

GenCore version 5.1.6  
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OM nucleic - nucleic search, using SW model

Run on: April 25, 2005, 13:09:42 ; Search time 228.947 Seconds  
(without alignments)  
517.127 Million cell updates/sec

Title: US-08-887-505B-28

Perfect score: 20

Sequence: 1 TTCCGACCACTACTC 20

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	2	AAT80332
2	20	100.0	20	2	AAT80337
3	20	100.0	20	2	AAT80336
4	20	100.0	20	2	AAT80338
5	20	100.0	20	2	AAT80329
6	20	100.0	20	2	AAT80330
7	20	100.0	20	2	AAT80333
8	20	100.0	20	2	AAT80339
9	20	100.0	20	2	AAT80340
10	20	100.0	20	2	AAT80238
11	20	100.0	20	2	AAT80334
12	20	100.0	20	2	AAT80335
13	20	100.0	20	2	AAT80331
14	20	100.0	20	6	AB865922
15	20	100.0	20	6	AB865918
16	20	100.0	20	6	AB865924
17	20	100.0	20	6	AB865920
18	20	100.0	20	6	AB865917
19	20	100.0	20	6	AB865923
20	20	100.0	20	6	AB865921

21	20	100.0	20	6	AB865913	AB865913 Inhibitor
22	20	100.0	20	6	AB865916	AB865916 Inhibitor
23	20	100.0	20	6	AB865919	AB865919 Inhibitor
24	20	100.0	20	6	AB865914	AB865914 Inhibitor
25	20	100.0	20	6	AB865915	AB865915 Inhibitor
26	20	100.0	20	6	AB865822	AB865822 Inhibitor
27	20	100.0	20	6	AB865822	AB865822 Inhibitor
28	20	100.0	20	6	AB865925	AB865925 Inhibitor
29	20	100.0	20	3	AA774631	AA774631 HCV probe
30	20	100.0	20	2	AAT80341	AAT80341 HCV
31	20	100.0	20	6	AB865925	AB865925 Inhibitor
32	20	100.0	20	3	AAA96562	AAA96562 Nucleotide
33	20	100.0	20	3	AAA91665	AAA91665 HCV(-)RNA
34	20	100.0	20	3	AA774630	AA774630 HCV probe
35	20	100.0	20	6	ABA99710	ABA99710 HCV sub-d
36	20	100.0	20	7	ABA99715	ABA99715 HCV sub-d
37	20	100.0	20	8	AA153726	AA153726 Hepatitis
38	20	100.0	20	7	AD49658	AD49658 Hepatitis
39	20	100.0	20	10	AD865926	AD865926 Stem-loop
40	20	100.0	20	2	AAT80278	AAT80278 HCV
41	20	100.0	20	2	AAT80284	AAT80284 HCV
42	20	100.0	20	6	AB865862	AB865862 Inhibitor
43	20	100.0	20	6	AB865868	AB865868 Inhibitor
44	20	100.0	20	6	ABK15311	ABK15311 Hepatitis
45	20	100.0	20	10	ADCS4069	ADCS4069 HCV 5'UTR
46	20	100.0	20	3	AAQ31157	AAQ31157 Probe 126
47	20	100.0	20	3	AAQ46463	AAQ46463 Hepatitis
48	20	100.0	20	3	AAV07837	AAV07837 HCV .33.8
49	20	100.0	20	3	AAV83065	AAV83065 Amplifier
50	20	100.0	20	4	AAA86970	AAA86970 Probe for
51	20	100.0	20	4	AAA93199	AAA93199 Hepatitis
52	20	100.0	20	10	ADCA45968	ADCA45968 Synthesis
53	20	100.0	20	4	ADP87787	ADP87787 TEX on ml
54	20	100.0	20	12	ADP87774	ADP87774 TEX contr
55	20	100.0	20	12	ADP87786	ADP87786 TEX synth
56	20	100.0	20	4	AAQ98098	AAQ98098 Capture e
57	20	100.0	20	10	ADCS4055	ADCS4055 Genotype
58	20	100.0	20	9	ACCB0000	ACCB0000 Hepatitis
59	20	100.0	20	10	ADCA45965	ADCA45965 Synthesis
60	20	100.0	20	8	ADCA45966	ADCA45966 Synthesis
61	20	100.0	20	10	AD080850	AD080850 Hepatitis
62	20	100.0	20	12	AAT09185	AAT09185 Hepatitis
63	20	100.0	20	6	AAV20727	AAV20727 Hepatitis
64	20	100.0	20	2	AAV22777	AAV22777 Amp-probe
65	20	100.0	20	6	ABK86847	ABK86847 Hepatitis
66	20	100.0	20	8	AD056324	AD056324 Hepatitis
67	20	100.0	20	12	ADQ74924	ADQ74924 HCV Amp p
68	20	100.0	20	10	ADCS4054	ADCS4054 Genotype
69	20	100.0	20	4	AA810487	AA810487 HCV 5'-UT
70	20	100.0	20	2	AAQ43061	AAQ43061 -255 to -
71	20	100.0	20	2	AAQ43068	AAQ43068 -255 to -
72	20	100.0	20	2	AAQ43060	AAQ43060 -255 to -
73	20	100.0	20	2	AAQ43067	AAQ43067 -255 to -
74	20	100.0	20	2	AAT11272	AAT11272 Hepatitis
75	20	100.0	20	2	AAQ43059	AAQ43059 -255 to -
76	20	100.0	20	2	AA810486	AA810486 HCV 5'-UT
77	20	100.0	20	2	AAQ43073	AAQ43073 -255 to -
78	20	100.0	20	2	AAQ43074	AAQ43074 -255 to -
79	20	100.0	20	2	AAQ43072	AAQ43072 -255 to -
80	20	100.0	20	2	AAQ43058	AAQ43058 -255 to -
81	20	100.0	20	2	AAQ43070	AAQ43070 -255 to -
82	20	100.0	20	2	AAQ43075	AAQ43075 -255 to -
83	20	100.0	20	19	AD534710	AD534710 gRNA-7 P
84	20	100.0	20	6	AB141919	AB141919 DNA comp
85	20	100.0	20	8	ADA93664	ADA93664 Competito
86	20	100.0	20	12	AD005658	AD005658 HCV temp
87	20	100.0	20	12	AD005662	AD005662 PCR ampli
88	20	100.0	20	12	AD005661	AD005661 PCR ampli
89	20	100.0	20	2	AAV70460	AAV70460 Partial s
90	20	100.0	20	6	AB146070	AB146070 Hepatitis
91	20	100.0	20	12	ADK82260	ADK82260 Hepatitis
92	20	100.0	20	2	AAV70459	AAV70459 Partial s
93	20	100.0	20	2	AAV70455	AAV70455 Partial s

C 94	20	100.0	239	6	ABL46065	Abi46065 Hepatitis	C 167	20	100.0	299	10	AAD55565	Aad55565 IS57272 H
C 95	20	100.0	239	6	ABL46069	Abi46069 Hepatitis	C 168	20	100.0	301	10	ACD27586	Ac227586 Hepatitis
C 96	20	100.0	239	12	ADK82255	Adk82255 Hepatitis	C 169	20	100.0	305	10	AAT87088	Aat87088 HCV ampli
C 97	20	100.0	239	12	ADK82259	Adk82259 Hepatitis	C 170	20	100.0	305	6	ABN79969	Abn79969 Hepatitis
C 98	20	100.0	240	2	AAV70458	Aav70458 Partial s	C 171	20	100.0	305	6	ABN79970	Abn79970 Hepatitis
C 99	20	100.0	240	2	AAV70456	Aav70456 Partial s	C 172	20	100.0	305	6	ABN79974	Abn79974 Hepatitis
C 100	20	100.0	240	2	AAV70461	Aav70461 Partial s	C 173	20	100.0	306	2	AAO67079	Aao67079 Hepatitis
C 101	20	100.0	240	6	ABL46066	Abi46066 Hepatitis	C 174	20	100.0	306	6	ABSS3053	Abss3053 Hepatitis
C 102	20	100.0	240	6	ABL46068	Abi46068 Hepatitis	C 175	20	100.0	308	3	AAV75294	Aav75294 Novel hep
C 103	20	100.0	240	6	ABL46071	Abi46071 Hepatitis	C 176	20	100.0	308	12	ADN35973	Adn35973 HCV CDNA
C 104	20	100.0	240	12	ADK82261	Adk82261 Hepatitis	C 177	20	100.0	310	6	ABK70877	Abk70877 HCV genom
C 105	20	100.0	240	12	ADK82258	Adk82258 Hepatitis	C 178	20	100.0	312	3	AAZ36198	Aaz36198 Adapted H
C 106	20	100.0	240	12	ADK82256	Adk82256 Hepatitis	C 179	20	100.0	314	3	AAZ36197	Aaz36197 Adapted H
C 107	20	100.0	241	6	AAD43290	Aad43290 HCV tarpe	C 180	20	100.0	323	6	ABK70883	Abk70883 HCV genom
C 108	20	100.0	241	6	ABL46059	Abi46059 Hepatitis	C 181	20	100.0	323	6	ABK70882	Abk70882 HCV genom
C 109	20	100.0	244	6	AAV70454	Aav70454 Partial s	C 182	20	100.0	326	6	ABK70880	Abk70880 HCV genom
C 110	20	100.0	244	2	AAV70449	Aav70449 HCV subty	C 183	20	100.0	326	12	ADP20410	Adp20410 Hepatitis
C 111	20	100.0	244	2	AAV70450	Aav70450 HCV subty	C 184	20	100.0	327	3	AAZ36159	Aaz36159 Adapted H
C 112	20	100.0	244	2	AAV70452	Aav70452 HCV subty	C 185	20	100.0	327	6	ABK70884	Abk70884 HCV genom
C 113	20	100.0	244	6	ABL46062	Abi46062 Hepatitis	C 186	20	100.0	328	6	AAI77074	Aai77074 Hepatitis
C 114	20	100.0	244	6	ABL46059	Abi46059 Hepatitis	C 187	20	100.0	328	6	ABL46275	Abi46275 Hepatitis
C 115	20	100.0	244	6	ABL46060	Abi46060 Hepatitis	C 188	20	100.0	328	6	ABL46278	Abi46278 Hepatitis
C 116	20	100.0	244	6	ABL46064	Abi46064 Hepatitis	C 189	20	100.0	328	6	ABL46273	Abi46273 Hepatitis
C 117	20	100.0	244	12	ADK82254	Adk82254 Hepatitis	C 190	20	100.0	328	6	AAI53724	Aai53724 Hepatitis
C 118	20	100.0	244	12	ADK82351	Adk82351 Hepatitis	C 191	20	100.0	328	8	AAI53724	Aai53724 Hepatitis
C 119	20	100.0	244	12	ADK82350	Adk82350 Hepatitis	C 192	20	100.0	328	6	ABK70871	Abk70871 HCV genom
C 120	20	100.0	244	12	ADK82347	Adk82347 Hepatitis	C 193	20	100.0	329	6	ABK70867	Abk70867 HCV genom
C 121	20	100.0	244	12	ADK82252	Adk82252 Hepatitis	C 194	20	100.0	333	6	ABK70881	Abk70881 HCV genom
C 122	20	100.0	244	12	ADK82350	Adk82350 Hepatitis	C 195	20	100.0	333	6	ABK70879	Abk70879 HCV genom
C 123	20	100.0	244	12	ADK82249	Adk82249 Hepatitis	C 196	20	100.0	333	6	ABK70876	Abk70876 HCV genom
C 124	20	100.0	244	12	ADK82348	Adk82348 Hepatitis	C 197	20	100.0	334	6	AAQ98272	Aaq98272 Hepatitis
C 125	20	100.0	244	12	ADK82348	Adk82348 Hepatitis	C 198	20	100.0	334	6	ABK70869	Abk70869 HCV genom
C 126	20	100.0	252	2	AAQ31071	Aaq31071 HCV-1 gen	C 199	20	100.0	335	6	ABK70868	Abk70868 HCV genom
C 127	20	100.0	252	2	AAQ31069	Aaq31069 HCV-1 gen	C 200	20	100.0	335	6	ABK70885	Abk70885 HCV genom
C 128	20	100.0	252	2	AAQ31070	Aaq31070 HCV-1 gen	C 201	20	100.0	335	6	ABK70885	Abk70885 HCV genom
C 129	20	100.0	252	2	AAQ31068	Aaq31068 HCV-1 gen	C 202	20	100.0	336	6	ABK70874	Abk70874 HCV genom
C 130	20	100.0	252	2	AAQ31081	Aaq31081 HCV-1 gen	C 203	20	100.0	337	2	AAT76663	Aat76663 HCV.I tr
C 131	20	100.0	252	2	AAQ31080	Aaq31080 HCV-1 gen	C 204	20	100.0	337	6	AAV53895	Aav53895 HCV.I RN
C 132	20	100.0	252	2	AAQ31067	Aaq31067 HCV-1 gen	C 205	20	100.0	337	6	ABK70870	Abk70870 HCV genom
C 133	20	100.0	252	2	AAQ31066	Aaq31066 HCV-1 gen	C 206	20	100.0	337	6	ADSE2863	Adse2863 FEEN-1 rel
C 134	20	100.0	252	2	AAQ31072	Aaq31072 HCV-1 gen	C 207	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 135	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 208	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 136	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 209	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 137	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 210	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 138	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 211	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 139	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 212	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 140	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 213	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 141	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 214	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 142	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 215	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 143	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 216	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 144	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 217	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 145	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 218	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 146	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 219	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 147	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 220	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 148	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 221	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 149	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 222	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 150	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 223	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 151	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 224	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 152	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 225	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 153	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 226	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 154	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 227	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 155	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 228	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 156	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 229	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 157	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 230	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 158	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 231	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 159	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 232	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 160	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 233	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 161	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 234	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 162	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 235	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 163	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 236	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 164	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 237	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 165	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 238	20	100.0	341	2	AAO62945	Aao62945 HCV genom
C 166	20	100.0	256	2	AAQ32981	Aaq32981 HCV E1 5'	C 239	20	100.0	341	2	AAO62945	Aao62945 HCV genom



C 240	20	100.0	384	6	ABK15314	Hepatitis	C 313	20	100.0	1880	2	AAQ24466	AAQ24466	NANB	hepa
C 241	20	100.0	386	2	AAQ29117	Hepatitis	C 314	20	100.0	1880	2	AAQ24467	AAQ24467	NANB	hepa
C 242	20	100.0	386	9	ADB16253	Cleavage	C 315	20	100.0	2033	2	AAQ64913	AAQ64913	Hepatitis	
C 243	20	100.0	393	6	ABA96260	Hepatitis	C 316	20	100.0	2033	2	AAQ6788	AAQ6788	Hepatitis	
C 244	20	100.0	412	6	ABA96259	Hepatitis	C 317	20	100.0	2116	2	AAQ12242	AAQ12242	Encodes P	
C 245	20	100.0	420	12	AD080848	Hepatitis	C 318	20	100.0	2327	6	ABQ78074	ABQ78074	Partial P	
C 246	20	100.0	422	8	ACC79264	Hepatitis	C 319	20	100.0	2540	2	AAQ29628	AAQ29628	Hepatitis	
C 247	20	100.0	483	2	AAQ32446	HCV core-	C 320	20	100.0	2540	2	AAQ29627	AAQ29627	Hepatitis	
C 248	20	100.0	483	2	AAQ32445	HCV core-	C 321	20	100.0	2540	2	AAQ3889	AAQ3889	NANB	hepa
C 249	20	100.0	483	2	AAQ32453	HCV core-	C 322	20	100.0	2540	2	AAQ43888	AAQ43888	NANB	hepa
C 250	20	100.0	483	2	AAQ32447	HCV core-	C 323	20	100.0	2540	2	AAQ63753	AAQ63753	NANBH ge	
C 251	20	100.0	483	2	AAQ32444	HCV core-	C 324	20	100.0	2540	2	AAQ63752	AAQ63752	NANBH ge	
C 252	20	100.0	500	13	ADS34658	Hepatitis	C 325	20	100.0	2674	6	ABQ78073	ABQ78073	Partial P	
C 253	20	100.0	500	13	ADS34660	Hepatitis	C 326	20	100.0	2771	6	ABQ78072	ABQ78072	Partial P	
C 254	20	100.0	500	13	ADS34661	Hepatitis	C 327	20	100.0	2829	2	AAV60673	AAV60673	Fragment	
C 255	20	100.0	500	13	ADS34659	Hepatitis	C 328	20	100.0	3360	2	AAV60677	AAV60677	Fragment	
C 256	20	100.0	504	2	AAQ12239	Clone 164	C 329	20	100.0	3401	2	AAQ64069	AAQ64069	Non-A, no	
C 257	20	100.0	552	2	AAQ79755	Hepatitis	C 330	20	100.0	3401	2	AAQ30387	AAQ30387	5'UTR/COR	
C 258	20	100.0	552	2	AAQ79749	Hepatitis	C 331	20	100.0	3461	2	AAQ64068	AAQ64068	Non-A, no	
C 259	20	100.0	552	2	AAQ79756	Hepatitis	C 332	20	100.0	3461	2	AAQ30386	AAQ30386	5'UTR/COR	
C 260	20	100.0	552	2	AAQ79757	Hepatitis	C 333	20	100.0	4987	2	AAQ65322	AAQ65322	Vaccinia	
C 261	20	100.0	552	2	AAQ207646	HCV C/E d	C 334	20	100.0	4987	2	AAQ67879	AAQ67879	Vaccinia	
C 262	20	100.0	552	2	AAQ207651	HCV C/E d	C 335	20	100.0	5860	6	ABQ78071	ABQ78071	PMU050 co	
C 263	20	100.0	552	2	AAQ207651	HCV C/E d	C 336	20	100.0	7141	6	AAQ25333	AAQ25333	Hepatitis	
C 264	20	100.0	552	2	AAQ26727	Consensus	C 337	20	100.0	7789	6	AAQ25330	AAQ25330	Hepatitis	
C 265	20	100.0	552	2	AAQ26732	Consensus	C 338	20	100.0	7848	6	AAQ25323	AAQ25323	Hepatitis	
C 266	20	100.0	552	2	AAQ66058	Hepatitis	C 339	20	100.0	7911	2	AAQ32436	AAQ32436	Hepatitis	
C 267	20	100.0	552	2	AAQ66048	Hepatitis	C 340	20	100.0	7979	10	ADD93729	ADD93729	Hepatitis	
C 268	20	100.0	556	2	AAQ79776	Hepatitis	C 341	20	100.0	7979	10	ADD93730	ADD93730	Hepatitis	
C 269	20	100.0	556	2	AAQ79776	Hepatitis	C 342	20	100.0	7979	10	ADD93732	ADD93732	Hepatitis	
C 270	20	100.0	556	2	AAQ00458	Hepatitis	C 343	20	100.0	7979	10	ADD93731	ADD93731	Hepatitis	
C 271	20	100.0	556	2	AAQ26743	Sequence	C 344	20	100.0	7980	10	ADD93724	ADD93724	Hepatitis	
C 272	20	100.0	560	2	AAQ207652	Hepatitis	C 345	20	100.0	7980	10	ADD93725	ADD93725	Hepatitis	
C 273	20	100.0	572	13	ADS34704	HCV J1 co	C 346	20	100.0	7983	10	ADD93727	ADD93727	Hepatitis	
C 274	20	100.0	587	3	AAQ57395	Hepatitis-1 P	C 347	20	100.0	7987	6	AAQ25329	AAQ25329	Hepatitis	
C 275	20	100.0	652	2	AAQ27966	Hepatitis	C 348	20	100.0	7987	6	AAQ25321	AAQ25321	Hepatitis	
C 276	20	100.0	665	3	AAQ75292	Novel hepd	C 349	20	100.0	7987	6	AAQ25324	AAQ25324	Hepatitis	
C 277	20	100.0	665	12	ADN35896	HCV CDNA	C 350	20	100.0	7987	13	ADR38452	ADR38452	Hepatitis	
C 278	20	100.0	685	2	AAQ11719	Hepatitis	C 351	20	100.0	7989	3	AAQ98968	AAQ98968	Hepatitis	
C 279	20	100.0	685	10	AAQ49755	HCV 5'UTR	C 352	20	100.0	7989	6	AAQ25322	AAQ25322	Hepatitis	
C 280	20	100.0	685	12	ADN03472	Hepatitis	C 353	20	100.0	7989	6	AAQ25326	AAQ25326	Hepatitis	
C 281	20	100.0	703	3	AAQ4921	Hepatitis	C 354	20	100.0	7989	6	AAQ25325	AAQ25325	Hepatitis	
C 282	20	100.0	713	3	AAQ57396	Hepatitis	C 355	20	100.0	7989	10	ADD93728	ADD93728	Hepatitis	
C 283	20	100.0	720	3	AAQ80907	Hepatitis	C 356	20	100.0	7989	10	ADD93726	ADD93726	Hepatitis	
C 284	20	100.0	720	3	ABQ52861	Hepatitis	C 357	20	100.0	7989	10	ADD93722	ADD93722	Hepatitis	
C 285	20	100.0	780	3	AAQ5789	Hepatitis	C 358	20	100.0	7989	10	ADD93733	ADD93733	Hepatitis	
C 286	20	100.0	803	2	AAQ70436	Recombina	C 359	20	100.0	7989	12	ADQ57845	ADQ57845	HCV repli	
C 287	20	100.0	803	2	AAQ70437	Recombina	C 360	20	100.0	7989	13	ADR38453	ADR38453	DNA encod	
C 288	20	100.0	803	2	AAQ70440	Recombina	C 361	20	100.0	7991	6	AAQ47279	AAQ47279	Hepatitis	
C 289	20	100.0	803	2	AAQ70438	Recombina	C 362	20	100.0	7992	6	AAQ47276	AAQ47276	Hepatitis	
C 290	20	100.0	803	2	AAQ70439	Recombina	C 363	20	100.0	7992	6	AAQ47280	AAQ47280	Hepatitis	
C 291	20	100.0	803	2	AAQ70439	Recombina	C 364	20	100.0	7992	6	AAQ47277	AAQ47277	Hepatitis	
C 292	20	100.0	807	2	AAQ20940	PCR-gener	C 365	20	100.0	7992	6	AAQ47281	AAQ47281	Hepatitis	
C 293	20	100.0	817	13	ADS34705	siRNA-2 P	C 366	20	100.0	7992	10	ADD93723	ADD93723	Hepatitis	
C 294	20	100.0	923	2	AAQ28348	Hepatitis	C 367	20	100.0	7995	6	AAQ47278	AAQ47278	Hepatitis	
C 295	20	100.0	1157	10	ADC64640	Hepatitis	C 368	20	100.0	8001	3	AAQ98967	AAQ98967	Hepatitis	
C 296	20	100.0	1270	2	AAV60668	Fragment	C 369	20	100.0	8085	10	AAQ48122	AAQ48122	HCV r	
C 297	20	100.0	1554	2	AAQ32451	HCV core-	C 370	20	100.0	8451	10	AAQ54425	AAQ54425	Hepatitis	
C 298	20	100.0	1562	2	AAV60672	Fragment	C 371	20	100.0	8637	3	AAQ98966	AAQ98966	Hepatitis	
C 299	20	100.0	1734	2	AAQ40436	Hepatitis	C 372	20	100.0	8637	6	AAQ88595	AAQ88595	Hepatitis	
C 300	20	100.0	1734	2	AAQ40432	Hepatitis	C 373	20	100.0	8638	6	AAQ88596	AAQ88596	Hepatitis	
C 301	20	100.0	1734	2	AAQ40433	Hepatitis	C 374	20	100.0	8638	6	AAQ88577	AAQ88577	Hepatitis	
C 302	20	100.0	1734	2	AAQ40434	Hepatitis	C 375	20	100.0	8638	6	AAQ88578	AAQ88578	Hepatitis	
C 303	20	100.0	1734	2	AAQ40431	Hepatitis	C 376	20	100.0	8639	6	AAQ88574	AAQ88574	Hepatitis	
C 304	20	100.0	1734	2	AAQ40428	Hepatitis	C 377	20	100.0	8642	6	AAQ88573	AAQ88573	Hepatitis	
C 305	20	100.0	1734	2	AAQ40435	Hepatitis	C 378	20	100.0	8643	6	AAQ88575	AAQ88575	Hepatitis	
C 306	20	100.0	1734	2	AAQ40430	Hepatitis	C 379	20	100.0	8648	6	AAQ88576	AAQ88576	Hepatitis	
C 307	20	100.0	1734	2	AAQ40429	Hepatitis	C 380	20	100.0	8649	6	AAQ98969	AAQ98969	Hepatitis	
C 308	20	100.0	1734	2	AAQ40425	Hepatitis	C 381	20	100.0	8732	10	AAQ48121	AAQ48121	HCV r	
C 309	20	100.0	1765	2	AAQ79141	Hepatitis	C 382	20	100.0	9133	2	AAQ05956	AAQ05956	Sense str	
C 310	20	100.0	1863	2	AAQ79143	Hepatitis	C 383	20	100.0	9185	2	AAQ10566	AAQ10566	Hepatitis	
C 311	20	100.0	1863	2	AAQ15363	Fragment	C 384	20	100.0	9185	2	AAQ10566	AAQ10566	Hepatitis	
C 312	20	100.0	1863	2	AAQ15362	Fragment	C 385	20	100.0	9185	2	AAQ10566	AAQ10566	Hepatitis	

C 386	20	100.0	9185	2	AAX00459	Aax00459	Hepatitis	C 459	20	100.0	9611	5	AAC86648	Aac86648	Nucleotid
C 387	20	100.0	9185	2	AAX26737	Aax26737	Nucleotid	C 460	20	100.0	9611	13	AD534713	Ad534713	Hepatitis
C 388	20	100.0	9185	2	ADF66068	Adf66068	Nucleotid	C 461	20	100.0	9618	11	ADN31102	Adn31102	Hepatitis
C 389	20	100.0	9185	3	AAW5297	Aaw5297	Sene Str	C 462	20	100.0	9622	10	AAW54424	Aaw54424	Hepatitis
C 390	20	100.0	9185	12	AAZ55979	Aaz55979	HCV cDNA	C 463	20	100.0	9646	2	AAV59361	Aav59361	Hepatitis
C 391	20	100.0	9365	6	AAD25518	Aad25518	Hepatitis	C 464	20	100.0	9646	8	ACA62466	Ac62466	Hepatitis
C 392	20	100.0	9365	6	AAQ36209	Aaq36209	Composite	C 465	20	100.0	9646	8	ACA62466	Ac62466	Hepatitis
C 393	20	100.0	9365	6	AAQ38959	Aaq38959	Hepatitis	C 466	20	100.0	9646	8	ACA62466	Ac62466	Hepatitis
C 394	20	100.0	9365	6	AAQ38959	Aaq38959	Hepatitis	C 467	20	100.0	9646	8	ACA62466	Ac62466	Hepatitis
C 395	20	100.0	9365	6	AAQ64175	Aaq64175	NANBHV E1	C 468	20	100.0	9690	6	ABK91443	Abk91443	Hepatitis
C 396	20	100.0	9400	13	AAQ21744	Aaq21744	Compiled	C 469	20	100.0	9690	6	ABK91435	Abk91435	Hepatitis
C 397	20	100.0	9400	13	AAQ21744	Aaq21744	Compiled	C 470	20	100.0	9690	6	ABK91243	Abk91243	Hepatitis
C 398	20	100.0	9401	2	AAI22710	Aai22710	Hepatitis	C 471	20	100.0	9690	6	ABK91440	Abk91440	Hepatitis
C 399	20	100.0	9401	2	AAI22710	Aai22710	Hepatitis	C 472	20	100.0	9690	6	ABK91434	Abk91434	Hepatitis
C 400	20	100.0	9401	2	AAI22710	Aai22710	Hepatitis	C 473	20	100.0	9690	6	ABK91417	Abk91417	Hepatitis
C 401	20	100.0	9401	2	AAI22710	Aai22710	Hepatitis	C 474	20	100.0	9690	6	ACA61697	Ac61697	Hepatitis
C 402	20	100.0	9401	2	AAI22710	Aai22710	Hepatitis	C 475	20	100.0	9690	10	ADCB3762	Adcb3762	Hepatitis
C 403	20	100.0	9401	13	ADR29358	Adr29358	Hepatitis	C 476	20	100.0	9691	6	ABK91423	Abk91423	Hepatitis
C 404	20	100.0	9402	2	AAQ41345	Aaq41345	Human hep	C 477	20	100.0	9691	6	ABK91439	Abk91439	Hepatitis
C 405	20	100.0	9405	2	AAQ04046	Aaq04046	DNA encod	C 478	20	100.0	9693	6	ABK91443	Abk91443	Hepatitis
C 406	20	100.0	9413	2	AAQ08049	Aaq08049	DNA encod	C 479	20	100.0	9693	6	ABK91438	Abk91438	Hepatitis
C 407	20	100.0	9413	2	AAQ08155	Aaq08155	Hepatitis	C 480	20	100.0	9693	10	ADCB7945	Adcb7945	Hepatitis
C 408	20	100.0	9413	2	AAQ08155	Aaq08155	Hepatitis	C 481	20	100.0	9693	10	ABX10617	Abx10617	Modified
C 409	20	100.0	9413	2	AAQ08155	Aaq08155	Hepatitis	C 482	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 410	20	100.0	9413	6	AAQ08155	Aaq08155	Hepatitis	C 483	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 411	20	100.0	9413	8	AAQ08155	Aaq08155	Hepatitis	C 484	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 412	20	100.0	9413	8	AAQ08155	Aaq08155	Hepatitis	C 485	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 413	20	100.0	9413	10	AAQ08155	Aaq08155	Hepatitis	C 486	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 414	20	100.0	9413	13	AAQ08155	Aaq08155	Hepatitis	C 487	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 415	20	100.0	9416	2	AAQ02068	Aaq02068	Hepatitis	C 488	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 416	20	100.0	9416	2	AAQ02068	Aaq02068	Hepatitis	C 489	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 417	20	100.0	9416	2	AAQ02068	Aaq02068	Hepatitis	C 490	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 418	20	100.0	9416	2	AAQ02068	Aaq02068	Hepatitis	C 491	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 419	20	100.0	9416	2	AAQ02068	Aaq02068	Hepatitis	C 492	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 420	20	100.0	9416	6	AAQ02068	Aaq02068	Hepatitis	C 493	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 421	20	100.0	9416	6	AAQ02068	Aaq02068	Hepatitis	C 494	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 422	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 495	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 423	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 496	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 424	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 497	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 425	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 498	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 426	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 499	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 427	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 500	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 428	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 501	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 429	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 502	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 430	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 503	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 431	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 504	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 432	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 505	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 433	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 506	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 434	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 507	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 435	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 508	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 436	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 509	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 437	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 510	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 438	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 511	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 439	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 512	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 440	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 513	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 441	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 514	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 442	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 515	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 443	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 516	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 444	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 517	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 445	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 518	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 446	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 519	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 447	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 520	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 448	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 521	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 449	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 522	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 450	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 523	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 451	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 524	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 452	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 525	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 453	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 526	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 454	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 527	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 455	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 528	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 456	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 529	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 457	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 530	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc
C 458	20	100.0	9416	10	AAQ02068	Aaq02068	Hepatitis	C 531	20	100.0	9693	6	AAAD5331	Aaad5331	MKO-Z nuc

C 532	19	95.0	40	12	ADP87793	Adp87793 HCV cDNA	605	16	80.0	16	6	AB865870	Ab865870 Inhibitor
C 533	19	95.0	177	2	AAQ79456	AaQ79456 HCV iso1a	C 606	16	80.0	17	8	ACDS6911	AcD6911 HCV DNAzy
C 534	19	95.0	177	2	AAQ68087	AaQ68087 HCV iso1a	C 607	16	80.0	17	8	ACDS6912	AcD6912 HCV DNAzy
C 535	19	95.0	177	2	AAQ79452	AaQ79452 HCV iso1a	C 608	16	80.0	17	12	AD182811	Ad182811 HCV DNAzy
C 536	19	95.0	177	2	AAQ79459	AaQ79459 HCV iso1a	C 609	16	80.0	17	12	AD182812	Ad182812 HCV DNAzy
C 537	19	95.0	177	2	AAQ68068	AaQ68068 HCV iso1a	C 610	16	80.0	19	10	ADFS1556	AdF51556 Hepatitis
C 538	19	95.0	177	2	AAQ79454	AaQ79454 HCV iso1a	C 611	16	80.0	19	10	ADFS1574	AdF51574 Hepatitis
C 539	19	95.0	177	2	AAQ68065	AaQ68065 HCV iso1a	C 612	16	80.0	19	10	ADFS2252	AdF52252 Hepatitis
C 540	19	95.0	177	2	AAQ68070	AaQ68070 HCV iso1a	C 613	16	80.0	19	10	ADFS2270	AdF52270 Hepatitis
C 541	19	95.0	177	2	AAQ79457	AaQ79457 HCV iso1a	C 614	16	80.0	20	2	AAQ44886	AaQ44886 Antisense
C 542	19	95.0	177	2	AAQ68063	AaQ68063 HCV iso1a	C 615	16	80.0	20	2	AAQ49205	AaQ49205 Phosphoro
C 543	19	95.0	177	2	AAQ79460	AaQ79460 HCV iso1a	C 616	16	80.0	20	2	AAQ51069	AaQ51069 Oligo #26
C 544	19	95.0	177	2	AAQ79449	AaQ79449 HCV iso1a	C 617	16	80.0	20	2	AAQ80240	AaQ80240 Oligo HCV
C 545	19	95.0	177	2	AAQ79455	AaQ79455 HCV iso1a	C 618	16	80.0	20	3	AAAS2567	AaA2567 Oligonuc1
C 546	19	95.0	177	2	AAQ68066	AaQ68066 HCV iso1a	C 619	16	80.0	20	3	AAAB9758	AaA9758 HCV RNA a
C 547	19	95.0	177	2	AAQ79448	AaQ79448 HCV iso1a	C 620	16	80.0	20	6	AB190976	Ab190976 Hepatitis
C 548	19	95.0	177	2	AAQ79453	AaQ79453 HCV iso1a	C 621	16	80.0	20	6	AB658220	Ab658220 Inhibitor
C 549	19	95.0	177	2	AAQ79458	AaQ79458 HCV iso1a	C 622	16	80.0	20	6	AB658824	Ab658824 Inhibitor
C 550	19	95.0	178	2	AAQ68065	AaQ68065 HCV iso1a	C 623	16	80.0	20	10	ADBS68557	AdB68557 DNA oligo
C 551	19	95.0	178	2	AAQ68064	AaQ68064 HCV iso1a	C 624	16	80.0	20	10	ADBS68556	AdB68556 HCV R PCR
C 552	19	95.0	552	2	AAQ11075	AaQ11075 Fragment	C 625	16	80.0	20	10	ADCS9536	AdC9536 HCV R PCR
C 553	18	90.0	18	2	AAQ64960	AaQ64960 Antisense	C 626	16	80.0	20	10	ADCS9534	AdC9534 HCV R PCR
C 554	18	90.0	18	2	AAQ79435	AaQ79435 Oligo HCV	C 627	16	80.0	20	10	ADCS9532	AdC9532 HCV R PCR
C 555	18	90.0	18	2	AAQ80322	AaQ80322 Oligo HCV	C 628	16	80.0	20	10	ADP70300	AdP70300 Antisense
C 556	18	90.0	18	2	AAQ80322	AaQ80322 Oligo HCV	C 629	16	80.0	20	10	ADP70353	AdP70353 Antisense
C 557	18	90.0	18	6	AB655909	Ab655909 Inhibitor	C 630	16	80.0	20	12	AD113469	Ad113469 PCR prime
C 558	18	90.0	18	6	AB655906	Ab655906 Inhibitor	C 631	16	80.0	20	12	ADQ16464	AdQ16464 Control1e
C 559	18	90.0	18	12	ADP94800	Adp94800 Hepatitis	C 632	16	80.0	20	12	ADQ88603	AdQ88603 HCV DNA-R
C 560	18	90.0	18	12	ADM95051	Adm95051 Hepatitis	C 633	16	80.0	25	2	AAQ88545	AaQ88545 HCV DNA-R
C 561	18	90.0	19	10	ADFS2256	AdF52256 Hepatitis	C 634	16	80.0	25	6	AB655927	Ab655927 Inhibitor
C 562	18	90.0	19	10	ADFS1560	AdF51560 Hepatitis	C 635	16	80.0	26	2	AAQ37585	AaQ37585 HCV cone
C 563	18	90.0	19	10	ADFS2257	AdF52257 Hepatitis	C 636	16	80.0	26	2	AAQ64899	AaQ64899 Hepatitis
C 564	18	90.0	19	10	ADFS1561	AdF51561 Hepatitis	C 637	16	80.0	28	3	AAQ28892	AaQ28892 Hepatitis
C 565	18	90.0	20	2	AAQ64961	AaQ64961 Antisense	C 638	16	80.0	45	5	AAH23742	AaH23742 Oligonuc1
C 566	18	90.0	20	2	AAQ80236	AaQ80236 Oligo HCV	C 639	16	80.0	48	4	AAQ92377	AaQ92377 HCV-RNA w
C 567	18	90.0	20	2	AAQ80237	AaQ80237 Oligo HCV	C 640	16	80.0	102	4	AAQ92377	AaQ92377 HCV-RNA w
C 568	18	90.0	20	2	AAQ80239	AaQ80239 Oligo HCV	C 641	16	80.0	338	2	AAQ66173	AaQ66173 Tagged ge
C 569	18	90.0	20	6	ABAO2485	AbAO2485 Hepatitis	C 642	15	75.0	15	2	AAQ64956	AaQ64956 Antisense
C 570	18	90.0	20	6	AB655823	Ab655823 Inhibitor	C 643	15	75.0	15	2	AAQ64959	AaQ64959 Antisense
C 571	18	90.0	20	6	AB655821	Ab655821 Inhibitor	C 644	15	75.0	15	2	AAQ62400	AaQ62400 Substrate
C 572	18	90.0	20	12	ADBS6855	AdB68555 DNA oligo	C 645	15	75.0	15	6	ABX00257	AbX00257 Hepatitis
C 573	18	90.0	20	12	ADBS6855	AdB68555 TEX exten	C 646	15	75.0	15	8	ACD65974	AcD65974 Anti-HCV
C 574	18	90.0	21	2	ADBS68379	AdB68379 Antisense	C 647	15	75.0	15	8	ADBS6972	AdB68972 Anti-HCV
C 575	18	90.0	25	12	ADBS68776	AdB68776 Hepatitis	C 648	15	75.0	15	12	AD187543	Ad187543 Anti-HCV
C 576	18	90.0	39	3	AAAS2555	AaA25555 Hepatitis	C 649	15	75.0	15	12	AD187541	Ad187541 Anti-HCV
C 577	18	90.0	39	6	AAAL45193	AaA15193 Target ge	C 650	15	75.0	17	8	ACD65757	AcD65757 HCV minus
C 578	18	90.0	60	10	ADCA6896	AdC6896 Synthesis	C 651	15	75.0	17	8	ACD65757	AcD65757 HCV minus
C 579	17	85.0	17	2	AAQ64957	AaQ64957 Antisense	C 652	15	75.0	17	12	AD187251	Ad187251 HCV DNAzy
C 580	17	85.0	17	2	AAQ80323	AaQ80323 Oligo HCV	C 653	15	75.0	17	12	AD187253	Ad187253 HCV DNAzy
C 581	17	85.0	17	2	AAQ80326	AaQ80326 Oligo HCV	C 654	15	75.0	19	10	ADFS2276	AdF52276 Hepatitis
C 582	17	85.0	17	6	AB655910	Ab655910 Inhibitor	C 655	15	75.0	19	10	ADFS2260	AdF52260 Hepatitis
C 583	17	85.0	17	6	AB655907	Ab655907 Inhibitor	C 656	15	75.0	19	10	ADFS1564	AdF51564 Hepatitis
C 584	17	85.0	17	8	ACD65758	AcD65758 HCV minus	C 657	15	75.0	19	10	ADFS1580	AdF51580 Hepatitis
C 585	17	85.0	17	12	AD187252	Ad187252 HCV DNAzy	C 658	15	75.0	19	13	ADBS1228	AdB1228 Hepatitis
C 586	17	85.0	17	12	ADBS68707	AdB68707 TEX exten	C 659	15	75.0	20	2	AAQ85811	AaQ85811 Anti-HCV
C 587	17	85.0	19	10	ADFS1563	AdF51563 Hepatitis	C 660	15	75.0	20	2	AAQ80327	AaQ80327 Oligo HCV
C 588	17	85.0	19	10	ADFS1566	AdF51566 Hepatitis	C 661	15	75.0	20	6	ABN80532	AbN80532 DNA-RNA h
C 589	17	85.0	19	10	ADFS2262	AdF52262 Hepatitis	C 662	15	75.0	25	9	AC154585	Ac154585 Human mAc
C 590	17	85.0	19	10	ADFS2259	AdF52259 Hepatitis	C 663	15	75.0	28	2	AAQ05220	AaQ05220 Hepatitis
C 591	17	85.0	20	2	AAQ49204	AaQ49204 Phosphoro	C 664	15	75.0	28	3	AAQ57755	AaQ57755 Hepatitis
C 592	17	85.0	20	2	AAQ51068	AaQ51068 Oligo #25	C 665	15	75.0	31	2	AAV41507	AaV41507 Nucleotid
C 593	17	85.0	20	6	AB190975	Ab190975 Hepatitis	C 666	15	75.0	31	2	AAV41506	AaV41506 Nucleotid
C 594	17	85.0	20	6	AB655911	Ab655911 Inhibitor	C 667	15	75.0	45	2	AAQ09177	AaQ09177 Hepatitis
C 595	17	85.0	21	2	AAV15314	AaV15314 Hepatitis	C 668	15	75.0	45	2	AAV20718	AaV20718 Hepatitis
C 596	17	85.0	21	5	AAQ28812	AaQ28812 Hepatitis	C 669	15	75.0	45	2	AAV22770	AaV22770 Capture/A
C 597	17	85.0	25	13	ADBS34696	AdB34696 Primer DS	C 670	15	75.0	45	6	ABR86839	AbR86839 Human imm
C 598	17	85.0	46	8	ACC79266	Acc79266 Hepatitis	C 671	15	75.0	45	8	AAQ56316	AaQ56316 Hepatitis
C 599	17	85.0	100	13	ADBS34711	AdB34711 siRNA-e p	C 672	15	75.0	45	12	ADQ74916	AdQ74916 HCV Captu
C 600	17	85.0	332	6	ABK70878	AbK70878 HCV genom	C 673	15	75.0	243	43	AAK70449	AaK70449 Human imm
C 601	17	85.0	398	2	AAQ01513	AaQ01513 Hepatitis	C 674	15	75.0	267	6	ABN79975	AbN79975 Hepatitis
C 602	17	85.0	398	2	AAQ01514	AaQ01514 Hepatitis	C 675	15	75.0	695	12	ADBS6809	AdB6809 Archaea 2
C 603	17	85.0	1734	2	AAQ040427	AaQ040427 Hepatitis	C 676	15	75.0	3696	4	AAQ61063	AaQ61063 P. putida
C 604	16	80.0	16	2	AAQ80286	AaQ80286 Oligo HCV	C 677	14	70.0	15	6	ABX01764	AbX01764 Hepatitis

C 678	14	70.0	17	8	ACD56910	AcD56910 HCV DNAzy	C 751	13	65.0	13	8	ACD65999	AdC65999 Anti-HCV	
C 679	14	70.0	17	8	ABZ24771	AbZ24771 Locked nu	C 752	13	65.0	13	8	ACD65973	AdC65973 Anti-HCV	
C 680	14	70.0	17	12	AD182810	Ad182810 HCV DNAzy	C 753	13	65.0	13	12	AD187542	Ad187542 Anti-HCV	
C 681	14	70.0	18	4	AAC90038	Aac90038 Oligonuc1	C 754	13	65.0	13	12	AD187568	Ad187568 Anti-HCV	
C 682	14	70.0	18	4	AAC92373	Aac92373 Oligonuc1	C 755	13	65.0	13	13	AA61843	Aa61843 HCV 5' no	
C 683	14	70.0	18	5	AAH23739	Aah23739 Oligonuc1	C 756	13	65.0	13	15	AA62401	Aa62401 Substrate	
C 684	14	70.0	19	2	AAO70441	Aao70441 Primer/pr	C 757	13	65.0	13	6	ABX03369	Abx03369 Hepatitis	
C 685	14	70.0	19	10	ADF51571	Adf51571 Hepatitis	C 758	13	65.0	13	15	6	ABX00229	Abx00229 Hepatitis
C 686	14	70.0	19	10	ADF51587	Adf51587 Hepatitis	C 759	13	65.0	13	8	ACD65998	AdC65998 Anti-HCV	
C 687	14	70.0	19	10	ADF52283	Adf52283 Hepatitis	C 760	13	65.0	13	12	AD187567	Ad187567 Anti-HCV	
C 688	14	70.0	19	10	ADF52267	Adf52267 Hepatitis	C 761	13	65.0	13	16	AAT90601	Aat90601 Hepatitis	
C 689	14	70.0	20	2	AAO44885	Aao44885 Antisense	C 762	13	65.0	13	3	AA13418	Aa13418 Hepatitis	
C 690	14	70.0	20	2	AAT01199	Aat01199 HCV gene	C 763	13	65.0	13	8	ABX74337	Abx74337 Hepatitis	
C 691	14	70.0	20	2	AAT45057	Aat45057 CM14 cDNA	C 764	13	65.0	13	17	8	ACD56913	AdC56913 HCV DNAzy
C 692	14	70.0	20	2	AAT80241	Aat80241 Oligo HCV	C 765	13	65.0	13	17	10	ADB88559	AdB88559 DNA Oligo
C 693	14	70.0	20	2	AAT80235	Aaa52568 Oligonuc1	C 766	13	65.0	13	17	12	AD182813	Ad182813 HCV DNAzy
C 694	14	70.0	20	3	AAA52568	Aaa52568 Oligonuc1	C 767	13	65.0	13	18	2	AAT94720	Aat94720 HCV
C 695	14	70.0	20	6	AB565825	Ab565825 Inhibitor	C 768	13	65.0	13	18	2	AAZ27490	Aaz27490 Probe for
C 696	14	70.0	20	6	AB565825	Ab565825 Inhibitor	C 769	13	65.0	13	18	2	AAZ27490	Aaz27490 Probe for
C 697	14	70.0	20	12	ADP87810	Adp87810 Extended	C 770	13	65.0	13	18	2	AAZ27490	Aaz27490 Probe for
C 698	14	70.0	20	12	ADP87810	Adp87810 Extended	C 771	13	65.0	13	18	2	AAZ27490	Aaz27490 Probe for
C 699	14	70.0	23	12	ADP87796	Adp87796 Extended	C 772	13	65.0	13	19	4	AAH03051	Aah03051 Microorga
C 700	14	70.0	23	12	ADP87796	Adp87796 Extended	C 773	13	65.0	13	19	9	AD27475	Ad27475 Microorga
C 701	14	70.0	25	13	AAO98285	Aao98285 Hepatitis	C 774	13	65.0	13	19	9	AD27475	Ad27475 Microorga
C 702	14	70.0	31	13	ADR82700	Adr82700 Peptide n	C 775	13	65.0	13	19	10	ADP52263	Adp52263 Hepatitis
C 703	14	70.0	31	13	ADR82701	Adr82701 Peptide n	C 776	13	65.0	13	19	10	ADP52271	Adp52271 Hepatitis
C 704	14	70.0	33	2	AAO53258	Aao53258 Hepatitis	C 777	13	65.0	13	19	10	ADP51575	Adp51575 Hepatitis
C 705	14	70.0	39	2	AAV37633	Aav37633 HCV detec	C 778	13	65.0	13	19	10	ADP51567	Adp51567 Hepatitis
C 706	14	70.0	42	2	AAV41501	Aav41501 Nucleotid	C 779	13	65.0	13	19	10	ADP51567	Adp51567 Hepatitis
C 707	14	70.0	43	2	AAV41501	Aav41501 Nucleotid	C 780	13	65.0	13	19	10	ADP51567	Adp51567 Hepatitis
C 708	14	70.0	46	2	AAV41499	Aav41499 Nucleotid	C 781	13	65.0	13	21	4	AAH03051	Aah03051 Microorga
C 709	14	70.0	47	2	AAV41517	Aav41517 Nucleotid	C 782	13	65.0	13	21	6	AAI40739	Aai40739 Human IRS
C 710	14	70.0	53	2	AAO98138	Aao98138 Hepatitis	C 783	13	65.0	13	22	2	AAV72983	Aav72983 Hepatitis
C 711	14	70.0	57	2	AAO63223	Aao63223 Hepatitis	C 784	13	65.0	13	24	12	ADP87804	Adp87804 TEX on mi
C 712	14	70.0	64	2	AAO98120	Aao98120 Hepatitis	C 785	13	65.0	13	24	12	ADP87798	Adp87798 TEX on mi
C 713	14	70.0	180	2	AAQ31083	Aaq31083 HCV-1 ext	C 786	13	65.0	13	25	2	AAQ37583	Aaq37583 HCV conse
C 714	14	70.0	182	10	ADCO2538	Adco2538 HCV-1 gen	C 787	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 715	14	70.0	529	10	ABAI3309	Abai3309 Human ner	C 788	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 716	14	70.0	656	10	ACD97117	AcD97117 Human col	C 789	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 717	14	70.0	924	8	ACA46928	Ac46928 Prokaryot	C 790	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 718	14	70.0	924	8	ACA46928	Ac46928 Prokaryot	C 791	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 719	14	70.0	927	4	AAH53169	Aah53169 S. epider	C 792	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 720	14	70.0	930	6	ABN90739	Abn90739 Staphyloc	C 793	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 721	14	70.0	930	13	ADSO2805	Adso2805 Staphyloc	C 794	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 722	14	70.0	1386	4	AAH87946	Aah87946 Bottom fe	C 795	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 723	14	70.0	1387	4	AAH87946	Aah87946 Bottom fe	C 796	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 724	14	70.0	1387	4	AAH87946	Aah87946 Bottom fe	C 797	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 725	14	70.0	1482	11	ABD12849	Abd12849 Saccharom	C 798	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 726	14	70.0	1634	6	ABO49122	Abq49122 Oligonuc1	C 799	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 727	14	70.0	1634	6	ABO49122	Abq49122 Oligonuc1	C 800	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 728	14	70.0	2000	6	ABZ16777	Abz16777 Arabidops	C 801	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 729	14	70.0	2352	2	AAT63604	Aat63604 Dehiscenc	C 802	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 730	14	70.0	4069	4	AAH54612	Aah54612 S. epider	C 803	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 731	14	70.0	5020	8	ABZ10105	Abz10105 Haematopo	C 804	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 732	14	70.0	5506	6	ABN80229	Abn80229 Human che	C 805	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 733	14	70.0	5506	6	ABN80229	Abn80229 Human che	C 806	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 734	14	70.0	6175	6	ABL33306	Ab133306 Human imm	C 807	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 735	14	70.0	6224	6	ABL33306	Ab133306 Human imm	C 808	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 736	14	70.0	6224	6	ABL33306	Ab133306 Human imm	C 809	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 737	14	70.0	6380	4	ABL13596	Ab13596 Chemocall	C 810	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 738	14	70.0	8020	10	ADBE4209	Adbe4209 Pirocephal	C 811	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 739	14	70.0	8020	13	ADBE4209	Adbe4209 Pirocephal	C 812	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 740	14	70.0	9707	6	ABL33421	Ab133421 Human lym	C 813	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 741	14	70.0	10717	6	ABL33694	Ab133694 Human imm	C 814	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 742	14	70.0	10717	6	ABL33694	Ab133694 Human imm	C 815	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 743	14	70.0	15600	10	ACF03818	Acf03818 Human par	C 816	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 744	14	70.0	17959	6	ABL53575	Ab153575 Chemocall	C 817	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 745	14	70.0	17959	6	ABL53575	Ab153575 Chemocall	C 818	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 746	14	70.0	23683	6	ABL34622	Ab134622 Human met	C 819	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 747	14	70.0	23683	6	ABL34622	Ab134622 Human met	C 820	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 748	14	70.0	23683	6	ABL34622	Ab134622 Human met	C 821	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 749	14	70.0	23683	6	ABL34622	Ab134622 Human met	C 822	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse
C 750	14	70.0	23683	6	ABL34622	Ab134622 Human met	C 823	13	65.0	13	25	2	AAQ37580	Aaq37580 HCV conse

AdC65999	Anti-HCV	AdC65973	Anti-HCV	Ad187542	Anti-HCV	Ad187568	Anti-HCV	Aa61843	HCV 5' no	Aa62401	Substrate	Abx03369	Hepatitis	Abx00229	Hepatitis	AdC65998	Anti-HCV	Ad187567	Anti-HCV	Aat90601	Hepatitis	Aa13418	Hepatitis	AdC56913	HCV DNAzy	AdB88559	DNA Oligo	Ad182813	HCV DNAzy	Adp87837	TEX on mi	Adp87852	RT primer	Aat994720	Hepatitis	Aaz27490	Probe for	Aaz299215	Primer fo	Aah03051	Microorga	Adh027475	Microogan	Adf52263	Hepatitis	Adf52271	Hepatitis	Adf51575	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	Hepatitis	Adf51567	H
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824	13	65.0	712	6	ABQ23075	Abq23075 Oligonucle	897	13	65.0	2681	13	ACN43252	Acn43252 Human dia
825	13	65.0	712	6	ABQ23074	Abq23074 Oligonucle	898	13	65.0	2599	13	ACN43251	Acn43251 Human dia
826	13	65.0	786	11	ABQ38552	Abq38552 Kliebsiehl	899	13	65.0	2706	10	ADG74697	Adg74697 Human kin
827	13	65.0	876	6	ABQ38784	Abq38784 Oligonucle	900	13	65.0	2801	3	AACT7062	Aac77062 Human ORP
828	13	65.0	876	6	ABQ38785	Abq38785 Oligonucle	901	13	65.0	3091	12	ADL27527	Adl27527 Genomic s
829	13	65.0	960	6	ACA44732	Ac444732 Prokaryot	902	13	65.0	3183	10	ADA52620	Ada52620 Human cod
830	13	65.0	963	10	ADF02210	Adf02210 Bacterial	903	13	65.0	3329	6	ABQ78455	Abq78455 Nucleotid
831	13	65.0	1162	6	ABO50240	Abq50240 Oligonucle	904	13	65.0	3329	6	ABQ78456	Abq78456 Nucleotid
832	13	65.0	1162	6	ABO50241	Abq50241 Oligonucle	905	13	65.0	3402	6	ABQ79786	Abq79786 Human met
833	13	65.0	1173	6	ABZ13078	Abz13078 Arabidops	906	13	65.0	3403	6	ABQ79785	Abq79785 Human 334
834	13	65.0	1239	6	ACF70523	Abq470523 Photornab	907	13	65.0	3403	6	ABQ79785	Abq79785 Human met
835	13	65.0	1281	6	ABQ44106	Abq44106 Oligonucle	908	13	65.0	3403	6	ABQ78454	Abq78454 Nucleotid
836	13	65.0	1281	6	ABQ44107	Abq44107 Oligonucle	909	13	65.0	3403	6	ABQ78454	Abq78454 Human met
837	13	65.0	1296	8	ACA29505	Ac29505 Prokaryot	910	13	65.0	3471	6	ABQ78456	Abq78456 Nucleotid
838	13	65.0	1419	12	ADI02491	Adi02491 DNA encod	911	13	65.0	3471	6	ABQ78456	Abq78456 Nucleotid
839	13	65.0	1437	3	ACA40487	Aac40487 Arabidops	912	13	65.0	3571	6	ABZ11529	Abz11529 Human pol
840	13	65.0	1446	6	ABL50838	Abi50838 Human Akt	913	13	65.0	3571	12	ADM44047	Adm44047 Novel hum
841	13	65.0	1560	12	ADM91317	Adm91317 DNA homol	914	13	65.0	3766	6	ABK85766	Abk85766 DNA encod
842	13	65.0	1593	12	ADQ84311	Adq84311 Human tum	915	13	65.0	3861	8	ABT19704	Abt19704 Aspergill
843	13	65.0	1593	12	ADQ84311	Adq84311 Human tum	916	13	65.0	3877	13	ADR07592	Adr07592 Full leng
844	13	65.0	1593	13	ADQ83643	Adq83643 Human tum	917	13	65.0	3897	13	ACN43263	Acn43263 Human dia
845	13	65.0	1593	13	ADQ85783	Adq85783 Human tum	918	13	65.0	4077	12	ADL16376	Adl16376 Human pro
846	13	65.0	1593	13	ACN40577	Acn40577 Tumour-as	919	13	65.0	4253	6	ABS58376	Abs58376 Protein m
847	13	65.0	1599	2	AAAT71252	Aat71252 Mouse Akt	920	13	65.0	5433	4	ABL04331	Abi04331 Human imm
848	13	65.0	1599	3	AAA08448	Aaa08448 Human Akt	921	13	65.0	5878	6	ABL33540	Abi33540 Human imm
849	13	65.0	1599	3	AAZ60814	Aaz60814 Nucleotid	922	13	65.0	5883	6	ABL33733	Abi33733 Human imm
850	13	65.0	1599	11	ADC26887	Adc26887 DNA encod	923	13	65.0	5891	6	ABL33439	Abi33439 Human imm
851	13	65.0	1599	11	ADI31678	Adi31678 Human CDN	924	13	65.0	6237	10	ADR82762	Adr82762 Human alp
852	13	65.0	1599	12	ADN71937	Adn71937 Human pro	925	13	65.0	6352	6	ABK31340	Abk31340 Signal tr
853	13	65.0	1617	12	ADL27528	Adl27528 CDNA sequ	926	13	65.0	6352	6	ABK70563	Abi70563 Chemical
854	13	65.0	1701	10	ADB78667	Adb78667 Human nlc	927	13	65.0	6352	6	AA661235	Aa661235 Human gen
855	13	65.0	1715	6	ABV94263	Abv94263 Breast ca	928	13	65.0	6356	3	AAA51877	Aa51877 A. fumiga
856	13	65.0	1715	12	ADP48783	Adp48783 Human Akt	929	13	65.0	6381	4	ABL16414	Abi16414 Drosoephil
857	13	65.0	1722	10	ADB07335	Adb07335 Novel cod	930	13	65.0	7002	4	ABL09667	Abi09667 Drosoephil
858	13	65.0	1771	6	ADZ6345	Adz6345 Human mut	931	13	65.0	7162	4	ABL16436	Abi16436 Drosoephil
859	13	65.0	1771	10	ADB78665	Adb78665 Human nlc	932	13	65.0	7297	4	ABR21079	Ab21079 Human ner
860	13	65.0	1771	10	ADB78665	Adb78665 Human nlc	933	13	65.0	7726	5	ABR21079	Ab21079 Human ner
861	13	65.0	1771	10	ADB78666	Adb78666 Human nlc	934	13	65.0	10637	4	ABL09666	Abi09666 Drosoephil
862	13	65.0	1771	10	ADB78675	Adb78675 Human nlc	935	13	65.0	11942	4	AA515342	Aa515342 Human CHR
863	13	65.0	1771	10	ADB78664	Adb78664 Human nlc	936	13	65.0	12046	6	ABL33633	Abi33633 Human imm
864	13	65.0	1771	10	ADB78674	Adb78674 Human nlc	937	13	65.0	12222	4	AA654045	Aa654045 Human alp
865	13	65.0	1771	10	ADB78677	Adb78677 Human nlc	938	13	65.0	14756	10	ADC87364	Adc87364 Human GPC
866	13	65.0	1771	10	ADB78676	Adb78676 Human nlc	939	13	65.0	15954	6	ABK31494	Abk31494 Signal tr
867	13	65.0	1771	10	ADB78678	Adb78678 Human nlc	940	13	65.0	15954	6	ABT70467	Abt70467 Chemical
868	13	65.0	1854	3	AACT39548	Aac39548 Arabidops	941	13	65.0	17131	6	ABJ33052	Abj33052 Human imm
869	13	65.0	1947	4	ADA06387	Ada06387 Murine be	942	13	65.0	17590	3	AA250904	Aa250904 Human TBC
870	13	65.0	1957	10	ADF81647	Adf81647 Human cod	943	13	65.0	25559	10	ACF65388_12	Acf65388_12 Confinuaction (13 o
871	13	65.0	2040	6	ABQ99595	Abq99595 Human cod	944	13	65.0	32328	4	ABL09994	Abi09994 Drosoephil
872	13	65.0	2112	6	ABQ99595	Abq99595 Human cod	945	13	65.0	36471	3	AAA81453	Aa81453 N. mening
873	13	65.0	2125	13	ACN43262	Acn43262 Human dia	946	13	65.0	37030	10	ADB74276	Adb74276 Mycobacte
874	13	65.0	2199	13	ACN43261	Acn43261 Human dia	947	13	65.0	48829	11	ACN44868	Acn44868 Mouse gen
875	13	65.0	2272	13	ACN43260	Acn43260 Human dia	948	13	65.0	54732	13	ABD33335	Abd33335 Human can
876	13	65.0	2297	13	ACN43259	Acn43259 Human dia	949	13	65.0	55211	12	ADQ97266_3	Adq97266_3 Confinuaction (4 o
877	13	65.0	2307	13	ACN43258	Acn43258 Human dia	950	13	65.0	58909	4	AA678543	Aa678543 Genomic f
878	13	65.0	2325	13	ACN43257	Acn43257 Human dia	951	13	65.0	59748	13	ABD33260	Abd33260 Human can
879	13	65.0	2345	13	ACN43256	Acn43256 Human dia	952	13	65.0	65186	10	ADH10017_3	Adh10017_3 Confinuaction (4 o
880	13	65.0	2447	10	ADZ55029	Adz55029 Rat gene	953	13	65.0	68571	12	ADH56913	Adh56913 Human CAR
881	13	65.0	2447	10	ADZ55025	Adz55025 Rat gene	954	13	65.0	98300	12	ADO79403	Ado79403 KIAA0783
882	13	65.0	2448	2	AAV12201	Aav12201 Human neu	955	13	65.0	104900	13	ABD32848	Abd32848 Human can
883	13	65.0	2448	2	AAV12201	Aav12201 Human neu	956	13	65.0	107280	13	ABD33169	Abd33169 Murine can
884	13	65.0	2448	2	ABSS4876	Abss4876 Human neu	957	13	65.0	110000	3	AAA81489_2	Aa81489_2 Confinuaction (3 o
885	13	65.0	2448	6	ABV73249	Abv73249 Human neu	958	13	65.0	110000	10	ACF67367_36	Acf67367_36 Confinuaction (37 o
886	13	65.0	2448	9	ADAI0866	Adai0866 Human neu	959	13	65.0	110000	12	ADQ97266_2	Adq97266_2 Confinuaction (3 o
887	13	65.0	2448	11	ADM68423	Adm68423 Human nlc	960	13	65.0	110000	13	ABD32806_00	Abd32806_00 Human can
888	13	65.0	2452	13	ADQ85169	Adq85169 Human tum	961	13	65.0	110000	13	ABD32806_0	Abd32806_0 Human can
889	13	65.0	2452	13	ACN43265	Acn43265 Human dia	962	13	65.0	149062	13	ABD32780_0	Abd32780_0 Human can
890	13	65.0	2543	13	ACN43255	Acn43255 Human dia	963	13	65.0	149062	13	ABD32608	Abd32608 Human can
891	13	65.0	2562	13	ABD33336	Abd33336 Human can	964	13	65.0	347001	12	ADP43517	Adp43517 Human MAD
892	13	65.0	2582	13	ACN43254	Acn43254 Human dia	965	13	65.0	349980	3	AA672161	Aa672161 Neisseria
893	13	65.0	2583	5	AA584487	Aa584487 DNA encod	966	12	60.0	12	2	AA180311	Aa180311 Oligo HCV
894	13	65.0	2583	5	AD160351	Ad160351 Secreted	967	12	60.0	12	5	AB119088	Ab119088 Oligonucle
895	13	65.0	2600	13	ACN43253	Acn43253 Human dia	968	12	60.0	12	6	AB565895	Ab565895 Inhibitor
896	13	65.0	2605	13	ACN43264	Acn43264 Human dia	969	12	60.0	13	5	ABC87845	Abc87845 Oligonucle

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c 970      12      60.0      13      5      ABC87844      Abc87844 Oligonucle
c 971      12      60.0      13      8      ACD65997      Acd65997 Anti-HCV
c 972      12      60.0      13      12      ADI87566      Adi87566 Anti-HCV
c 973      12      60.0      15      3      AAZ62399      Aaz62399 Substrate
c 974      12      60.0      15      6      ABX00256      Abx00256 Hepatitis
c 975      12      60.0      15      6      ABX01765      Abx01765 Hepatitis
c 976      12      60.0      15      8      ACD65975      Acd65975 Anti-HCV
c 977      12      60.0      15      12      ADI87544      Adi87544 Anti-HCV
c 978      12      60.0      17      8      ACD65760      Acd65760 HCV minus
c 979      12      60.0      17      8      ACD65756      Acd65756 HCV minus
c 980      12      60.0      17      12      ADI87250      Adi87250 HCV DNAzy
c 981      12      60.0      17      12      ADI87254      Adi87254 HCV DNAzy
c 982      12      60.0      17      12      ADP87811      Adp87811 Extension
c 983      12      60.0      18      8      ABZ10900      Abz10900 Haematopo
c 984      12      60.0      18      10      ABT23632      Abt23632 Stabilisi
c 985      12      60.0      19      10      ADP51577      Adp51577 Hepatitis
c 986      12      60.0      19      10      ADP51577      Adp51577 Hepatitis
c 987      12      60.0      19      10      ADP52294      Adp52294 Hepatitis
c 988      12      60.0      19      10      ADP51598      Adp51598 Hepatitis
c 989      12      60.0      19      10      ADP52273      Adp52273 Hepatitis
c 990      12      60.0      20      2      AAQ44916      Aaq44916 Antisense
c 991      12      60.0      20      2      AAT80242      Aat80242 Oligo HCV
c 992      12      60.0      20      6      ABS65826      Abs65826 Inhibitor
c 993      12      60.0      25      9      ACI25526      Aci25526 Human mic
c 994      12      60.0      25      9      ACK17513      Ack17513 Human mic
c 995      12      60.0      25      9      ACI55212      Aci55212 Human mic
c 996      12      60.0      25      9      ACI54584      Aci54584 Human mic
c 997      12      60.0      29      2      AAQ52823      Aaq52823 HCV target
c 998      12      60.0      29      2      AAQ52822      Aaq52822 HCV target
c 999      12      60.0      45      3      AAA07134      Aaa07134 S. pyogen
1000      12      60.0      45      3      AAA07121      Aaa07121 S. pyogen

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## ALIGNMENTS

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RESULT 1
ID AAT80332 standard; RNA; 20 BP.
XX
AC AAT80332;
XX
DT 16-OCT-1997 (first entry)
XX
DE Oligo HCV1 9x5, targeted to HCV mRNA position -67 to -86.
XX
KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW inhibition; replication; expression; detection; chronic hepatitis;
KW acute hepatitis; hepatocarcinoma; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FH modified_base 1..9
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FT /note= "2'-OMe RNA"
FT modified_base 10..11
FT /*tag= b
FT /note= "Comprises phosphorothioate linkages"
FT modified_base 12..20
FT /*tag= c
FT /note= "2'-OMe RNA"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOFF-) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
PA

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XX Frank BL, Goodchild J, Hamlin HA, Kilukuskie RE, Roberts NA;
PI Roberts PC, Walther DM, Wolfe JL;
XX WPI, 1997-043122/04.
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX carcinoma.
XX
XX Claim 1; Page 18; 100bp; English.
XX
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX which are complementary to a portion of the 5' untranslated region (UTR)
XX of hepatitis C virus (HCV). These sequences may be used in a
XX pharmaceutical composition for the control or prevention of HCV
XX infection. They may be used to inhibit replication or expression of HCV
XX or for detecting the presence of HCV in a sample. They may be used to
XX inhibit HCV replication in a cell and are therefore useful in the
XX treatment of HCV infections such as chronic and acute hepatitis and
XX hepatocarcinoma
XX
XX Sequence 20 BP; 5 A; 9 C; 2 G; 0 T; 4 U; 0 Other;
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XX Best Local Similarity 80.0%; Pred. No. 0.061;
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XX 1 TTGGCGACCCACACTATC 20
XX 1 UUCGCGACCCACACACUACUC 20

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RESULT 2
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XX
AC AAT80337;
XX
DT 16-OCT-1997 (first entry)
XX
DE Oligo HCV1 9x5, targeted to HCV mRNA position -67 to -86.
XX
KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW inhibition; replication; expression; detection; chronic hepatitis;
KW acute hepatitis; hepatocarcinoma; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
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FT /note= "2'-OMe RNA"
FT modified_base 10..15
FT /*tag= b
FT /note= "Comprises phosphorothioate linkages"
FT modified_base 16..20
FT /*tag= c
FT /note= "2'-OMe RNA"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOFF-) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
PA
XX Frank BL, Goodchild J, Hamlin HA, Kilukuskie RE, Roberts NA;
XX Roberts PC, Walther DM, Wolfe JL;
PI

```

```
XX DR WPI; 1997-043122/04.
XX
XX PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX carcinoma.
XX
XX PS Claim 1; Page 18; 100pp; English.
XX
XX CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX which are complementary to a portion of the 5' untranslated region (UTR)
XX of hepatitis C virus (HCV). These sequences may be used in a
XX pharmaceutical composition for the control or prevention of HCV
XX infection. They may be used to inhibit replication or expression of HCV
XX or for detecting the presence of HCV in a sample. They may be used to
XX inhibit HCV replication in a cell and are therefore useful in the
XX treatment of HCV infections such as chronic and acute hepatitis and
XX hepatocarcinoma
XX
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XX Best Local Similarity 100.0%; Pred. No. 0.061;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX DB 1 TTGCGACCCCAACTACTC 20
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XX
XX AC AAT80336;
XX
XX DT 16-OCT-1997 (first entry)
XX
XX DE Oligo HCV1 11x3, targeted to HCV mRNA position -67 to -86.
XX
XX KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX inhibition; replication; expression; detection; chronic hepatitis;
XX acute hepatitis; hepatocarcinoma; ss.
XX
XX OS Synthetic.
XX
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XX FT /note= "Comprises phosphorothioate linkages"
XX modified_base 18..20
XX FT /tag= c
XX FT /note= "2'-Ome RNA"
XX
XX PN WO9639500-A2.
XX PD 12-DEC-1996.
XX PF 04-JUN-1996; 96WO-EP002427.
XX PR 06-JUN-1995; 95US-00471968.
XX
XX PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
XX
XX PI Frank BL, Goodchild J, Hamlin HA, Kilukuskie RE, Roberts NA;
XX Roberts PC, Walther DM, Wolfe JL;
XX WPI; 1997-043122/04.
XX
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```
PT PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT carcinoma.
PT
PT PS Claim 1; Page 18; 100pp; English.
PT
PT CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
PT which are complementary to a portion of the 5' untranslated region (UTR)
PT of hepatitis C virus (HCV). These sequences may be used in a
PT pharmaceutical composition for the control or prevention of HCV
PT infection. They may be used to inhibit replication or expression of HCV
PT or for detecting the presence of HCV in a sample. They may be used to
PT inhibit HCV replication in a cell and are therefore useful in the
PT treatment of HCV infections such as chronic and acute hepatitis and
PT hepatocarcinoma
PT
PT SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
PT
PT Query Match 100.0%; Score 20; DB 2; Length 20;
PT Best Local Similarity 100.0%; Pred. No. 0.061;
PT Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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PT 1 TTGCGACCCCAACTACTC 20
PT DB 1 TTGCGACCCCAACTACTC 20
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PT ID AAT80338 standard; RNA; 20 BP.
PT
PT AC AAT80338;
PT
PT DT 16-OCT-1997 (first entry)
PT
PT DE Oligo HCV1 5x9, targeted to HCV mRNA position -67 to -86.
PT
PT KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
PT inhibition; replication; expression; detection; chronic hepatitis;
PT acute hepatitis; hepatocarcinoma; ss.
PT
PT OS Synthetic.
PT
PT FH Key Location/Qualifiers
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PT modified_base 6..11
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PT FT /note= "Comprises phosphorothioate linkages"
PT modified_base 12..20
PT FT /tag= c
PT FT /note= "2'-Ome RNA"
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PT PN WO9639500-A2.
PT PD 12-DEC-1996.
PT PF 04-JUN-1996; 96WO-EP002427.
PT PR 06-JUN-1995; 95US-00471968.
PT
PT PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PT (HYBR-) HYBRIDON INC.
PT
PT PI Frank BL, Goodchild J, Hamlin HA, Kilukuskie RE, Roberts NA;
PT Roberts PC, Walther DM, Wolfe JL;
PT WPI; 1997-043122/04.
PT
PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT carcinoma.
PT
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XX Claim 1; Page 18; 100pp; English.

PS The sequences given in AAT80211-382 represent synthetic oligonucleotides

CC which are complementary to a portion of the 5' untranslated region (UTR)

CC of hepatitis C virus (HCV). These sequences may be used in a

CC pharmaceutical composition for the control or prevention of HCV

CC infection. They may be used to inhibit replication or expression of HCV

CC or for detecting the presence of HCV in a sample. They may be used to

CC inhibit HCV replication in a cell and are therefore useful in the

CC treatment of HCV infections such as chronic and acute hepatitis and

CC hepatocarcinoma

XX

Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTGCGACCCACACTACTC 20

RESULT 5

AAT80329

ID AAT80329 standard; DNA; 20 BP.

XX AAT80329;

AC

XX 16-OCT-1997 (first entry)

DT

XX

DE Oligo HCV1 OX4, targeted to HCV mRNA position -67 to -86.

XX

OS Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;

KW inhibition; replication; expression; detection; chronic hepatitis;

KW acute hepatitis; hepatocarcinoma; ss.

XX

OS Synthetic.

XX

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XX

XX WO9639500-A2.

XX

XX 12-DEC-1996.

XX

XX 04-JUN-1996; 96WO-EP002427.

XX

XX 06-JUN-1995; 95US-00471968.

XX

XX (HOF ) HOFFMANN LA ROCHE & CO AG F.

XX (HYBR-) HYBRIDON INC.

XX

XX Frank BL, Goodchild J, Hamlin HA, Kilukie RE, Roberts NA;

PI Roberts PC, Walther DM, Wolfe JL;

XX

XX WPI; 1997-043122/04.

XX

XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in

PT the treatment and detection of HCV infection, esp. hepatitis and hepato-

PT carcinoma.

XX

XX Claim 1; Page 18; 100pp; English.

PS The sequences given in AAT80211-382 represent synthetic oligonucleotides

CC which are complementary to a portion of the 5' untranslated region (UTR)

CC of hepatitis C virus (HCV). These sequences may be used in a

CC treatment of HCV infections such as chronic and acute hepatitis and

CC hepatocarcinoma

CC

CC pharmaceutical composition for the control or prevention of HCV

CC infection. They may be used to inhibit replication or expression of HCV

CC or for detecting the presence of HCV in a sample. They may be used to

CC inhibit HCV replication in a cell and are therefore useful in the

CC treatment of HCV infections such as chronic and acute hepatitis and

CC hepatocarcinoma

XX

Sequence 20 BP; 5 A; 9 C; 2 G; 3 T; 1 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;

Best Local Similarity 95.0%; Pred. No. 0.061;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACTACTC 20

Db 1 TTGCGACCCACACTACTC 20

RESULT 6

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ID AAT80330 standard; DNA; 20 BP.

XX AAT80330;

AC

XX 16-OCT-1997 (first entry)

DT

XX

DE Oligo HCV1 OX3, targeted to HCV mRNA position -67 to -86.

XX

OS Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;

KW inhibition; replication; expression; detection; chronic hepatitis;

KW acute hepatitis; hepatocarcinoma; ss.

XX

OS Synthetic.

XX

XX Key Location/Qualifiers

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XX

XX WO9639500-A2.

XX

XX 12-DEC-1996.

XX

XX 04-JUN-1996; 96WO-EP002427.

XX

XX 06-JUN-1995; 95US-00471968.

XX

XX (HOF ) HOFFMANN LA ROCHE & CO AG F.

XX (HYBR-) HYBRIDON INC.

XX

XX Frank BL, Goodchild J, Hamlin HA, Kilukie RE, Roberts NA;

PI Roberts PC, Walther DM, Wolfe JL;

XX

XX WPI; 1997-043122/04.

XX

XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in

PT the treatment and detection of HCV infection, esp. hepatitis and hepato-

PT carcinoma.

XX

XX Claim 1; Page 18; 100pp; English.

PS The sequences given in AAT80211-382 represent synthetic oligonucleotides

CC which are complementary to a portion of the 5' untranslated region (UTR)

CC of hepatitis C virus (HCV). These sequences may be used in a

CC pharmaceutical composition for the control or prevention of HCV

CC infection. They may be used to inhibit replication or expression of HCV

CC or for detecting the presence of HCV in a sample. They may be used to

CC inhibit HCV replication in a cell and are therefore useful in the

CC treatment of HCV infections such as chronic and acute hepatitis and

CC hepatocarcinoma

CC



XX Sequence 20 BP; 5 A; 9 C; 2 G; 3 T; 1 U; 0 Other;  
SQ Query Match 100.0%; Score 20; DB 2; Length 20;  
Best Local Similarity 95.0%; Pred. No. 0.061;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
1 TTGGGACCCCAACTACTC 20  
Db 1 TTGGGACCCCAACTACTC 20

RESULT 7  
AAT80333  
ID AAT80333 standard; RNA; 20 BP.  
XX AAT80333;  
AC AAT80333;  
XX 16-OCT-1997 (first entry)  
DT  
XX Oligo HCV1 8x8, targeted to HCV mRNA position -67 to -86.  
DE  
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KW inhibition; replication; expression; detection; chronic hepatitis;  
KM acute hepatitis; hepatocarcinoma; ss.  
XX Synthetic.  
OS

XX Key Location/Qualifiers  
FH modified\_base 1..8  
FT /tag= a  
FT /note= "2'-OME RNA"  
FT modified\_base 9..12  
FT /tag= b  
FT /note= "Comprises phosphorothioate linkages"  
FT modified\_base 13..20  
FT /tag= c  
FT /note= "2'-OME RNA"  
XX  
XX WO9639500-A2.  
XX 12-DEC-1996.  
XX  
XX 04-JUN-1996; 96WO-EP002427.  
XX  
XX 06-JUN-1995; 95US-00471968.  
XX  
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.  
XX (HYBR-) HYBRIDON INC.  
XX  
XX Frank BL, Goodchild J, Hamlin HA, Kilukuskie RE, Roberts NA;  
PI Roberts PC, Walther DM, Wolfe JL;  
XX  
XX WPI: 1997-043122/04.  
XX  
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
XX Claim 1; Page 18; 100pp; English.  
XX  
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma  
XX  
XX Sequence 20 BP; 5 A; 9 C; 2 G; 0 T; 4 U; 0 Other;

Qy Query Match 100.0%; Score 20; DB 2; Length 20;  
Best Local Similarity 80.0%; Pred. No. 0.061;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
1 TTGGGACCCCAACTACTC 20  
Db 1 TTGGGACCCCAACTACTC 20

RESULT 8  
AAT80339  
ID AAT80339 standard; RNA; 20 BP.  
XX AAT80339;  
AC AAT80339;  
XX 16-OCT-1997 (first entry)  
DT  
XX Oligo HCV1 3x11, targeted to HCV mRNA position -67 to -86.  
DE  
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KW inhibition; replication; expression; detection; chronic hepatitis;  
KM acute hepatitis; hepatocarcinoma; ss.  
XX Synthetic.  
OS

XX Key Location/Qualifiers  
FH modified\_base 1..3  
FT /tag= a  
FT /note= "2'-OME RNA"  
FT modified\_base 4..9  
FT /tag= b  
FT /note= "Comprises phosphorothioate linkages"  
FT modified\_base 10..20  
FT /tag= c  
FT /note= "2'-OME RNA"  
XX  
XX WO9639500-A2.  
XX 12-DEC-1996.  
XX  
XX 04-JUN-1996; 96WO-EP002427.  
XX  
XX 06-JUN-1995; 95US-00471968.  
XX  
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.  
XX (HYBR-) HYBRIDON INC.  
XX  
XX Frank BL, Goodchild J, Hamlin HA, Kilukuskie RE, Roberts NA;  
PI Roberts PC, Walther DM, Wolfe JL;  
XX  
XX WPI: 1997-043122/04.  
XX  
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
XX Claim 1; Page 18; 100pp; English.  
XX  
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma  
XX  
XX Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.061;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
 DB 1 TTGGGACCCCAACTACTC 20

## RESULT 9

AAT80340  
 ID AAT80340 standard; RNA; 20 BP.

AC AAT80340;

DT 16-OCT-1997 (first entry)

DE Oligo HCV1 0x14, targeted to HCV mRNA position -67 to -86.

KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KW inhibition; replication; expression; detection; chronic hepatitis;  
 XX acute hepatitis; hepatocarcinoma; ss.

OS Synthetic.

PH Key Location/Qualifiers

FT modified\_base 1..6

FT /\*tag= a

FT /note= "Comprises phosphorothioate linkages"

FT modified\_base 7..20

FT /\*tag= b

FT /note= "2'-OME RNA"

PN WO9639500-A2.

PD 12-DEC-1996.

PF 04-JUN-1996; 96WO-EP002427.

PR 06-JUN-1995; 95US-00471968.

PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PA (HYBR-) HYBRIDON INC.

PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
 PI Roberts PC, Walther DM, Wolfe JL;

DR WPI; 1997-043122/04.

PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
 PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
 XX carcinoma.

PS Claim 1; Page 18; 100pp; English.

CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
 CC which are complementary to a portion of the 5' untranslated region (UTR)  
 CC of hepatitis C virus (HCV). These sequences may be used in a  
 CC pharmaceutical composition for the control or prevention of HCV  
 CC infection. They may be used to inhibit replication or expression of HCV  
 CC or for detecting the presence of HCV in a sample. They may be used to  
 CC inhibit HCV replication in a cell and are therefore useful in the  
 CC treatment of HCV infections such as chronic and acute hepatitis and  
 CC hepatocarcinoma

SO Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.061;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
 DB 1 TTGGGACCCCAACTACTC 20

RESULT 10  
 AAT80238  
 ID AAT80238 standard; DNA; 20 BP.

AC AAT80238;

DT 15-OCT-1997 (first entry)

DE Oligo HCV1, targeted to HCV mRNA RNase sensitive region C.

KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KW inhibition; replication; expression; detection; chronic hepatitis;  
 XX acute hepatitis; hepatocarcinoma; ss.

OS Synthetic.

PH Key Location/Qualifiers

FT modified\_base 1..20

FT /\*tag= a

FT /note= "Comprises phosphorothioate linkages"

PN WO9639500-A2.

PD 12-DEC-1996.

PF 04-JUN-1996; 96WO-EP002427.

PR 06-JUN-1995; 95US-00471968.

PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PA (HYBR-) HYBRIDON INC.

PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
 PI Roberts PC, Walther DM, Wolfe JL;

DR WPI; 1997-043122/04.

PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
 PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
 XX carcinoma.

PS Claim 1; Page 25; 100pp; English.

CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
 CC which are complementary to a portion of the 5' untranslated region (UTR)  
 CC of hepatitis C virus (HCV). These sequences may be used in a  
 CC pharmaceutical composition for the control or prevention of HCV  
 CC infection. They may be used to inhibit replication or expression of HCV  
 CC or for detecting the presence of HCV in a sample. They may be used to  
 CC inhibit HCV replication in a cell and are therefore useful in the  
 CC treatment of HCV infections such as chronic and acute hepatitis and  
 CC hepatocarcinoma. This oligo was used in an RNase H assay to determine  
 CC whether it binds successfully to its target. Three regions of HCV mRNA  
 CC were investigated as RNase sensitive sites. This oligo binds to position  
 CC -67 to -86

SO Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.061;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
 DB 1 TTGGGACCCCAACTACTC 20

## RESULT 11

AAT80334  
 ID AAT80334 standard; RNA; 20 BP.

AC AAT80334;  
 XX

DT	16-OCT-1997	(first entry)
DE	Oligo HCV1 7x7,	targetted to HCV mRNA position -67 to -86.
XX		
KW	Complementary; 5'	untranslated region; UTR; hepatitis C virus; HCV;
KM	inhibition; replication;	expression; detection; chronic hepatitis;
KW	acute hepatitis; hepatocarcinoma;	ss.
XX		
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	modified_base	1..7
FT		/tag= "a"
FT		/note= "2'-OME RNA"
FT	modified_base	8..13
FT		/tag= "b"
FT		/note= "Compriees phosphorothioate linkages"
FT	modified_base	14..20
FT		/tag= "c"
FT		/note= "2'-OME RNA"
PN	WO9639500-A2.	
XX		
PD	12-DEC-1996.	
XX		
PF	04-JUN-1996;	96WO-EP002427.
PR	06-JUN-1995;	95US-00471968.
XX		
PA	(HOFF ) HOFFMANN LA ROCHE & CO AG F.	
XX	(HYBR-) HYBRIDON INC.	
PI	Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;	
P1	Roberts PC, Walther DM, Wolfe JL;	
XX		
DR	WPI, 1997-043122/04.	
XX		
PT	Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in	
PT	the treatment and detection of HCV infection, esp. hepatitis and hepato-	
PT	carcinoma.	
PS	Claim 1; Page 18; 100pp; English.	
CC	The sequences given in AAT80211-382 represent synthetic oligonucleotides	
CC	which are complementary to a portion of the 5' untranslated region (UTR)	
CC	of hepatitis C virus (HCV). These sequences may be used in a	
CC	pharmaceutical composition for the control or prevention of HCV	
CC	infection. They may be used to inhibit replication or expression of HCV	
CC	or for detecting the presence of HCV in a sample. They may be used to	
CC	inhibit HCV replication in a cell and are therefore useful in the	
CC	treatment of HCV infections such as chronic and acute hepatitis and	
CC	hepatocarcinoma	
XX		
SQ	Sequence 20 BP; 5 A; 9 C; 2 G; 0 T; 4 U; 0 Other;	
OY	Query Match	100.0%; Score 20; DB 2; Length 20;
	Best Local Similarity	80.0%; Pred.No.0.061;
	Matches 16; Conservative	4; Mismatches 0; Indels 0; Gaps 0
DB	1 TTGGGACCCCAACTACTC 20	
	:::     :: :	
	1 UUCCGACCACAACUACUC 20	
RESULT 12		
ID	AAT80335	
XX	AAT80335 standard; RNA; 20 BP.	
XX		
AC	AAT80335;	
XX		
DT	16-OCT-1997	(first entry)
XX		
DE	Oligo HCV1 6x6, targetted to HCV mRNA position -67 to -86.	

Key	Location/Qualifiers
modified_base	1..6
modified_base	/*tag= a
modified_base	/note= "2'-OME RNA"
modified_base	7..14
modified_base	/*tag= b
modified_base	/note= "Comprises phosphorothioate linkages"
modified_base	15..20
modified_base	/*tag= c
modified_base	/note= "2'-OME RNA"
WO9639500-A2.	
12-DEC-1996.	
04-JUN-1996.	96WO-EP002427.
06-JUN-1995.	95US-00471968.
(HOFF) HOFFMANN LA ROCHE & CO AG F.	
(HYBR-) HYBRIDON INC.	
Frank BL, Goodchild J, Hamlin HA, Kilkuetie RE, Roberts NA;	
Roberts PC, Walthers DM, Wolfe JL;	
WPI; 1997-043122/04.	
Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in	
the treatment and detection of HCV infection, esp. hepatitis and hepato-	
carcinoma.	
Claim 1; Page 18; 100pp; English.	
The sequences given in AAT80211-382 represent synthetic oligonucleotides	
which are complementary to a portion of the 5' untranslated region (UTR)	
of hepatitis C virus (HCV). These sequences may be used in a	
pharmaceutical composition for the control or prevention of HCV	
infection. They may be used to inhibit replication or expression of HCV	
or for detecting the presence of HCV in a sample. They may be used to	
inhibit HCV replication in a cell and are therefore useful in the	
treatment of HCV infections such as chronic and acute hepatitis and	
hepatocarcinoma	
Sequence 20 BP; 5 A; 9 C; 2 G; 4 U; 0 Other;	
Query Match	100.0%; Score 20; DB 2; Length 20;
Best Local Similarity	80.0%; Pred. No. 0.061; 0; Indels 0; Gaps 0
Matches	16; Conservative 4; Mismatches 0; Indels 0; Gaps 0
1 TTTCGACCCACACTACTC 20	
1 UUGCGACCCACACACUACUC 20	
RESULT 13	
AAT80331	
AAT80331 standard; DNA; 20 BP.	
AAT80331;	
16-OCF-1997 (first entry)	
Oligo HCV OX2, targeted to HCV mRNA position -67 to -86.	
Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;	
inhibition; replication; expression; detection; chronic hepatitis;	
inhibition; replication; expression; detection; chronic hepatitis;	

KW acute hepatitis; hepatocarcinoma; ss.  
 XX Synthetic.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /tag= a  
 FT /note= "Comprises phosphothioate linkages"  
 FT 19..20  
 FT /tag= b  
 FT /note= "2'-OME RNA"  
 FT  
 XX  
 PN WO639500-A2.  
 PD 12-DEC-1996.  
 XX  
 XX  
 PF 04-JUN-1996; 96WO-EP002427.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 XX  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 PA (HYBR-) HYBRIDON INC.  
 XX  
 PI Frank BL, Goodchild J, Hamlin HA, Kiluskie RE, Roberts NA,  
 PI Roberts PC, Walther DM, Wolfe JL;  
 XX WPI; 1997-043122/04.  
 DR  
 XX  
 PT Oligonucleotide(s) complementary to HCV 5' untranslated region - used in  
 PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
 PT carcinoma.  
 XX  
 PS Claim 1; Page 18; 100pp; English.  
 XX  
 CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
 CC which are complementary to a portion of the 5' untranslated region (UTR)  
 CC of hepatitis C virus (HCV). These sequences may be used in a  
 CC pharmaceutical composition for the control or prevention of HCV  
 CC infection. They may be used to inhibit replication or expression of HCV  
 CC or for detecting the presence of HCV in a sample. They may be used to  
 CC inhibit HCV replication in a cell and are therefore useful in the  
 CC treatment of HCV infections such as chronic and acute hepatitis and  
 CC hepatocarcinoma  
 CC  
 SQ Sequence 20 BP; 5 A; 9 C; 2 G; 3 T; 1 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 2; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 0.061;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGGGACCCCACTACTC 20  
 Db 1 TTGGGACCCCACTACTC 20  
 RESULT 14  
 ABS65922  
 ID ABS65922 standard; DNA; 20 BP.  
 XX  
 AC ABS65922;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #128.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KW gene therapy; ss; DNA-RNA hybrid.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002081577-A1.  
 FN

XX  
 PD 27-JUN-2002.  
 XX  
 PF 02-JUL-1997; 97US-00887505.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
 XX  
 PA (KILK) KILUSKIE R L.  
 PA (FRANK) FRANK B L.  
 PA (GOOD) GOODCHILD J.  
 PA (WOLFE) WOLFE J L.  
 PA (ROBE) ROBERTS P C.  
 PA (HAML) HAMLIN H A.  
 PA (ROBE) ROBERTS N A.  
 PA (WALT) WALTHER D M.  
 XX  
 PI Kiluskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,  
 PI Hamlin HA, Roberts NA, Walther DM;  
 XX WPI; 2002-537132/57.  
 DR  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.  
 XX  
 PS Claim 1; Page 6; 74pp; English.  
 XX  
 CC The invention describes synthetic oligonucleotides complementary to a  
 CC portion of the 5' untranslated region of hepatitis C virus. The  
 CC oligonucleotides may be used in methods for controlling, preventing, and  
 CC treating hepatitis C virus infection, in antisense technology and gene  
 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
 CC HCV replication and expression of HCV  
 CC  
 SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.061;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGGGACCCCACTACTC 20  
 Db 1 TTGGGACCCCACTACTC 20  
 RESULT 15  
 ABS65918  
 ID ABS65918 standard; DNA; 20 BP.  
 XX  
 AC ABS65918;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #124.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KW gene therapy; ss; DNA-RNA hybrid.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002081577-A1.  
 XX  
 PD 27-JUN-2002.

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XX 02-JUL-1997; 97US-00887505.
PR 06-JUN-1995; 95US-00471968.
PR 02-JUL-1996; 96US-0021104P.
XX (KILK/) KILKUSKIE R L.
PA (FRAN/) FRANK B L.
PA (GOOD/) GOODCHILD J.
PA (WOLF/) WOLFE J L.
PA (ROBE/) ROBERTS P C.
PA (HAML/) HAMLIN H A.
PA (ROBE/) ROBERTS N A.
PA (WALT/) WALTHER D M.
XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
PI Hamlin HA, Roberts NA, Walther DM;
DR WPI, 2002-537132/57.
XX Synthetic oligonucleotides complementary to a portion of the 5'
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and
PT treating HCV infections and hepatocellular carcinoma.
XX Claim 1; Page 6; 74pp; English.
XX The invention describes synthetic oligonucleotides complementary to a
CC portion of the 5' untranslated region of hepatitis C virus. The
CC oligonucleotides may be used in methods for controlling, preventing, and
CC treating hepatitis C virus infection, in antisense technology and gene
CC therapy, and of detecting the presence of hepatitis C virus in a sample.
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
CC -B, acute and chronic hepatitis, and has been associated with
CC hepatocellular carcinoma. The invention describes methods and kits for
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic
CC acid and protein, and for treating HCV infections. This sequence
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting
CC HCV replication and expression of HCV
XX
SQ Sequence 20 BP; 5 A; 9 C; 2 G; 0 T; 4 U; 0 Other;
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 0.061;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGACCCCAACTACTC 20
Db 1 TTCCGACCCCAACTACTC 20
1 UUCGCGACCCCAACTACTC 20
RESULT 16
ABS65924
ID ABS65924 standard; DNA; 20 BP.
XX
AC ABS65924;
XX
DT 15-NOV-2002 (first entry)
XX
DE Inhibitory oligonucleotide specific for hepatitis C virus #130.
XX
KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
KW non-B hepatitis; acute hepatitis; chronic hepatitis;
KW hepatocellular carcinoma; viraemia; cytostatic; antisense therapy;
KW gene therapy; ss; DNA-RNA hybrid.
XX
OS Synthetic.
XX
PN US2002081577-A1.
XX
PD 27-JUN-2002.
XX
PR 02-JUL-1997; 97US-00887505.

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XX 06-JUN-1995; 95US-00471968.
PR 02-JUL-1996; 96US-0021104P.
XX (KILK/) KILKUSKIE R L.
PA (FRAN/) FRANK B L.
PA (GOOD/) GOODCHILD J.
PA (WOLF/) WOLFE J L.
PA (ROBE/) ROBERTS P C.
PA (HAML/) HAMLIN H A.
PA (ROBE/) ROBERTS N A.
PA (WALT/) WALTHER D M.
XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
PI Hamlin HA, Roberts NA, Walther DM;
DR WPI, 2002-537132/57.
XX Synthetic oligonucleotides complementary to a portion of the 5'
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and
PT treating HCV infections and hepatocellular carcinoma.
XX Claim 1; Page 6; 74pp; English.
XX The invention describes synthetic oligonucleotides complementary to a
CC portion of the 5' untranslated region of hepatitis C virus. The
CC oligonucleotides may be used in methods for controlling, preventing, and
CC treating hepatitis C virus infection, in antisense technology and gene
CC therapy, and of detecting the presence of hepatitis C virus in a sample.
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
CC -B, acute and chronic hepatitis, and has been associated with
CC hepatocellular carcinoma. The invention describes methods and kits for
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic
CC acid and protein, and for treating HCV infections. This sequence
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting
CC HCV replication and expression of HCV
XX
SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGACCCCAACTACTC 20
Db 1 TTCCGACCCCAACTACTC 20
1 TTCCGACCCCAACTACTC 20
RESULT 17
ABS65920
ID ABS65920 standard; DNA; 20 BP.
XX
AC ABS65920;
XX
DT 15-NOV-2002 (first entry)
XX
DE Inhibitory oligonucleotide specific for hepatitis C virus #126.
XX
KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
KW non-B hepatitis; acute hepatitis; chronic hepatitis;
KW hepatocellular carcinoma; viraemia; cytostatic; antisense therapy;
KW gene therapy; ss; DNA-RNA hybrid.
XX
OS Synthetic.
XX
PN US2002081577-A1.
XX
PD 27-JUN-2002.
XX
PR 02-JUL-1997; 97US-00887505.
PR 06-JUN-1995; 95US-00471968.

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PR 02-JUL-1996; 96US-0021104P.  
 XX (KILK/) KILKUSKIE R L.  
 PA (FRAN/) FRANK B L.  
 PA (GOOD/) GOODCHILD J.  
 PA (WOLF/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.  
 PA (HAML/) HAMLIN H A.  
 PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.  
 XX  
 PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,  
 PI Hamlin HA, Roberts NA, Walther DM;  
 XX WPI, 2002-537132/57.  
 XX  
 DR WPI, 2002-537132/57.  
 XX  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
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 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
 CC HCV replication and expression of HCV  
 XX  
 SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.061;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCACACTACTC 20  
 Db 1 TTGCGACCCACACTACTC 20  
 RESULT 18  
 ABS65917  
 ID ABS65917 standard; DNA; 20 BP.  
 XX  
 AC ABS65917;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #123.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; viraemia; cytosolic; antisense therapy;  
 KW gene therapy; ss; DNA-RNA hybrid.  
 XX  
 OS Synthetic.  
 XX  
 US2002081577-A1.  
 XX  
 PN 27-JUN-2002.  
 PD  
 XX  
 PF 02-JUL-1997; 97US-00887505.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
 XX

PA (KILK/) KILKUSKIE R L.  
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 PA (WALT/) WALTHER D M.  
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 PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,  
 PI Hamlin HA, Roberts NA, Walther DM;  
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 SQ Sequence 20 BP; 5 A; 9 C; 2 G; 0 T; 4 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 0.061;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCACACTACTC 20  
 Db 1 TTGCGACCCACACTACTC 20  
 RESULT 19  
 ABS65923  
 ID ABS65923 standard; DNA; 20 BP.  
 XX  
 AC ABS65923;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #129.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; viraemia; cytosolic; antisense therapy;  
 KW gene therapy; ss; DNA-RNA hybrid.  
 XX  
 OS Synthetic.  
 XX  
 US2002081577-A1.  
 XX  
 PN 27-JUN-2002.  
 PD  
 XX  
 PF 02-JUL-1997; 97US-00887505.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
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 PA (KILK/) KILKUSKIE R L.  
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 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
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 SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.061;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTCCGGACCCCAACTACTC 20  
 Db 1 TTCCGGACCCCAACTACTC 20  
 RESULT 20  
 ABS65921  
 ID ABS65921 standard; DNA; 20 BP.  
 XX  
 AC ABS65921;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #127.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KW gene therapy; ss; DNA-RNA hybrid.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002081577-A1.  
 XX  
 PD 27-JUN-2002.  
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 PF 02-JUL-1997; 97US-00887505.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
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 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
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 XX  
 SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.061;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTCCGGACCCCAACTACTC 20  
 Db 1 TTCCGGACCCCAACTACTC 20  
 RESULT 21  
 ABS65913  
 ID ABS65913 standard; DNA; 20 BP.  
 XX  
 AC ABS65913;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #119.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KW gene therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002081577-A1.  
 XX  
 PD 27-JUN-2002.  
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 PF 02-JUL-1997; 97US-00887505.  
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 PR 02-JUL-1996; 96US-0021104P.  
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 PI Kiluskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
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 DR WPI; 2002-537132/57.  
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 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
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 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic oligonucleotide used for inhibiting HCV  
 CC replication and expression of HCV  
 XX  
 SQ Sequence 20 BP; 5 A; 9 C; 2 G; 3 T; 1 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 20; DB 6; Length 20;  
 Best Local Similarity 95.0%; Pred. No. 0.061;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTTCGACCCCAACACTACTC 20  
 Db 1 TTTCGACCCCAACACTACTC 20  
 XX  
 RESULT 22  
 ABS65916  
 ID ABS65916 standard; DNA; 20 BP.  
 AC ABS65916;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #122.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; viraemia; cytostatic; antisense therapy;  
 KW gene therapy; ss; DNA-RNA hybrid.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002081577-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 02-JUL-1997; 97US-00887505.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
 XX  
 PA (KILK/) KILKUSKIE R L.  
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XX  
 PI Kiluskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
 PI Hamlin HA, Roberts NA, Walthers DM;  
 XX  
 DR WPI; 2002-537132/57.  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
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 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
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 XX  
 SQ Sequence 20 BP; 5 A; 9 C; 2 G; 0 T; 4 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 20; DB 6; Length 20;  
 Best Local Similarity 80.0%; Pred. No. 0.061;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTTCGACCCCAACACTACTC 20  
 Db 1 TTTCGACCCCAACACTACTC 20  
 XX  
 RESULT 23  
 ABS65919  
 ID ABS65919 standard; DNA; 20 BP.  
 AC ABS65919;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #125.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; viraemia; cytostatic; antisense therapy;  
 KW gene therapy; ss; DNA-RNA hybrid.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002081577-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 02-JUL-1997; 97US-00887505.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
 XX  
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 XX  
 PI Kiluskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;



PI Hamlin HA, Roberts NA, Walther DM;  
XX  
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SQ Sequence 20 BP; 5 A; 9 C; 2 G; 0 T; 4 U; 0 Other;  
Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 80.0%; Pred. No. 0.061;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTGGGACCCCAACTACTC 20  
1 TTTGGGACCCCAACTACTC 20  
DB 1 UUCGGACCCCAACTACTC 20  
RESULT 24  
ABS65914  
ID ABS65914 standard; DNA; 20 BP.  
XX  
AC ABS65914;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Inhibitory oligonucleotide specific for hepatitis C virus #120.  
XX  
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
KW gene therapy; ss; DNA-RNA hybrid.  
XX  
OS Synthetic.  
XX  
PN US2002081577-A1.  
XX  
PD 27-JUN-2002.  
XX  
PF 02-JUL-1997; 97US-00887505.  
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XX  
SQ Sequence 20 BP; 5 A; 9 C; 2 G; 3 T; 1 U; 0 Other;  
Query Match 100.0%; Score 20; DB 6; Length 20;  
Best Local Similarity 95.0%; Pred. No. 0.061;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTGGGACCCCAACTACTC 20  
1 TTTGGGACCCCAACTACTC 20  
DB 1 TTGGGACCCCAACTACTC 20  
RESULT 25  
ABS65915  
ID ABS65915 standard; DNA; 20 BP.  
XX  
AC ABS65915;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Inhibitory oligonucleotide specific for hepatitis C virus #121.  
XX  
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
KW gene therapy; ss; DNA-RNA hybrid.  
XX  
OS Synthetic.  
XX  
PN US2002081577-A1.  
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PD 27-JUN-2002.  
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 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
 CC HCV replication and expression of HCV

SQ Sequence 20 BP; 5 A; 9 C; 2 G; 3 T; 1 U; 0 Other;

Query Match  
 Best Local Similarity 100.0%; Score 20; DB 6; Length 20;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGCGACCCACACTACTC 20  
 Db 1 TTCCGCGACCCACACTACTC 20

RESULT 26  
 ABS65822  
 ID ABS65822 standard; DNA; 20 BP.

AC ABS65822;

DT 15-NOV-2002 (first entry)

DE Inhibitory oligonucleotide specific for hepatitis C virus #28.

KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; vironcide; cytostatic; antisense therapy;  
 KW gene therapy; ss.

OS Synthetic.

PN US2002081577-A1.

PD 27-JUN-2002.

PF 02-JUL-1997; 97US-00887505.

PR 06-JUN-1995; 95US-00471968.

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WP; 2002-537132/57.  
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 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
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 CC replication and expression of HCV

SQ Sequence 20 BP; 5 A; 9 C; 2 G; 4 T; 0 U; 0 Other;

Query Match  
 Best Local Similarity 100.0%; Score 20; DB 6; Length 20;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGCGACCCACACTACTC 20  
 Db 1 TTCCGCGACCCACACTACTC 20

RESULT 27  
 AAT80285  
 ID AAT80285 standard; DNA; 24 BP.

AC AAT80285;

DT 15-OCT-1997 (first entry)

DE Oligo HCV34, targeted to HCV RNA RNase sensitive region.

KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KW inhibition; replication; expression; detection; chronic hepatitis;  
 KW acute hepatitis; hepatocarcinoma; ss.

OS Synthetic.

PN WO9639500-A2.

PD 12-DEC-1996.

PF 04-JUN-1996; 96WO-EP002427.

PR 06-JUN-1995; 95US-00471968.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PA (HYBR-) HYBRIDON INC.

PA (ROBE/) ROBERTS P. C.

PA (HAML/) HAMLIN H. A.

PA (ROBE/) ROBERTS N. A.

PA (WALT/) WALTHER D. M.

PI Kilkuskie R., Frank B., Goodchild J., Wolfe J., Roberts P.,

PI Hamlin H., Roberts N., Walther D.,

WP; 1997-043122/04.  
 Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
 the treatment and detection of HCV infection, esp. hepatitis and hepato-  
 carcinoma.

Claim 1, Page 26, 100pp; English.

The sequences given in AAT80211-382 represent synthetic oligonucleotides

CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This oligo was used in an RNase H assay to determine  
CC whether it binds successfully to its target. Three regions of HCV mRNA  
CC were investigated as RNase sensitive sites. This oligo binds to position  
CC -88 to -65  
XX  
SQ Sequence 24 BP; 5 A; 10 C; 4 G; 5 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.061;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGAGCCCAACACTACTC 20  
Db 3 TTGCGAGCCCAACACTACTC 22  
RESULT 28  
ABS65869  
ID ABS65869 standard; DNA; 24 BP.  
XX  
AC ABS65869;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Inhibitory oligonucleotide specific for hepatitis C virus #75.  
XX  
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
KM non-B hepatitis; acute hepatitis; chronic hepatitis;  
KM hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
KM gene therapy; ss.  
XX  
OS Synthetic.  
XX  
XX US2002081577-A1.  
PN  
XX  
PD 27-JUN-2002.  
XX  
XX 02-JUL-1997; 97US-00887505.  
PF  
XX  
PR 06-JUN-1995; 95US-00471968.  
PR 02-JUL-1996; 96US-0021104P.  
XX  
PA (KILIK/) KILIKUSKIE R L.  
PA (FRANK/) FRANK B L.  
PA (GOOD/) GOODCHILD J.  
PA (WOLF/) WOLFE J L.  
PA (ROBE/) ROBERTS P C.  
PA (HAML/) HAMLIN H A.  
PA (ROBE/) ROBERTS N A.  
PA (WALT/) WALTHER D M.  
PI Kiliuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,  
PI Hamlin HA, Roberts NA, Walther DM;  
XX  
DR WPI; 2002-537132/57.  
XX  
XX Synthetic oligonucleotides complementary to a portion of the 5'  
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
PT treating HCV infections and hepatocellular carcinoma.  
XX  
XX  
PS Claim 1; Page 9; 74pp; English.  
XX  
XX The invention describes synthetic oligonucleotides complementary to a  
CC portion of the 5' untranslated region of hepatitis C virus. The  
CC oligonucleotides may be used in methods for controlling, preventing, and  
CC treating hepatitis C virus infection, in antisense technology and gene

CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
CC -B, acute and chronic hepatitis, and has been associated with  
CC hepatocellular carcinoma. The invention describes methods and kits for  
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic oligonucleotide used for inhibiting HCV  
CC replication and expression of HCV  
XX  
SQ Sequence 24 BP; 5 A; 10 C; 4 G; 5 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.061;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGAGCCCAACACTACTC 20  
Db 3 TTGCGAGCCCAACACTACTC 22  
RESULT 29  
AAA74631  
ID AAA74631 standard; DNA; 25 BP.  
XX  
AC AAA74631;  
XX  
DT 08-JAN-2001 (first entry)  
XX  
DE HCV probe C252-25-PRB.  
XX  
XX Hepatitis C virus; HCV; HCV detection; probe; ss.  
KM  
XX  
OS Hepatitis C virus.  
OS  
XX  
PN EP1026262-A2.  
XX  
PD 09-AUG-2000.  
XX  
XX 01-FEB-2000; 2000EP-00300763.  
PF  
XX  
PR 03-FEB-1999; 99US-0118497P.  
XX  
PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
XX  
XX Linnen JM, Gorman KM;  
PI  
XX  
DR WPI; 2000-507254/46.  
XX  
XX  
PT Detecting hepatitis C virus in biological sample involves amplifying  
PT reverse transcribed products of virus RNA using amplification primers  
PT whose sequences correspond to 5' or 3' non-coding region of the virus  
PT RNA.  
XX  
PS Claim 30; Page 27; 28pp; English.  
XX  
XX The present sequence is a probe used in a method for detecting hepatitis  
CC C virus (HCV) RNA in biological samples. The HCV RNA is reverse  
CC transcribed to generate cDNA. This is then amplified with primers  
CC corresponding to the 5' or 3' non-coding region of HCV. The product was  
CC captured by hybridisation to oligonucleotide probes, including the  
CC present sequence, which were covalently attached to latex particles and  
CC deposited on the surface of a flow through membrane. The probe/product  
CC complex was reacted with streptavidin-horseradish peroxidase conjugate,  
CC which catalyses the oxidative conversion of a dye precursor to a blue  
CC dye. The method is useful for the diagnosis of HCV infection in patients,  
CC in testing the efficacy of anti-HCV therapeutic regimes, and in screening  
CC blood for HCV-infected samples. The method provides an improved single-  
CC round, reverse transcription/amplification assay which detects low copy  
CC levels of HCV RNA. The primers and assay system are designed to allow the  
CC co-amplification of multiple regions of the HCV genome, multiple viral  
CC species, and an internal positive control (IPC) RNA (or DNA).  
CC Simultaneous amplification/detection of multiple regions of the HCV

CC genome increases assay sensitivity and the co-amplification of an IPC  
 CC decreases the likelihood of false negative results because of PCR  
 CC inhibition

XX SQ Sequence 25 BP; 5 A; 10 C; 4 G; 6 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 20; DB 3; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0.061;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCACTACTC 20  
 2 TTGCGAGCCCACTACTC 21

Db

RESULT 30  
 AAT80341  
 ID AAT80341 standard; DNA; 26 BP.  
 XX  
 AC AAT80341;  
 XX  
 DT 16-OCT-1997 (first entry)  
 XX  
 DE Oligo HCV-1ss1, targeted to HCV mRNA position -67 to -86.  
 XX  
 KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KW inhibition; replication; expression; detection; chronic hepatitis;  
 KW acute hepatitis; hepatocarcinoma; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..20  
 FT /tag= a  
 FT /note= "Comprises phosphorothioate linkages"  
 FT stem\_loop 10..26  
 FT /tag= b  
 FT misc\_feature 21..26  
 FT /tag= c  
 FT /note= "Nucleotides included for the purpose of base  
 FT pairing, not complementary to the target sequence"  
 XX  
 PN WO9639500-A2.  
 XX  
 PD 12-DEC-1996.  
 XX  
 PF 04-JUN-1996; 96MO-EP002427.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 XX  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 PA (HYBR-) HYBRIDON INC.  
 XX  
 PI Frank BL, Goodchild J, Hamlin HA, Kiluskie RE, Roberts NA;  
 PI Roberts PC, Walther DM, Wolfe JL;  
 XX  
 DR WPI; 1997-043122/04.  
 XX  
 PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
 PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
 PT carcinoma.  
 XX  
 PS Claim 1; Page 19; 100pp; English.  
 XX  
 CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
 CC which are complementary to a portion of the 5' untranslated region (UTR)  
 CC of hepatitis C virus (HCV). These sequences may be used in a  
 CC pharmaceutical composition for the control or prevention of HCV  
 CC infection. They may be used to inhibit replication or expression of HCV  
 CC or for detecting the presence of HCV in a sample. They may be used to  
 CC inhibit HCV replication in a cell and are therefore useful in the  
 CC treatment of HCV infections such as chronic and acute hepatitis and  
 CC hepatocarcinoma

XX SQ Sequence 26 BP; 5 A; 9 C; 5 G; 7 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 20; DB 2; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 0.06;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCACTACTC 20  
 1 TTGCGAGCCCACTACTC 20

Db

RESULT 31  
 ABS65925  
 ID ABS65925 standard; DNA; 26 BP.  
 XX  
 AC ABS65925;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #131.  
 XX  
 KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KW gene therapy; ss.  
 XX  
 OS Synthetic.  
 XX  
 FN US2002081577-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 02-JUL-1997; 97US-00887505.  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
 XX  
 PA (KILK) KILUSKIE R L.  
 PA (FRAN) FRANK B L.  
 PA (GOOD) GOODCHILD J.  
 PA (WOLF) WOLFE J L.  
 PA (ROBE) ROBERTS P C.  
 PA (HAML) HAMLIN H A.  
 PA (ROBE) ROBERTS N A.  
 PA (WALT) WALTHER D M.  
 XX  
 PI Kiluskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
 PI Hamlin HA, Roberts NA, Walther DM;  
 XX  
 DR WPI; 2002-537132/57.  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.  
 XX  
 PS Claim 1; Page 6; 74pp; English.  
 XX  
 CC The invention describes synthetic oligonucleotides complementary to a  
 CC portion of the 5' untranslated region of hepatitis C virus. The  
 CC oligonucleotides may be used in methods for controlling, preventing, and  
 CC treating hepatitis C virus infection, in antisense technology and gene  
 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic oligonucleotide used for inhibiting HCV  
 CC replication and expression of HCV  
 XX  
 SQ Sequence 26 BP; 5 A; 9 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 0.06;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
 |||||  
 DB 1 TTGGGACCCCACTACTC 20

RESULT 32  
 AAA96562  
 ID AAA96562 standard; DNA; 27 BP.  
 AC AAA96562;  
 XX 08-FEB-2001 (first entry)  
 DE Nucleotide sequence of a probe specific for HCV.  
 KM HCV, HIV, viral detection; probe; ss.  
 XX  
 OS Hepatitis C virus.  
 XX CA2296044-A1.  
 PN 03-AUG-2000.  
 PD 01-FEB-2000; 2000CA-02296044.  
 PF 03-FEB-1999; 99US-0118498P.  
 PR (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
 PA Linen JM, Song K, Patterson DR, Gorman KM;  
 PI WPI, 2000-594741/57.  
 DR New methods for the simultaneous detection of hepatitis C virus and human  
 PT immunodeficiency virus in biological samples from humans.  
 XX  
 PS Claim 7; Page 23; 45pp; English.  
 CC The specification describes a method for co-detecting Hepatitis C Virus  
 CC (HCV) RNA and human immunodeficiency virus (HIV) RNA in a biological  
 CC sample. The method uses HCV and HIV specific reverse transcription  
 CC primers, either separately or in combination. The reverse transcribed  
 CC products are then amplified using primers specific for the 5' noncoding  
 CC region of HCV and/or HIV. The presence of specific products indicates the  
 CC presence of the appropriate RNA in the sample. The method is used for the  
 CC simultaneous detection of the presence of HCV RNA and HIV RNA in a  
 CC sample. The present sequence represents a probe specific for HCV  
 XX  
 SQ Sequence 27 BP; 5 A; 12 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.06;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
 |||||  
 DB 4 TTGGGACCCCACTACTC 23

RESULT 33  
 AAA91665/C  
 ID AAA91665 standard; RNA; 27 BP.  
 AC AAA91665;  
 XX 03-JAN-2001 (first entry)  
 DT HCV(-) RNA oligonucleotide.  
 XX

XX Hepatitis C virus; HCV, HCV RNA replication inhibitor; ribozyme;  
 KM antiviral; ss.  
 XX  
 XX Hepatitis C virus.  
 OS  
 XX US6107028-A.  
 PN 22-AUG-2000.  
 PD 15-MAY-1996; 96US-00648272.  
 PF 14-DEC-1994; 94US-00357508.  
 PR 07-JUN-1995; 95US-00476257.  
 PR 11-SEP-1995; 95US-00534220.  
 XX  
 PA (UNIW ) UNIV WASHINGTON.  
 XX  
 PI Lieber A, Kay MA;  
 DR WPI, 2000-578530/54.  
 DR  
 XX  
 PT Inhibiting hepatitis C viral RNA replication in an infected cell for  
 PT treating or preventing viral infection, comprises introducing ribozymes  
 PT specific for a minus strand of the viral 5' non-coding sequence.  
 XX  
 PS Example 2; Col 17; 28pp; English.  
 XX  
 CC The present sequence is an oligonucleotide which was used for in solution  
 CC hybridization to quantitate hepatitis C virus (HCV) RNA following  
 CC ribozyme expression. Ribozymes were identified that can specifically  
 CC cleave HCV RNA in a HCV 5' non-coding sequence, the capsid sequence, the  
 CC NS-5 sequence or any other conserved region of the hepatitis C RNA.  
 CC Ribozymes may be introduced into a cell infected with HCV in order to  
 CC inhibit HCV RNA replication or expression. Unlike prior art compositions  
 CC and methods, compositions comprising these ribozymes effectively reduce  
 CC and eradicate HCV from the infected cells and significantly impair the  
 CC ability of the virus to replicate, thus preventing further dissemination  
 CC of the disease. The composition is inherently specific for HCV and has  
 CC negligible toxicity  
 XX  
 SQ Sequence 27 BP; 6 A; 4 C; 12 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.06;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
 |||||  
 DB 24 TTGGGACCCCACTACTC 5

RESULT 34  
 AAA74630  
 ID AAA74630 standard; DNA; 27 BP.  
 AC AAA74630;  
 XX 08-JAN-2001 (first entry)  
 DT HCV probe C252-27-PRB.  
 XX  
 DE HCV probe C252-27-PRB.  
 XX  
 KM Hepatitis C virus; HCV, HCV detection; probe; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN EP1026262-A2.  
 PD 09-AUG-2000.  
 PF 01-FEB-2000; 2000EP-00300763.  
 PR 03-FEB-1999; 99US-0118497P.  
 XX

```

XX PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX PT
XX FI Linmen JM, Gorman KM;
XX DR WPI; 2000-507254/46.
XX PT
XX PT Detecting hepatitis C virus in biological sample involves amplifying
XX PT reverse transcribed products of virus RNA using amplification primers
XX PT whose sequences correspond to 5' or 3' non-coding region of the virus
XX PT RNA.
XX PS Claim 30; Page 27; 28pp; English.
XX CC
XX CC The present sequence is a probe used in a method for detecting hepatitis
XX CC C virus (HCV) RNA in biological samples. The HCV RNA is reverse
XX CC transcribed to generate cDNA. This is then amplified with primers
XX CC corresponding to the 5' or 3' non-coding region of HCV. The product was
XX CC captured by hybridisation to oligonucleotide probes, including the
XX CC present sequence, which were covalently attached to latex particles and
XX CC deposited on the surface of a flow through membrane. The probe/product
XX CC complex was reacted with streptavidin-horse radish peroxidase conjugate,
XX CC which catalyses the oxidative conversion of a dye precursor to a blue
XX CC dye. The method is useful for the diagnosis of HCV infection in patients,
XX CC in testing the efficacy of anti-HCV therapeutic regimens, and in screening
XX CC blood for HCV-infected samples. The method provides an improved single-
XX CC round, reverse transcription/amplification assay which detects low copy
XX CC levels of HCV RNA. The primers and assay system are designed to allow the
XX CC co-amplification of multiple regions of the HCV genome, multiple viral
XX CC species, and an internal positive control (IPC) RNA (or DNA).
XX CC Simultaneous amplification/detection of multiple regions of the HCV
XX CC genome increases assay sensitivity and the co-amplification of an IPC
XX CC decreases the likelihood of false negative results because of PCR
XX CC inhibition
XX SQ Sequence 27 BP; 5 A; 12 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 3; Length 27;
XX Best Local Similarity 100.0%; Pred. No. 0.06;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TTTCGGACCCCAACTACTC 20
XX Db 4 TTTCGGACCCCAACTACTC 23
XX
XX RESULT 35
XX ABA9710/c
XX ID ABA9710 standard; RNA; 27 BP.
XX AC
XX AC ABA9710;
XX XX
XX DT 07-AUG-2003 (revised)
XX DT 06-JUN-2002 (first entry)
XX XX
XX DE HCV sub-domain IIId polymorphic fragment IIId_gc.pdb.
XX XX
XX KW Sub-domain IIId; screening; internal ribosome entry site; IRES; virucide;
XX KW molecular modelling; hepatitis C infection; protein co-ordinate data; ss.
XX XX
XX OS Hepatitis C virus.
XX XX
XX Key Location/Qualifiers
XX FH stem_loop 1..27
XX FT /*tag= a
XX FT
XX FT misc_binding 1..3
XX FT /*tag= b
XX FT /bound_molety= "IIId_gc.pdb"
XX FT /note= "This region binds to nucleotides 27 to 25,
XX FT forming a stem loop structure"
XX FT 9..11
XX FT /*tag= c
XX FT /bound_molety= "IIId_gc.pdb"

```

```

XX FT
XX FT /note= "This region binds to nucleotides 20 to 18,
XX FT forming a stem loop structure"
XX FT 18..20
XX FT /*tag= d
XX FT /bound_molety= "IIId_gc.pdb"
XX FT /note= "This region binds to nucleotides 11 to 9, forming
XX FT a stem loop structure"
XX FT 25..27
XX FT /*tag= e
XX FT /bound_molety= "IIId_gc.pdb"
XX FT /note= "This region binds to nucleotides 3 to 1, forming
XX FT a stem loop structure"
XX FT
XX PN W0200181627-A2.
XX XX
XX PD 01-NOV-2001.
XX XX
XX XX 26-APR-2001; 2001WC-GB001871.
XX XX
XX XX 26-APR-2000; 2000GB-00010173.
XX XX
XX XX 26-APR-2000; 2000US-019773P.
XX XX
XX PA (RIBO-) RIBOTARGETS LTD.
XX XX
XX PI Kinick R, Walker S, Afshar M, Collier A, Aboul-Ela F, Westhof E;
XX XX
XX DR WPI; 2002-062037/08.
XX XX
XX PT Identifying compound that interacts with hepatitis C virus internal
XX PT ribosome entry site sub-domain IIId, comprises providing atomic co-
XX PT ordinates of domain in computer storage medium, applying molecular
XX PT modeling techniques.
XX XX
XX PS Disclosure; Fig 6; 56pp; English.
XX XX
XX CC This invention describes a novel in silico method, for identifying a
XX CC compound that interacts with sub-domain IIId of the hepatitis C virus
XX CC (HCV) internal ribosome entry site (IRES). The method comprises providing
XX CC atomic co-ordinates of the sub-domain IIId in a storage medium on a
XX CC computer, and using the computer to apply molecular modelling techniques
XX CC to the co-ordinates. The compounds identified by the method of the
XX CC invention are useful in an assay for displacement from a fragment of the
XX CC HCV IRES, by contacting the compound with the HCV IRES and assaying the
XX CC interaction between them. The products of the invention also have
XX CC manufacture of a medicament for treating hepatitis C infection, and for
XX CC treating hepatitis C infection. This sequence represents the Hepatitis c
XX CC virus IRES sub-domain IIId fragment IIId_gc.pdb which is used to
XX CC illustrate the method of the invention. (Updated on 07-AUG-2003 to
XX CC correct OS field.)
XX XX
XX SQ Sequence 27 BP; 5 A; 5 C; 12 G; 0 T; 5 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 6; Length 27;
XX Best Local Similarity 100.0%; Pred. No. 0.06;
XX Matches 20; Conservative 100; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TTTCGGACCCCAACTACTC 20
XX Db 23 TTTCGGACCCCAACTACTC 4
XX
XX RESULT 36
XX ABA9715/c
XX ID ABA9715 standard; RNA; 27 BP.
XX AC
XX AC ABA9715;
XX XX
XX DT 07-AUG-2003 (revised)
XX DT 06-JUN-2002 (first entry)
XX XX
XX DE HCV sub-domain IIId loop fragment RNA.
XX XX

```

Query Match	Best Local Similarity	100.0%	Score 20;	DB 6;	Length 27;
Matches	20;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0

1 TTCGGACCAACTACTC 20

```

Db          23 TTGGGAGCCCAACTACTCTC 4
|||||
RESULT 37
AAL53726/c
ID AAL53726 standard; RNA; 27 BP.
XX
AC AAL53726;
XX
DT 27-OCT-2003 (revised)
DT 07-FEB-2003 (first entry)
XX
DE Hepatitis C Virus target motif SEQ ID NO 20.
XX
KW Target RNA; target RNA:support-attached test compound; flow cytometry;
KM mass spectrometry; high-throughput screening; RNA motif; ss.
XX
OS Hepatitis C virus; Virus.
XX
WO200283837-A1.
XX
EN 24-OCT-2002.
XX
PD 11-APR-2002; 2002MO-US011758.
XX
PF 11-APR-2001; 2001US-0282966P.
XX
PR 11-APR-2001; 2001US-0282966P.
XX
PA (PTCT-) PTC THERAPEUTICS INC.
PI Alimstead NG;
XX
DR WPI; 2003-075534/07.
XX
PT Identifying a test compound that binds to a target RNA molecule by
PT separating the detectably labeled target RNA:support-attached test
PT compound complex from uncomplexed target RNA molecules and test compounds
PT by flow cytometry.
XX
PS Example; Page 60; 131pp; English.
XX
CC The invention relates to a novel method for identifying a test compound
CC that binds to a target RNA molecule comprising separating the detectably
CC labeled target RNA:support-attached test compound complex from
CC uncomplexed target RNA molecules and test compounds. The separating
CC process is carried out by flow cytometry and determining a structure of
CC the type of test compound of the RNA:support-attached test compound
CC complex by mass spectrometry. The method is useful for high-throughput
CC screening of libraries of compounds to identify pharmaceutical leads.
CC This polynucleotide sequence represents one of the target RNA motifs/
CC regions of the invention. (Updated on 27-Oct-2003 to standardise OS
CC field)
XX
SO Sequence 27 BP; 5 A; 5 C; 12 G; 0 T; 5 U; 0 Other;
Query Match 100.0%; Score 20; DB 8; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1 TTGGGAGCCCAACTACTCTC 20
DB 23 TTGGGAGCCCAACTACTCTC 4
|||||
RESULT 38
AAD49658/c
ID AAD49658 standard; RNA; 27 BP.
XX
AC AAD49658;
XX
DT 24-MAR-2003 (first entry)
DT Hepatitis C virus internal ribosome entry site subdomain IIId RNA.
DE

```

XX Amyloidosis; haemophilia; Alzheimer's disease; atherosclerosis; cancer;  
 KW gigantism; dwarfism; hypothyroidism; hyperthyroidism; cystic fibrosis;  
 KW autoimmune disorder; aging; inflammation; diabetes; obesity; anorectic;  
 KW neurodegenerative disorder; Parkinson's disease; gene therapy; virucide;  
 KW haemostatic; antibacterial; nootropic; neuroprotective; cytosolic; HCV;  
 KW fungicide; Hepatitis C virus; internal ribosome entry site; IRES; ss.  
 XX Hepatitis C virus.  
 OS  
 XX WO200283953-A1.  
 XX  
 XX 24-OCT-2002.  
 XX  
 XX 11-APR-2002; 2002WO-US011757.  
 XX  
 XX 11-APR-2001; 2001US-0282965P.  
 XX  
 XX (PCT-) PTC THERAPEUTICS INC.  
 XX  
 XX Rando R, Welch E;  
 XX  
 XX WPI; 2003-075561/07.  
 XX  
 XX  
 PT Identifying a test compound that binds to a target RNA molecule for  
 PT treating or preventing amyloidosis, hemophilia, cancer, gigantism,  
 PT diabetes, by contacting a detectably labeled target RNA molecule with a  
 PT library of test compounds.  
 XX  
 XX  
 XX Example; Page 69; 152pp; English.  
 XX  
 CC The invention relates to a method for identifying a test compound that  
 CC binds to a target RNA molecule, which comprises contacting a detectably  
 CC labelled target RNA molecule with a library of test compounds under  
 CC conditions that permit direct binding of the labelled target RNA to a  
 CC member of the library of test compounds so that a detectably labeled  
 CC target RNA-test compound complex is formed. The method is useful for  
 CC screening libraries of compounds for those that are selectively bind to a  
 CC pre-selected target RNA. The compounds are useful for inhibiting the  
 CC formation of a specific bound RNA: host cell factor complexes in vivo.  
 CC They are also useful for treating or preventing diseases associated with  
 CC overproduction or decreased protein function, such as amyloidosis,  
 CC haemophilia, Alzheimer's disease, atherosclerosis, cancer, gigantism,  
 CC inflammation, hypothyroidism, hyperthyroidism, autoimmune disorders, aging,  
 CC disorders, Parkinson's disease or infections (bacterial, viral, fungal).  
 CC The invention is also used in gene therapy. The present sequence is  
 CC Hepatitis C virus (HCV) internal ribosome entry site (IRES) subdomain  
 CC I11d RNA. This sequence is used to illustrate the method of the invention  
 CC  
 SQ Sequence 27 BP; 5 A; 5 C; 12 G; 0 T; 5 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 8; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.06;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 23 TTGCGACCCCAACTACTC 4  
 RESULT 39  
 ADB85926/c  
 ID ADB85926 standard; RNA; 27 BP.  
 XX  
 XX ADB85926;  
 XX  
 XX 29-JAN-2004 (first entry)  
 XX  
 XX Stem-loop forming RNA from HCV subdomain I11d.  
 XX  
 XX Toll-like receptor; immunostimulant; antimicrobial; antiallergic;  
 KM cytosolic; vaccine; HCV; ss.

XX Hepatitis C virus.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FT stem\_loop 1..27  
 FT /\*tag= a  
 XX  
 XX WO2003086280-A2.  
 XX  
 XX 23-OCT-2003.  
 XX  
 XX 04-APR-2003; 2003WO-US010406.  
 XX  
 XX 04-APR-2002; 2002US-0370515P.  
 XX  
 XX 29-OCT-2002; 2002US-0421966P.  
 XX  
 XX (COLE-) COLEY PHARM GMBH.  
 XX  
 XX Lipford G, Bauer S;  
 XX  
 XX WPI; 2003-845251/78.  
 XX  
 XX  
 PT New immunostimulatory composition, useful in inducing an immune response  
 PT against microbial or cancer antigen or allergen.  
 XX  
 XX Disclosure; SEQ ID NO 4; 220pp; English.  
 XX  
 CC The present sequence is that of a stem-loop forming 27-mer from hepatitis  
 CC C virus (HCV) subdomain I11d. This sequence has been reported to be  
 CC critical in HCV internal ribosome entry site (IRES)-mediated translation.  
 CC The invention relates to immunostimulatory RNA oligomers that contain at  
 CC least one guanine and at least one uracil. Such immunostimulatory RNAs  
 CC are known to occur in the context of an IRES. Claimed immunostimulatory  
 CC RNA oligomers are thought to signal through an MyD88-dependent pathway,  
 CC probably through Toll-like receptor (TLR) 7 or TLR8, and are believed to  
 CC be ligands of TLR7 or TLR8. Claimed immunostimulatory compositions  
 CC comprise a G-U-containing RNA oligomer and optionally an antigen,  
 CC especially an allergen, cancer antigen or microbial antigen. Methods are  
 CC provided for activating an immune cell, inducing an immune response,  
 CC stimulating TLR8 or TLR7 signaling, and supplementing a TLR8- or TLR7-  
 CC mediated immune response. The methods and compositions are useful for  
 CC activating immune cells in vivo, in vitro and ex vivo, treating  
 CC infection, treating cancer, identifying a target receptor, and screening  
 CC for additional immunostimulatory compounds.  
 CC  
 SQ Sequence 27 BP; 5 A; 5 C; 12 G; 0 T; 5 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 10; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 0.06;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 23 TTGCGACCCCAACTACTC 4  
 RESULT 40  
 AAT80278  
 ID AAT80278 standard; DNA; 28 BP.  
 XX  
 XX AAT80278;  
 XX  
 XX 15-OCT-1997 (first entry)  
 XX  
 XX Oligo HCV36, targeted to HCV mRNA RNase sensitive region.  
 XX  
 XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KM inhibition; replication; expression; detection; chronic hepatitis;  
 XX acute hepatitis; hepatocarcinoma; ss.  
 OS  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH



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FT modified_base 1..28
FT /tag= a
FT /note= "Comprises phosphorothioate linkages"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
XX
XX Frank BL, Goodchild J, Hamlin HA, Kilukskie RE, Roberts NA;
XX Roberts PC, Walther DM, Wolfe JL;
XX
XX WPI; 1997-043122/04.
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX carcinoma.
XX
XX Claim 1; Page 26; 100pp; English.
XX
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX which are complementary to a portion of the 5' untranslated region (UTR)
XX of hepatitis C virus (HCV). These sequences may be used in a
XX pharmaceutical composition for the control or prevention of HCV
XX infection. They may be used to inhibit replication or expression of HCV
XX or for detecting the presence of HCV in a sample. They may be used to
XX inhibit HCV replication in a cell and are therefore useful in the
XX treatment of HCV infections such as chronic and acute hepatitis and
XX hepatocarcinoma. This oligo was used in an RNase H assay to determine
XX whether it binds successfully to its target. Three regions of HCV mRNA
XX were investigated as RNase sensitive sites. This oligo binds to position
XX -94 to -67
XX
XX Sequence 28 BP; 7 A; 11 C; 5 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 28;
XX Best Local Similarity 100.0%; Pred. No. 0.06;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TTGCGGACCCCAACTACTC 20
XX 1 TTGCGGACCCCAACTACTC 20
XX
XX Db 1 TTGCGGACCCCAACTACTC 20
XX
XX RESULT 41
XX AAT80284
XX ID AAT80284 standard; DNA; 28 BP.
XX
XX AC AAT80284;
XX
XX DT 15-OCT-1997 (first entry)
XX
XX DE Oligo HCV35, targeted to HCV mRNA RNase sensitive region.
XX
XX KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX inhibition; replication; expression; detection; chronic hepatitis;
XX acute hepatitis; hepatocarcinoma; ss.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..28
XX /tag= a
XX /note= "Comprises phosphorothioate linkages"
XX
XX WO9639500-A2.
XX

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PD 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
XX
XX Frank BL, Goodchild J, Hamlin HA, Kilukskie RE, Roberts NA;
XX Roberts PC, Walther DM, Wolfe JL;
XX
XX WPI; 1997-043122/04.
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX carcinoma.
XX
XX Claim 1; Page 26; 100pp; English.
XX
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX which are complementary to a portion of the 5' untranslated region (UTR)
XX of hepatitis C virus (HCV). These sequences may be used in a
XX pharmaceutical composition for the control or prevention of HCV
XX infection. They may be used to inhibit replication or expression of HCV
XX or for detecting the presence of HCV in a sample. They may be used to
XX inhibit HCV replication in a cell and are therefore useful in the
XX treatment of HCV infections such as chronic and acute hepatitis and
XX hepatocarcinoma. This oligo was used in an RNase H assay to determine
XX whether it binds successfully to its target. Three regions of HCV mRNA
XX were investigated as RNase sensitive sites. This oligo binds to position
XX -90 to -63
XX
XX Sequence 28 BP; 5 A; 12 C; 5 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 28;
XX Best Local Similarity 100.0%; Pred. No. 0.06;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TTGCGGACCCCAACTACTC 20
XX 5 TTGCGGACCCCAACTACTC 24
XX
XX Db 5 TTGCGGACCCCAACTACTC 24
XX
XX RESULT 42
XX ABS65862
XX ID ABS65862 standard; DNA; 28 BP.
XX
XX AC ABS65862;
XX
XX DT 15-NOV-2002 (first entry)
XX
XX DE Inhibitory oligonucleotide specific for hepatitis C virus #68.
XX
XX KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
XX non-B hepatitis; acute hepatitis; chronic hepatitis;
XX hepatocellular carcinoma; virucide; cytostatic; antisense therapy;
XX gene therapy; ss.
XX
XX OS Synthetic.
XX
XX US2002081577-A1.
XX
XX PD 27-JUN-2002.
XX
XX PF 02-JUL-1997; 97US-00887505.
XX
XX PR 06-JUN-1995; 95US-00471968.
XX 02-JUL-1996; 96US-0021104P.
XX
XX (KILK/) KILKUSKIE R L.
XX (FRAN/) FRANK B L.
XX (GOOD/) GOODCHILD J.
XX

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PA (WOLFE/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.  
 PA (HAML/) HAMLIN H A.  
 PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.  
 PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,  
 PI Hamlin HA, Roberts NA, Walther DM;  
 DR WPI: 2002-537132/57.  
 XX  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.  
 XX  
 XX  
 PS Claim 1; Page 9; 74pp; English.  
 CC The invention describes synthetic oligonucleotides complementary to a  
 CC portion of the 5' untranslated region of hepatitis C virus. The  
 CC oligonucleotides may be used in methods for controlling, preventing, and  
 CC treating hepatitis C virus infection, in antisense technology and gene  
 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic oligonucleotide used for inhibiting HCV  
 CC replication and expression of HCV  
 SO Sequence 28 BP; 7 A; 11 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 28;  
 Best Local Similarity 100.0%; Pred. NO. 0.06;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 1 TTGCGACCCCAACTACTC 20  
 RESULT 43  
 ID ABS65868 standard; DNA; 28 BP.  
 AC ABS65868;  
 XX  
 XX  
 DT 15-NOV-2002 (first entry)  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #74.  
 XX  
 XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KW gene therapy; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 XX US2002081577-A1.  
 XX  
 XX  
 PD 27-JUN-2002.  
 XX  
 XX  
 PF 02-JUL-1997; 97US-00887505.  
 XX  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
 XX  
 XX (KILK/) KILKUSKIE R L.  
 PA (FRAN/) FRANK B L.  
 PA (GOOD/) GOODCHILD J.  
 PA (WOLFE/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.

PA (HAML/) HAMLIN H A.  
 PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.  
 XX  
 XX  
 PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,  
 PI Hamlin HA, Roberts NA, Walther DM;  
 DR WPI: 2002-537132/57.  
 XX  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.  
 XX  
 XX  
 PS Claim 1; Page 9; 74pp; English.  
 CC The invention describes synthetic oligonucleotides complementary to a  
 CC portion of the 5' untranslated region of hepatitis C virus. The  
 CC oligonucleotides may be used in methods for controlling, preventing, and  
 CC treating hepatitis C virus infection, in antisense technology and gene  
 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic oligonucleotide used for inhibiting HCV  
 CC replication and expression of HCV  
 SO Sequence 28 BP; 5 A; 12 C; 5 G; 6 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 28;  
 Best Local Similarity 100.0%; Pred. NO. 0.06;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 5 TTGCGACCCCAACTACTC 24  
 RESULT 44  
 ID ABK15311/c  
 AC ABK15311;  
 XX  
 XX  
 DT 08-MAY-2002 (first entry)  
 DE Hepatitis C virus IRES element domain IIId RNA sequence.  
 XX  
 XX Hepatitis C virus; HCV; internal ribosome entry site element; IRES; ss;  
 KW 40S ribosome subunit; domain IIId; domain IIIE.  
 XX  
 XX Hepatitis C virus.  
 OS  
 XX  
 XX  
 FH Key  
 FT stem\_loop  
 FT 1..29  
 FT /tag= a  
 FT 5..88  
 FT /tag= c  
 FT /note= "Forms characteristic S turn in backbone"  
 FT 5..25  
 FT /tag= b  
 FT /note= "Form sheared base pair"  
 FT 6..24  
 FT /tag= d  
 FT /note= "Form parallel base pair"  
 FT 7  
 FT /tag= e  
 FT /note= "Bulged residue; forms a base triple with reversed  
 FT Hoogsteen pair (residues 8 and 23)"  
 FT 8..23  
 FT /tag= f

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FT FT      /note= "Form reverse Hoogsteen base pair"
FT FT      9..22
FT FT      /tag= h
FT FT      /note= "Form sheared base pair"
FT FT      9
FT FT      /tag= g
FT FT      /note= "Minor groove exposed Watson-Crick face"
FT FT      13..18
FT FT      /tag= i
FT FT      /note= "Hairpin loop"
FT FT      23
FT FT      /tag= j
FT FT      /note= "Minor groove exposed Watson-Crick face"
FT FT      24
FT FT      /tag= k
FT FT      /note= "Minor groove exposed Watson-Crick face"
FT FT      25
FT FT      /tag= l
FT FT      /note= "Minor groove exposed Watson-Crick face"
XX PN      WO200203919-A2.
XX PD      17-JAN-2002.
XX PF      10-JUL-2001; 2001WO-US021871.
XX PR      10-JUL-2000; 2000US-0217673P.
XX PA      (STRD ) UNIV LELAND STANFORD JUNIOR.
XX PI      Puglisi JD;
XX DR      WPI; 2002-179655/23.
XX FT      Computer for producing a three dimensional representation of a molecule
XX PT      hepatitis C virus entry site element comprises a machine-readable device,
XX XX      data storage medium, working memory, central processing unit and display.
XX PS      Claim 3; Fig 1c; 39pp; English.
XX CC      The present invention relates to a new computer for producing three
XX CC      dimensional representation of a molecule. The computer of the invention
XX CC      comprises a machine-readable data storage medium, a working memory for
XX CC      storing instructions, a central processing unit coupled to the working
XX CC      memory and machine-readable data storage medium and a display coupled to
XX CC      the central processing unit. The molecule comprises a hepatitis C virus
XX CC      (HCV) internal ribosomal entry site (IRES) element. The invention is
XX CC      useful for producing a three dimensional representation of a molecule
XX CC      comprising hepatitis virus C IRES element, for identifying potential
XX CC      inhibitors of hepatitis C virus translation and for modelling
XX CC      interactions of the IRES with its binding partner, the 40S ribosome
XX CC      subunit. The computer generates the three-dimensional graphical
XX CC      representations of molecules or their portions from a set of structure co-
XX CC      ordinates and displays graphical three-dimensional representation of the
XX CC      HCV IRES stem loops in at least one of domain IId or IIId. The
XX CC      structural data permits the identification of atoms that are important
XX CC      for 40S ribosomal subunit binding. The present nucleic acid sequence
XX CC      represents the hepatitis C virus internal ribosome entry site element
XX CC      domain IId of the invention. This sequence represents residues 252-280
XX CC      of ABK15309
XX SQ      Sequence 29 BP; 5 A; 6 C; 13 G; 0 T; 5 U; 0 Other;
XX
XX Query Match      100.0%; Score 20; DB 6; Length 29;
XX Best Local Similarity 100.0%; Pred. No. 0.06;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY      1 TTGGGAGCCCAACTACTC 20
XX DB      24 TTGGGAGCCCAACTACTC 5

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ADCS4069/C
XX ID      ADCS4069 standard; DNA; 29 BP.
XX AC      ADCS4069;
XX XX
XX DT      18-DEC-2003 (first entry)
XX XX
XX DE      HCV 5'UTR signal amplification probe, SEQ ID NO:20.
XX XX
XX KW      HCV; hepatitis C virus; classification; interferon therapy; 5'UTR;
XX KW      signal amplification; probe; ss.
XX OS      Hepatitis C virus.
XX XX
XX PN      JP2002345467-A.
XX PD      03-DEC-2002.
XX PF      17-APR-2001; 2001JP-00118810.
XX PR      23-OCT-2000; 2000JP-00322567.
XX PA      (SRLS-) SRL KK.
XX XX
XX DR      WPI; 2003-460879/44.
XX XX
XX PT      Probe and method for classification of hepatitis C virus (HCV) types used
XX PT      for forecast of therapeutic effect of interferon administration.
XX XX
XX PS      Disclosure; SEQ ID NO 20; 15pp; Japanese.
XX XX
XX CC      The invention relates to a nucleic acid probe for the classification of
XX CC      hepatitis C virus (HCV) into 3 genotypes. The 3 HCV genotypes are H1, H2 and
XX CC      (type 1), H2a, H2b, H2c, H2d, H2e, H2f, H2g, H2h, H2i, H2j, H2k, H2l, H2m, H2n, H2o, H2p, H2q, H2r, H2s, H2t, H2u, H2v, H2w, H2x, H2y, H2z, H3, H4, H5, H6, H7, H8, H9, H10, H11, H12, H13, H14, H15, H16, H17, H18, H19, H20, H21, H22, H23, H24, H25, H26, H27, H28, H29, H30, H31, H32, H33, H34, H35, H36, H37, H38, H39, H40, H41, H42, H43, H44, H45, H46, H47, H48, H49, H50, H51, H52, H53, H54, H55, H56, H57, H58, H59, H60, H61, H62, H63, H64, H65, H66, H67, H68, H69, H70, H71, H72, H73, H74, H75, H76, H77, H78, H79, H80, H81, H82, H83, H84, H85, H86, H87, H88, H89, H90, H91, H92, H93, H94, H95, H96, H97, H98, H99, H100, H101, H102, H103, H104, H105, H106, H107, H108, H109, H110, H111, H112, H113, H114, H115, H116, H117, H118, H119, H120, H121, H122, H123, H124, H125, H126, H127, H128, H129, H130, H131, H132, H133, H134, H135, H136, H137, H138, H139, H140, H141, H142, H143, H144, H145, H146, H147, H148, H149, H150, H151, H152, H153, H154, H155, H156, H157, H158, H159, H160, H161, H162, H163, H164, H165, H166, H167, H168, H169, H170, H171, H172, H173, H174, H175, H176, H177, H178, H179, H180, H181, H182, H183, H184, H185, H186, H187, H188, H189, H190, H191, H192, H193, H194, H195, H196, H197, H198, H199, H200, H201, H202, H203, H204, H205, H206, H207, H208, H209, H210, H211, H212, H213, H214, H215, H216, H217, H218, H219, H220, H221, H222, H223, H224, H225, H226, H227, H228, H229, H230, H231, H232, H233, H234, H235, H236, H237, H238, H239, H240, H241, H242, H243, H244, H245, H246, H247, H248, H249, H250, H251, H252, H253, H254, H255, H256, H257, H258, H259, H260, H261, H262, H263, H264, H265, H266, H267, H268, H269, H270, H271, H272, H273, H274, H275, H276, H277, H278, H279, H280, H281, H282, H283, H284, H285, H286, H287, H288, H289, H290, H291, H292, H293, H294, H295, H296, H297, H298, H299, H300, H301, H302, H303, H304, H305, H306, H307, H308, H309, H310, H311, H312, H313, H314, H315, H316, H317, H318, H319, H320, H321, H322, H323, H324, H325, H326, H327, H328, H329, H330, H331, H332, H333, H334, H335, H336, H337, H338, H339, H340, H341, H342, H343, H344, H345, H346, H347, H348, H349, H350, H351, H352, H353, H354, H355, H356, H357, H358, H359, H360, H361, H362, H363, H364, H365, H366, H367, H368, H369, H370, H371, H372, H373, H374, H375, H376, H377, H378, H379, H380, H381, H382, H383, H384, H385, H386, H387, H388, H389, H390, H391, H392, H393, H394, H395, H396, H397, H398, H399, H400, H401, H402, H403, H404, H405, H406, H407, H408, H409, H410, H411, H412, H413, H414, H415, H416, H417, H418, H419, H420, H421, H422, H423, H424, H425, H426, H427, H428, H429, H430, H431, H432, H433, H434, H435, H436, H437, H438, H439, H440, H441, H442, H443, H444, H445, H446, H447, H448, H449, H450, H451, H452, H453, H454, H455, H456, H457, H458, H459, H460, H461, H462, H463, H464, H465, H466, H467, H468, H469, H470, H471, H472, H473, H474, H475, H476, H477, H478, H479, H480, H481, H482, H483, H484, H485, H486, H487, H488, H489, H490, H491, H492, H493, H494, H495, H496, H497, H498, H499, H500, H501, H502, H503, H504, H505, H506, H507, H508, H509, H510, H511, H512, H513, H514, H515, H516, H517, H518, H519, H520, H521, H522, H523, H524, H525, H526, H527, H528, H529, H530, H531, H532, H533, H534, H535, H536, H537, H538, H539, H540, H541, H542, H543, H544, H545, H546, H547, H548, H549, H550, H551, H552, H553, H554, H555, H556, H557, H558, H559, H560, H561, H562, H563, H564, H565, H566, H567, H568, H569, H570, H571, H572, H573, H574, H575, H576, H577, H578, H579, H580, H581, H582, H583, H584, H585, H586, H587, H588, H589, H590, H591, H592, H593, H594, H595, H596, H597, H598, H599, H600, H601, H602, H603, H604, H605, H606, H607, H608, H609, H610, H611, H612, H613, H614, H615, H616, H617, H618, H619, H620, H621, H622, H623, H624, H625, H626, H627, H628, H629, H630, H631, H632, H633, H634, H635, H636, H637, H638, H639, H640, H641, H642, H643, H644, H645, H646, H647, H648, H649, H650, H651, H652, H653, H654, H655, H656, H657, H658, H659, 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XX 08-MAY-1991; 91US-00697326.
XX (CHIR ) CHIRON CORP.
XX Cha T, Beall E, Irvine B, Kolberg J, Urdea MS,
XX WPI; 1992-398869/48.
XX
XX Compsn. comprising a non-hepatitis C virus-1 nucleotide sequence -
XX related to HCV-1, useful for treating and detecting HCV-1 infections and
XX as a vaccine.
XX
XX Claim 63; Page 140; 106pp; English.
XX
XX A sandwich hybridisation assay can be used for HCV-1 genotyping analysis.
XX One example uses nucleotide sequences which correspond to sequences in
XX the C gene and the 5' UT region of HCV isolates as either capture or
XX detection probes. Probe 126 is preferably used as a labelled probe.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 33 BP; 8 A; 13 C; 6 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 0.06;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TTGCGACCCCAACTACTC 20
XX 10 TTGCGACCCCAACTACTC 29
XX
XX Db
XX
XX RESULT 47
XX AAQ46463
XX ID AAQ46463 standard; DNA; 33 BP.
XX
XX AAQ46463;
XX
XX 25-MAR-2003 (revised)
XX 13-DEC-1993 (first entry)
XX
XX Hepatitis C virus RNA assay label probe HCV.33.8.
XX
XX Detection; HCV; reduced background signal; improved reproducibility;
XX hybridisation; 5'-untranslated region; C gene; ss.
XX
XX Synthetic.
XX
XX WO9313224-A1.
XX
XX 08-JUL-1993.
XX
XX 22-DEC-1992; 92WO-US011343.
XX
XX 23-DEC-1991; 91US-00813338.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Sheridan P, Chang C, Running J;
XX
XX WPI; 1993-227338/28.
XX
XX Immobilising nucleic acid probe on styreneI, useful for HCV sequence
XX detection - by using intermediate passively adsorbed polymer having
XX functional gps. for covalently bonding to probe via its base-stable
XX linkages.
XX
XX Example; Fig 3.1; 34pp; English.
XX
XX The sequence is that of a synthetic label probe which is complementary to
XX nucleotide sequences in the hepatitis C virus C gene and the 5'-
XX untranslated region. It may be used in an assay for the detection of HCV
XX RNA. (Updated on 25-MAR-2003 to correct PN field.)

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XX Sequence 33 BP; 8 A; 13 C; 6 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 0.06;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TTGCGACCCCAACTACTC 20
XX 10 TTGCGACCCCAACTACTC 29
XX
XX Db
XX
XX RESULT 48
XX AAV07837
XX ID AAV07837 standard; DNA; 33 BP.
XX
XX AAV07837;
XX
XX 27-AUG-2003 (revised)
XX 25-MAR-2003 (revised)
XX 10-DEC-1998 (first entry)
XX
XX HCV.33.8 amplifier probe.
XX
XX Comb-type branched polynucleotide; amplification multimer; analyte;
XX hybridisation assay; hepatitis C virus; HCV; amplifier probe; ss.
XX
XX Synthetic.
XX
XX Hepatitis C virus.
XX
XX US5710264-A.
XX
XX 20-JAN-1998.
XX
XX 07-JUN-1995; 95US-00478085.
XX
XX 27-JUL-1990; 90US-00558897.
XX 23-DEC-1991; 91US-00813588.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Chang C, Fultz TJ, Warner B, Urdea MS, Horn T;
XX
XX WPI; 1998-109872/10.
XX
XX New large comb-type branched polynucleotides - useful as amplification
XX multimers in nucleic acid hybridisation assays.
XX
XX Example 6; Col 25; 33pp; English.
XX
XX The invention relates to a large comb-type branched polynucleotide of
XX formula 3'-A-S-(S'-X')m-S'-5'; where X' is a branched site joined to -
XX (R)n-S'-E-L; A = an oligonucleotide complementary to an analyte nucleic
XX acid sequence; S = a first spacer segment of 1-50 linked monomers where
XX each monomer is selected from nucleotides and a cleavable linker R; S' =
XX a branching site spacer segment of 0-15 linked monomers where each of the
XX monomers is selected from nucleotides and cleavable linker R; X' = a
XX multifunctional nucleotide that provides a branch site; m = 1-100; S' =
XX a second spacer segment of 0-10 linked monomers where each of the
XX monomers is selected from nucleotides and cleavable linker R; R = a
XX cleavable linker molecule; n = 0 or 1; S'' = a third spacer segment of 0
XX -10 linked monomers where each of the monomers is selected from
XX nucleotides and cleavable linker R; E = an oligonucleotide segment of 5-
XX 10 nucleotides; L = an oligonucleotide containing 2-10 iterations of a
XX nucleotide sequence complementary to a labelled nucleic acid probe. The
XX invention also relates to a branched nucleic acid polymer. The poly-
XX nucleotides are useful as amplification multimers in nucleic acid
XX clinical diagnostics. Since the polynucleotide multimers include a large
XX number (at least 20) iterations of a sequence that are available for
XX specific hybridisation, they permit a greater degree of amplification and
XX decrease the threshold level of a detectable analyte. The present
XX sequence represents a hepatitis C virus (HCV) amplifier probe. (Updated

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CC on 25-MAR-2003 to correct PF field.) (Updated on 27-AUG-2003 to correct  
CC OS field.)

Sequence 33 BP; 8 A; 13 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.06;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 10 TTGGGACCCCAACTACTC 29

#### RESULT 49

AAV83065  
ID AAV83065 standard; DNA; 33 BP.

AC AAV83065;

DT 24-FEB-1999 (first entry)

DE Amplifier probe HCV.33.8.

XX Comb-type branched polynucleotide; amplifier probe;

KW multifunctional nucleotide; pendant polynucleotide, sidechain;

XX hybridisation assay; amplification multimer; sandwich assay; ss.

OS Synthetic.

XX Hepatitis C virus.

PN US5649481-A.

PD 15-DEC-1998.

PF 05-JUN-1995; 95US-00470124.

PR 27-JUL-1990; 90US-00558897.

PR 23-DEC-1991; 91US-00813586.

PA (CHIR ) CHIRON CORP.

PT Improved nucleic acid hybridisation assays - using large comb-type

PT polypeptide(s).

PS Example 6; Col 24; 31pp; English.

XX Oligonucleotides AAV83063-80 represent amplifier probes, used in a

CC sandwich hybridisation assay for Hepatitis C virus (HCV) DNA. The

CC sandwich hybridisation assay utilises the comb-type branched

CC polynucleotide amplification multimer of the invention. This large comb-

CC type branched polynucleotide comprises a polynucleotide backbone having

CC at least 15 multifunctional nucleotides each defining a sidechain having

CC and pendant polynucleotide sidechains extending from the multifunctional

CC nucleotides, each comprising iterations of an single stranded

CC oligonucleotide unit capable of binding specifically to a second single-

CC stranded polynucleotide sequence. The total number of iterations in all

CC sidechains is at least 20. The first single-stranded polynucleotide

CC sequence is a labelled polynucleotide, directly or indirectly linked to a

CC nucleic acid analyte. In the nucleic acid hybridisation assay of the

CC invention, the labelled nucleic acid probe is hybridised to the branched

CC polymeric nucleotide via the second single-stranded oligonucleotide unit.

CC The comb-type branched polynucleotides are used as amplification

CC multimers in nucleic acid hybridisation assays and other assays such as

CC direct, indirect and sandwich assays

XX Sequence 33 BP; 8 A; 13 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 33;

Best Local Similarity 100.0%; Pred. No. 0.06;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 10 TTGGGACCCCAACTACTC 29

#### RESULT 50

AAA86970/C  
ID AAA86970 standard; DNA; 40 BP.

AC AAA86970;

DT 15-JAN-2001 (first entry)

DE Probe for Hepatitis C.

XX Detection; nucleic acid hybrid; depolymerisation; analysis; SNP;

KW single nucleotide polymorphism; identification; viral load; probe;

XX genotyping; medical marker diagnostic; primer; target; mutation;

OS Hepatitis C virus.

PN WO200049180-A1.

PD 24-AUG-2000.

PF 18-FEB-2000; 2000MO-US004242.

PR 18-FEB-1999; 99US-00252436.

PR 21-JUL-1999; 99US-00358972.

PR 25-AUG-1999; 99US-00383316.

PA (PROM-) PROMEGA CORP.

PI Shultz JW, Lewis MK, Leippe D, Mandrekar M, Kephart D, Rhodes RB;

PI Andrews CA, Hartnett JR, Gu T, Olson RJ, Wood KV, Welch R;

DR WPI; 2000-565377/52.

PT Determining presence or absence of a predetermined endogenous nucleic

PT acid sequence by using an enzyme that depolymerizes the 3' end of an

PT oligonucleotide probe hybridized to a target sequence to release

PT identifier nucleotides.

PS Example; Page 349; 389pp; English.

XX The present invention describes a method (M1) for determining the

CC presence or absence of a predetermined endogenous nucleic acid target

CC sequence (ENMT). The method comprises hybridising a probe having an

CC identifier nucleotide (IN) with ENMT which is treated with an enzyme that

CC depolymerises the 3' end of hybridised NA to release the INs. M1 is used

CC for determining the number of known sequence repeats present in a nucleic

CC acid target sequence in a nucleic acid sample. The method is also useful

CC for determining whether a nucleic acid target sequence in a sample is an

CC allele from a homozygous or heterozygous locus. The method is also useful

CC for detection of mutations, translocations and SNPs in nucleic acids

CC (including those associated with genetic disease), determination of viral

CC load, species identification, sample contamination, and analysis of

CC forensic samples. AAA86971 to AAA87079 and AAA812817 represent sequence

CC which are used in the exemplification of the present invention. N.B.

CC There is a discrepancy between the SEQ ID NO: and sequences given in the

CC examples, and the SEQ ID NO: and sequences given in the sequence listing

CC from the present invention

XX Sequence 40 BP; 6 A; 8 C; 16 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 40;

Best Local Similarity 100.0%; Pred. No. 0.059;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



DB 3 TTGGGACCCCAACTACTC 22

RESULT 53  
ADP87787/C  
ID ADP87787 standard; DNA; 40 BP.  
XX  
XX ADP87787;  
AC  
XX 09-SEP-2004 (first entry)  
DT  
XX  
XX  
DE TEX on microarray template M3.  
XX  
XX  
KW TEX; thermodynamic equilibrium extension of primers; template; ss.  
XX  
OS Synthetic.  
XX  
XX US2004115643-A1.  
XX  
XX 17-JUN-2004.  
XX  
XX 12-DEC-2002; 2002US-00318416.  
XX  
XX 12-DEC-2002; 2002US-00318416.  
XX  
XX 12-DEC-2002; 2002US-00318416.  
XX  
XX (LIZA/) LIZARDI P M.  
XX (GRIB/) GRIBANOV O G.  
XX  
XX Lizardi PM, Gribanov OG;  
PI  
XX  
XX MPI; 2004-468050/44.  
DR  
XX  
XX  
PT Amplifying nucleic acid for detecting nucleic acid, by extension of one  
PT or more primers using target templates having replication terminating  
PT feature, dissociation of primer from templates to produce multiple  
PT extended primers.  
XX  
XX  
PS Example; SEQ ID NO 19; 75bp; English.  
XX  
XX The invention relates to amplifying (M1) a nucleic acid, involving  
CC contacting one or more extension primers (EP) and target templates (TT)  
CC and incubating under conditions to promote interaction of (EP) and  
CC templates, extension of (EP) using the interacting (TT), and dissociation  
CC of the extended (EP) from (TT), to produce multiple extended (EP) from at  
CC least one (TT), where each (TT) comprise a replication terminating  
CC feature. In (M1), (EP) and target templates are incubated under  
CC isothermal conditions or single set of conditions. The target templates  
CC are nucleic acid sequences of interest. Each of (EP) comprises or  
CC consists of a target complement portion, preferably nucleotides, where  
CC the nucleotides consist of the target complement portion. Each (EP)  
CC can be amplified in the same reaction by targeting multiple sequences  
CC with (EP). Simultaneous amplification and detection is facilitated using  
CC detection probes associated with a substrate. Multiple detection can be  
CC facilitated by an array of detection probes with different detection  
CC probes at different locations of a substrate. The present sequence is a  
CC synthetic template sequence used to demonstrate the method of the  
CC invention.  
XX  
XX Sequence 40 BP; 7 A; 9 C; 15 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 31 TTGGGACCCCAACTACTC 12

RESULT 54  
ADP87774/C  
ID ADP87774 standard; DNA; 40 BP.  
XX  
XX ADP87774;  
AC  
XX  
XX 09-SEP-2004 (first entry)  
DT  
XX  
XX  
DE TEX control template sequence.  
XX  
XX  
KW TEX; thermodynamic equilibrium extension of primers; ss; target.  
XX  
XX  
OS Synthetic.  
XX  
XX US2004115643-A1.  
XX  
XX 17-JUN-2004.  
XX  
XX 12-DEC-2002; 2002US-00318416.  
XX  
XX 12-DEC-2002; 2002US-00318416.  
XX  
XX 12-DEC-2002; 2002US-00318416.  
XX  
XX (LIZA/) LIZARDI P M.  
XX (GRIB/) GRIBANOV O G.  
XX  
XX Lizardi PM, Gribanov OG;  
PI  
XX  
XX MPI; 2004-468050/44.  
DR  
XX  
XX  
PT Amplifying nucleic acid for detecting nucleic acid, by extension of one  
PT or more primers using target templates having replication terminating  
PT feature, dissociation of primer from templates to produce multiple  
PT extended primers.  
XX  
XX  
PS Example; SEQ ID NO 6; 75bp; English.  
XX  
XX The invention relates to amplifying (M1) a nucleic acid, involving  
CC contacting one or more extension primers (EP) and target templates (TT)  
CC and incubating under conditions to promote interaction of (EP) and  
CC templates, extension of (EP) using the interacting (TT), and dissociation  
CC of the extended (EP) from (TT), to produce multiple extended (EP) from at  
CC least one (TT), where each (TT) comprise a replication terminating  
CC feature. In (M1), (EP) and target templates are incubated under  
CC isothermal conditions or single set of conditions. The target templates  
CC are nucleic acid sequences of interest. Each of (EP) comprises or  
CC consists of a target complement portion, preferably nucleotides, where  
CC the nucleotides consist of the target complement portion. Each (EP)  
CC further comprises non-target complement portion. The method is known as  
CC TEX (thermodynamic equilibrium extension of primers). The method is  
CC useful for amplifying nucleic acid and for detecting nucleic acid  
CC sequences which involves performing (M1), and detecting one or more of  
CC the extended (EP). In (M1), only those sequences targeted by (EP) are  
CC amplified, thus allowing specific sequences to be targeted for  
CC amplification. Flexibility in the location of replication terminating  
CC feature allows flexibility in targeting sequences. If a targeted sequence  
CC is not present, the sequence will not be amplified. Multiple sequences  
CC can be amplified in the same reaction by targeting multiple sequences  
CC with (EP). Simultaneous amplification and detection is facilitated using  
CC detection probes associated with a substrate. Multiple detection can be  
CC facilitated by an array of detection probes with different detection  
CC probes at different locations of a substrate. The present sequence is a  
CC control target sequence used in an example demonstrating the method of  
CC the invention.  
XX  
XX Sequence 40 BP; 7 A; 8 C; 15 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.059;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTCCGACCCCAACTACTC 20  
 Db 31 TTCCGACCCCAACTACTC 12

RESULT 55  
 ADP87786/C  
 ID ADP87786 standard; DNA; 40 BP.

AC ADP87786;  
 XX  
 XX 09-SEP-2004 (first entry)  
 DT  
 XX  
 DE TEX synthetic spacer C3 #1.  
 XX  
 KW TEX; thermodynamic equilibrium extension of primers; template; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US2004115643-A1.  
 XX  
 PD 17-JUN-2004.  
 XX  
 PF 12-DEC-2002; 2002US-00318416.  
 XX  
 PR 12-DEC-2002; 2002US-00318416.  
 XX  
 PA (LIZA/) LIZARDI P M.  
 PA (GRIB/) GRIBANOV O G.  
 XX  
 PI Lizardi PM, Grihanov OG;  
 XX  
 DR WPI; 2004-468050/44.  
 XX

Amplifying nucleic acid for detecting nucleic acid, by extension of one or more primers using target templates having replication terminating feature, dissociation of primer from templates to produce multiple extended primers.

Example; SEQ ID NO 18; 75bp; English.

The invention relates to amplifying (M1) a nucleic acid, involving contacting one or more extension primers (EP) and target templates (TT) and incubating under conditions to promote interaction of (EP) and templates, extension of (EP) using the interacting (TT), and dissociation of the extended (EP) from (TT), to produce multiple extended (EP) from at least one (TT), where each (TT) comprises a replication terminating feature. In (M1), (EP) and target templates are incubated under isothermal conditions or single set of conditions. The target templates are nucleic acid sequences of interest. Each of (EP) comprises or consists of a target complement portion, preferably nucleotides, where the nucleotides consist of the target complement portion. Each (EP) further comprises non-target complement portion. The method is known as TEX (thermodynamic equilibrium extension of primers). The method is useful for amplifying nucleic acid and for detecting nucleic acid sequences which involve performing (M1), and detecting nucleic acid the extended (EP). In (M1), only those sequences targeted by (EP) are amplified, thus allowing specific sequences to be targeted for amplification. Flexibility in the location of replication terminating feature allows flexibility in targeting sequences. If a targeted sequence is not present, the sequence will not be amplified. Multiple sequences can be amplified in the same reaction by targeting multiple sequences with (EP). Simultaneous amplification and detection is facilitated using detection probes associated with a substrate. Multiplex detection can be facilitated by an array of detection probes with different detection probes at different locations of a substrate. The present sequence is a synthetic template sequence used to demonstrate the method of the invention.

Sequence 40 BP; 7 A; 8 C; 15 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 0.059;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
 Db 31 TTCCGACCCCAACTACTC 12.

RESULT 56  
 AAQ98098  
 ID AAQ98098 standard; DNA; 46 BP.

AC AAQ98098;  
 XX  
 XX 05-FEB-1996 (first entry)  
 DT  
 XX  
 DE Capture extender probe used in an improved sandwich hybridisation assay.

XX  
 KW Probe; nucleotide; solution phase sandwich hybridisation assay;  
 KW competitive; analyte binding sequence; background signal reduction; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FH misc\_binding 34..46  
 FT /\*tag= a  
 FT /note= "binds to immobilised capture probe"

WO9516055-A1.

15-JUN-1995.

07-DEC-1994; 94WO-US014119.

08-DEC-1993; 93US-00164388.

(CHIR) CHIRON CORP.

Urdea MS, Fultz T, Warner BD, Collins M;  
 WPI; 1995-224335/29.

Soln. phase sandwich hybridisation assays for nucleic acid(s) - with capture extender molecules or competitive oligo:nucleotide(s) to minimise background signal, increasing sensitivity and selectivity.

Example 1; Page 33; 86bp; English.

AAQ98098-098099 are capture extender probes (CEs) used in a new improved method of solution phase sandwich hybridisation assays. The capture extender probes contain an analyte binding sequence (ABS) and a support binding sequence (SBS) which hybridise to a sequence present in a capture probe when immobilised on a solid support. The analyte binding sequences are different in each capture extender probe and the capture probes contain two CE-binding sequences, so that two different CE can bind to a single capture probe. The new method minimises background signals (caused by non-specific hybridisation), this improves both sensitivity and selectivity of the assay without increasing cost or time

Sequence 46 BP; 9 A; 17 C; 11 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 0.059;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
 Db 10 TTCCGACCCCAACTACTC 29

RESULT 57  
 ADQ54055/C



ID ADC54055 standard; cDNA; 57 BP.  
XX  
AC ADC54055;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Genotype 3 HCV 5' non-coding region fragment, SEQ ID NO:6.  
XX  
KM HCV, hepatitis C virus; classification; interferon therapy; genotype 3;  
XX MHC3C; MHC3C'; 5' non-coding region; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN JP2002345467-A.  
XX  
PD 03-DEC-2002.  
XX  
PF 17-APR-2001; 2001JP-00118810.  
XX  
PR 23-OCT-2000; 2000JP-00322567.  
XX  
PA (SRLS-) SRL KK.  
XX  
DR WPI; 2003-460879/44.  
XX  
PT Probe and method for classification of hepatitis C virus (HCV) types used  
PT for forecast of therapeutic effect of interferon administration.  
XX  
PS Claim 10; SEQ ID NO 6; 15pp; Japanese.  
XX  
CC The invention relates to a nucleic acid probe for the classification of  
CC hepatitis C virus (HCV) into 3 genotypes. The 3 HCV genotypes are MH1am  
CC (type 1), MH2am (type 2) and MHC3C+MHC3C' (type 3). The probe can be  
CC used to classify HCV type to enable prediction of the success or  
CC otherwise of interferon therapy in a patient. The present sequence  
CC represents a specifically claimed HCV genotype 3 5' non-coding region  
CC fragment.  
XX  
SQ Sequence 57 BP; 10 A; 15 C; 22 G; 10 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 20; DB 10; Length 57;  
Best Local Similarity 100.0%; Pred. No. 0.058;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCGGACCCCAACTACTC 20  
DB 46 TTCGGACCCCAACTACTC 27  
RESULT 59  
ACCB0000/c  
ID ACCB0000 standard; DNA; 60 BP.  
XX  
AC ACCB0000;  
XX  
DT 12-SEP-2003 (first entry)  
XX  
DE Hepatitis C virus 60-mer oligonucleotide HCV0188 SEQ ID NO:1.  
XX  
KM Hepatitis C virus; HCV; HCV0188; control feature; polynucleotide array;  
KM diagnostic; screening; gene expression analysis; polymorphism detection;  
KM splice variant; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN EP1262566-A2.  
XX  
PD 04-DEC-2002.  
XX  
PF 29-MAY-2002; 2002EP-00253745.  
XX  
PR 30-MAY-2001; 2001US-00870939.  
XX

PA (AGIL-) AGILENT TECHNOLOGIES INC.  
XX  
PI Amorese DA, Shannon KM, Collins PJ, Wolber PK;  
XX  
DR WPI; 2003-543475/52.  
XX  
PT Polynucleotide array for genetic applications, has two sets of multiple  
PT features, with features of first set having longer polynucleotide  
PT molecules (400 nucleotides) than features of second set with 100  
PT nucleotides.  
XX  
PS Disclosure; Page 9; 18pp; English.  
XX  
CC The present invention describes a polynucleotide array (I), which  
CC comprises a first set of multiple features, where each feature  
CC independently has first polynucleotide molecules (PM1) of at least 400  
CC nucleotides in length, and a second set of features, where each feature  
CC independently has second polynucleotide molecules (PM2) of no more than  
CC 100 nucleotides in length. Also described: (1) a kit comprising (I) and  
CC polynucleotide controls which are, or their complements are, at least 70%  
CC complementary to sequences of respective second polynucleotides; and (2)  
CC fabricating (M) a polynucleotide array, by forming a first set of  
CC multiple features on a substrate, with each feature independently having  
CC PM1 and forming a second set of features on the substrate, with each  
CC feature independently having PM2. (I) is useful in a method involving  
CC exposing (I) to control targets, such that the control targets hybridise  
CC at least 100 times more efficiently to respective second features than  
CC they do to any of the first features, and simultaneously exposing (I) to  
CC a sample, where the second set of features hybridise more efficiently  
CC with control targets than any of the first set features hybridise to any  
CC control targets. The method further involves reading the array to obtain  
CC an image representing the amount of polynucleotides which have bound to  
CC first and second set features, and evaluating locations of first features  
CC in the image using the locations of second features in the image. (I) is  
CC useful in diagnostic, screening, gene expression analysis, and other  
CC applications. (I) is also useful for detecting polymorphisms or splice  
CC variants. The present sequence represents a Hepatitis C virus control  
CC features related 60-mer oligonucleotide, designated HCV0188, which is  
CC given in the exemplification of the present invention  
XX  
SQ Sequence 60 BP; 10 A; 11 C; 24 G; 15 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 20; DB 9; Length 60;  
Best Local Similarity 100.0%; Pred. No. 0.058;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCGGACCCCAACTACTC 20  
DB 24 TTCGGACCCCAACTACTC 5  
RESULT 59  
ADCC46965/c  
ID ADCC46965 standard; DNA; 80 BP.  
XX  
AC ADCC46965;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Synthesised bridge probe #SEQ ID 1.  
XX  
KM Oligonucleotide; amplification; gene detection; self-assembly; probe; ss.  
XX  
OS Synthetic.  
XX  
PN WO2003040367-A1.  
XX  
PD 15-MAY-2003.  
XX  
PF 30-OCT-2002; 2002WO-JP0111321.  
XX  
PR 08-NOV-2001; 2001JP-00342709.  
XX  
PR 08-MAY-2002; 2002JP-00132402.  
XX

XX (SANKO) SANKO JUNYAKU CO LTD.  
 XX Usui M, Mitsuoka M, Haki C;  
 XX WPI, 2003-441572/41.

PT Self-assembly formed from amplified target gene and probe pairs for  
 PT simple and accurate detection of the target gene.

XX Example Examples; Page 34; 123pp; Japanese.

XX The invention relates to a method for forming an oligonucleotide self-  
 CC assembly, in which oligonucleotides containing a target gene sequence are  
 CC first amplified by a conventional gene amplification method, and the  
 CC amplification product is then incorporated into the self-assembly by  
 CC reaction with one or more oligonucleotide probe pairs. Also disclosed is  
 CC the detection of a specific gene using the novel method. The  
 CC oligonucleotide probe pairs (which may consist of one pair, or two or  
 CC more different pairs) consist of at least three distinct hybridizing  
 CC regions which are each complementary to a region on the other probe of  
 CC the pair, or to a region on the target oligonucleotide. Preferably each  
 CC complementary region includes at least one G-C coupling. The regions  
 CC of the probe sequence and those complementary to the target  
 CC oligonucleotides at outer parts of the probe pair may be in the internal part  
 CC of the probe sequence and those complementary to the target  
 CC oligonucleotides at outer parts of the probe pair, by hybridisation of  
 CC the central complementary regions of the probes. This dimer is then  
 CC hybridised with the target oligonucleotides, each 3' or 5' terminal  
 CC portion of the probe dimer hybridizing to a different region on one or  
 CC other strand of the target oligonucleotide sequence. The probes may be  
 CC DNA, RNA, PNA or LNA. The 3' and/or 5' terminals of the probes may be  
 CC methylated. The oligonucleotides may be synthesised in the initial  
 CC amplification reaction from single or double stranded DNA or RNA and the  
 CC synthesis may include ligation of a target sequence to sequences  
 CC complementary to the probe pairs. They may be enzymatically cleavable by  
 CC exonuclease, RNase H or restriction enzymes. This method is an accurate,  
 CC specific and sensitive method for the detection of a target gene sequence  
 CC at low cost and without complicated procedures or apparatus. The current  
 CC sequence represents a synthesised bridge probe utilised in an example  
 CC from the invention.

XX Sequence 80 BP; 16 A; 21 C; 26 G; 17 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 80;  
 Best Local Similarity 100.0%; Pred. No. 0.057;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
 DB 78 TTGGGACCCCAACTACTC 59

RESULT 60

ID ADC46966 standard; DNA; 80 BP.

AC ADC46966;

DT 18-DEC-2003 (first entry)

DE Synthesised bridge probe #SEQ ID 2.

XX Oligonucleotide; amplification; gene detection; self-assembly; probe; ss.

OS Synthetic.

XX WO2003040367-A1.

XX 15-MAY-2003.

PF 30-OCT-2002; 2002MO-JP011321.

XX

PR 08-NOV-2001; 2001JP-00342709.

PR 08-MAY-2002; 2002JP-00132402.

XX (SANKO) SANKO JUNYAKU CO LTD.

XX Usui M, Mitsuoka M, Haki C;  
 XX WPI, 2003-441572/41.

PT Self-assembly formed from amplified target gene and probe pairs for  
 PT simple and accurate detection of the target gene.

XX Example Examples; Page 34-35; 123pp; Japanese.

XX The invention relates to a method for forming an oligonucleotide self-  
 CC assembly, in which oligonucleotides containing a target gene sequence are  
 CC first amplified by a conventional gene amplification method, and the  
 CC amplification product is then incorporated into the self-assembly by  
 CC reaction with one or more oligonucleotide probe pairs. Also disclosed is  
 CC the detection of a specific gene using the novel method. The  
 CC oligonucleotide probe pairs (which may consist of one pair, or two or  
 CC more different pairs) consist of at least three distinct hybridizing  
 CC regions which are each complementary to a region on the other probe of  
 CC the pair, or to a region on the target oligonucleotide. Preferably each  
 CC complementary region includes at least one G-C coupling. The regions  
 CC of the probe sequence and those complementary to the target  
 CC oligonucleotides at outer parts of the probe pair may be in the internal part  
 CC of the probe sequence and those complementary to the target  
 CC oligonucleotides at outer parts of the probe pair, by hybridisation of  
 CC the central complementary regions of the probes. This dimer is then  
 CC hybridised with the target oligonucleotides, each 3' or 5' terminal  
 CC portion of the probe dimer hybridizing to a different region on one or  
 CC other strand of the target oligonucleotide sequence. The probes may be  
 CC DNA, RNA, PNA or LNA. The 3' and/or 5' terminals of the probes may be  
 CC methylated. The oligonucleotides may be synthesised in the initial  
 CC amplification reaction from single or double stranded DNA or RNA and the  
 CC synthesis may include ligation of a target sequence to sequences  
 CC complementary to the probe pairs. They may be enzymatically cleavable by  
 CC exonuclease, RNase H or restriction enzymes. This method is an accurate,  
 CC specific and sensitive method for the detection of a target gene sequence  
 CC at low cost and without complicated procedures or apparatus. The current  
 CC sequence represents a synthesised bridge probe utilised in an example  
 CC from the invention.

XX Sequence 80 BP; 17 A; 26 C; 21 G; 16 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 80;  
 Best Local Similarity 100.0%; Pred. No. 0.057;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
 DB 3 TTGGGACCCCAACTACTC 22

RESULT 61

ID ADO80850 standard; DNA; 100 BP.

AC ADO80850;

DT 29-JUL-2004 (first entry)

DE Hepatitis C virus reference DNA with partial homology to target Seqid 3.

XX competitive PCR; quantitative; virus; viral infection; viraemia; ds.

XX Hepatitis C virus.

XX JP2004113194-A.

XX 15-APR-2004.

XX

PF	27-SEP-2002; 2002JP-00284452.
XX	
PR	27-SEP-2002; 2002JP-00284452.
XX	
PA	(TOKE ) TOSHIBA KK.
XX	
DR	WPI, 2004-360137/34.
XX	
PT	Quantitating target nucleic acid involves competitively amplifying target
PT	nucleic acid and reference sequences containing homologous sequences with
PT	respect to target, and determining amplified product obtained for the
PT	sequences.
XX	
PS	Claim 6; SEQ ID NO 3, 26pp; Japanese.
XX	
CC	This invention relates to a novel method for quantitating the amount of
CC	target nucleic acid molecules present in a sample. Specifically, it
CC	refers to competitively amplifying (using the same primer set) the target
CC	oligonucleotides and a number of reference sequences that are partially
CC	homologous to the target, where the concentration for each set is equal
CC	and amplified product obtained for each type of sequence can be
CC	determined and measured. The present invention describes this method as
CC	useful for quantitating target nucleic acids such as those derived from a
CC	viral genome or mRNA, in order to establish the presence and identity of
CC	a viral infection, as well as the degree of viremia. Accordingly, the
CC	method also enables measurement of the degree of responsiveness following
CC	treatment with a medicament by measuring target mRNA in the subject. This
CC	polynucleotide sequence is reference DNA from the hepatitis C virus that
CC	shares partial homology with the target nucleic acid of the invention.
XX	
SQ	Sequence 100 BP; 21 A; 36 C; 25 G; 18 T; 0 U; 0 Other;
Query Match	100.0%; Score 20; DB 12; Length 100;
Best Local Similarity	100.0%; Pred. No. 0.056;
Matches 20; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	1 TTTCGGACCCCAACTACTC 20       Db 69 TTTCGGACCCCAACTACTC 88
RESULT 62	
AAT09185	
ID	AAT09185 standard; DNA; 108 BP.
AC	
XX	AAT09185;
DT	21-OCT-2004 (revised)
DT	14-AUG-1996 (first entry)
XX	
DE	Hepatitis C virus specific amp-probe-2 (HCV C).
XX	
KM	Ligase dependent polymerase chain reaction; LD-PCR; probe; hybridisation;
KM	ligand binding pair; Ligase; paramagnetic bead; primer; amplification;
KW	hepatitis; untranslated region; UTR; rRNA; ss.
XX	
OS	Synthetic.
XX	
FH	Key
FT	misc_binding
FT	
FT	
FT	/tag= a
FT	/bound_moiety
FT	/note="complementary to a fragment of the hepatitis C
FT	virus 5' untranslated region"
FT	83..108
FT	misc_binding
FT	
FT	/tag= b
FT	/bound_moiety
FT	/note="complementary to a fragment of the hepatitis C
FT	virus 5' untranslated region"
XX	
PN	WO9535390-A1.
XX	
DD	28-DEC-1995.

XX		PF	14-JUN-1995;	95WO-US007671.
XX		PR	22-JUN-1994;	94US-00263937.
XX		PA	(MOUN ) MOUNT SINAI SCHOOL MEDICINE.	
XX		P1	Zhang DY,	
XX		DR	WPI; 1996-058427/06.	
PT		PT	Ligation dependent polymerase chain reaction - for the detection of infectious pathogens and abnormal human genes, e.g. HIV and neoplasia.	
XX		PS	Example B; Page 62; 100pp; English.	
CC		CC	A novel method of detecting a target nucleic acid (TNA) sequence involves use of the ligase dependent polymerase chain reaction method (LD-PCR). In this method, two probes are provided. The first probe contains a region at the 5' end which is complementary and will hybridise with the TNA, the 3' end of the first probe is generic and is bound to one half of a ligand binding pair (LBP). The second probe contains a region at the 5' end which is complementary to a region in the TNA which is immediately adjacent to the complementary region of the first probe. When the probes are bound to the TNA, they can be ligated together using a conventional ligase. The TNA-ligated probe complex can be isolated by binding the first probe to a paramagnetic bead to which is attached the second half of the LBP. The TNA can be dissociated from the ligated probe complex which can then be detected either by a label attached to the second probe, by using an external probe or by PCR using the ligated probes as a template. The capture probes AAT09176-7 are used to isolate a region of the Hepatitis C virus 5' untranslated region. This probe can be used to detect this region by hybridisation such that the 5' and 3' ends of the probe lie adjacent to each other when hybridised to the TNA, resulting in closed circular mol. after ligation. The ligated sequence can subsequently be detected by PCR amplification with the primers AAT09181-2	
CC		CC	Revised record issued on 21-OCT-2004 : Correction to Feature Table Key	
SQ		Sequence	108 BP; 28 A; 34 C; 21 G; 25 T; 0 U; 0 Other;	
		Query Match	100.0%; Score 20; DB 2; Length 108;	
		Best Local Similarity	100.0%; Pred. No. 0.056;	
		Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
CY		I	TTCGCGACCAACTACTC 20 	
DB		4	TTCGCGACCAACTACTCTC 23	
RESULT 63				
ID		AAV20727	standard; DNA, 108 BP.	
AC		AAV20727;		
DT		17-JUL-1998	(first entry)	
DE		Hepatitis C virus probe SEQ ID NO:31.		
KX		Hepatitis C virus; HCV; HIV; probe; detection; capture; amplification;		
XX		paramagnetic particle; ligation; ss.		
OS		Synthetic.		
XX		Hepatitis C virus.		
PN		MO9804745-A1.		
PD		05-FEB-1998.		
PF		30-JUL-1997;	97WO-US013390.	
R		31-JUL-1996;	96US-00690495.	

XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.  
 XX Zhang DY, Brandwein M;  
 XX WPI, 1998-159153/14.

XX Detection of target nucleic acids in samples - using capture and  
 PT amplification probes, paramagnetic particles and ligation to form a  
 PT nucleotide sequence which can be detected.

XX Example 8; Page 70; 136pp; English.

XX The present sequence represents a probe used in an example of the present  
 CC invention for the detection of HCV RNA in a sample. The present invention  
 CC describes methods for: (A) detecting a target nucleic acid (NA) in a  
 CC sample; (B) in situ detection of a target NA in a sample; (C) detecting  
 CC an antigen in a sample; and (D) detecting an antibody in a sample. The  
 CC methods can be used for the rapid automated detection and monitoring of  
 CC pathogenic organisms, as well as the detection of abnormal genes in an  
 CC individual. The methods allow for isolation, amplification and detection  
 CC of NA sequences corresponding to the target NA to be carried out in the  
 CC same receptacle, e.g. tube or micro-well plate. The method also allows  
 CC for standardisation of conditions, because only a pair of generic  
 CC amplification probes may be utilised in the present method for detecting  
 CC a variety of target NAs, thus allowing efficient multiplex amplification.  
 CC The method also allows the direct detection of RNA by probe amplification.  
 CC without the need for DNA template production. The amplification probes,  
 CC which may be covalently joined end to end, form a contiguous ligated  
 CC amplification sequence. The assembly of the amplifiable DNA by ligation  
 CC increase specificity, and makes possible the detection of a single  
 CC mutation in a target

SO Sequence 108 BP; 28 A; 34 C; 21 G; 25 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.056;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
 Db 4 TTGGGACCCCAACTACTC 23

RESULT 64

AAV22777  
 ID AAV22777 standard; DNA; 108 BP.

AC AAV22777;

XX 27-AUG-2003 (revised)

DT 22-JUL-1998 (first entry)

XX Amp-probe-2 (HCV C) for detecting Hepatitis C virus 5' UTR RNA.

XX Probe; Amp-probe-2 (HCV C); automated detection; Mycobacteri-  
 KM nucleic acid; monitoring; pathogenic organism; abnormal gene; ss.

XX Synthetic.  
 OS Hepatitis C virus.

XX W09804746-A1.

XX 05-FEB-1998.

XX 30-JUL-1997; 97MO-US013391.

XX 31-JUL-1996; 9GUS-00690494.

XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.

XX Zhang DY, Brandwein M, Hsu H TCH;

DR WPI, 1998-159154/14.

XX Detection of target nucleic acids in samples - using capture and  
 PT amplification probes, paramagnetic particles and ligation to form a  
 PT nucleotide sequence which is amplified.

XX Example 8; Page 67; 142pp; English.

XX The present sequence represents a probe, designated Amp-probe-2 (HCV C),  
 CC used for detecting the 5' untranslated region (5' UTR) of Hepatitis C  
 CC virus RNA. Nucleotides 1-26 at the 5' end of the probe are complementary  
 CC to a portion of the 5'UTR of the HCV genome. The probe is used to  
 CC exemplify the method of the invention, which describes the detection of a  
 CC target nucleic acid in a sample. The method comprises contacting the  
 CC paramagnetic particles coated with a ligand binding moiety. Each  
 CC capture/amplification probe has a ligand bound to its non-complementary  
 CC sequence that is capable of binding to and forming an affinity pair with  
 CC the ligand binding moiety coated onto the paramagnetic particles. The  
 CC oligonucleotide probes also comprise a probe that can be circularised, by  
 CC having the 3' and 5' ends ligated together. The circularised probe is  
 CC amplified with a DNA polymerase having strand displacement activity under  
 CC conditions whereby an extension primer is extended around the circle for  
 CC multiple revolutions to form a single stranded DNA of repeating units  
 CC complementary to the sequence of the circular probe, and multiple copies  
 CC of a second extension primer hybridizes to complementary regions of the  
 CC single stranded DNA and are extended by the DNA polymerase to provide  
 CC extension products. The extension products of the second extension primer  
 CC displace downstream copies of the second extension primer and  
 CC corresponding extension products to provide displaced single strands to  
 CC which multiple copies of the first extension primer bind and are extended  
 CC by the DNA polymerase. The amplified DNA is detected. The method can be  
 CC used for the rapid automated detection and monitoring of pathogenic  
 CC organisms as well as the detection of abnormal genes in an individual.  
 CC (Updated on 27-AUG-2003 to correct 05 field.)

SO Sequence 108 BP; 28 A; 34 C; 21 G; 25 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.056;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
 Db 4 TTGGGACCCCAACTACTC 23

RESULT 65

ABK86847  
 ID ABK86847 standard; DNA; 108 BP.

XX ABK86847;

DT 24-SEP-2002 (first entry)

XX Hepatitis C virus C amp-probe-2.

XX Hepatitis C; RNA detection; ss; probe; nucleic acid detection;  
 KM infectious disease.

XX Hepatitis C virus.

XX W0200244339-A2.

XX 06-JUN-2002.

XX 03-DEC-2001; 2001MO-US045822.

XX 01-DEC-2000; 2000US-00728265.

XX (ZHAN/) ZHANG D Y.  
 PA (BRAN/) BRANDWEIN M.  
 PA (HSU/) HSU H T C H.



CC oligonucleotide probe under conditions that allow hybridisation between  
 CC complementary sequences in the target nucleic acid and the circular  
 CC oligonucleotide probe, adding at least one forward primer comprising a  
 CC sequence complementary to a portion of the circular oligonucleotide  
 CC probe, adding an oligonucleotide primer pair comprising a first primer  
 CC and a second primer where the first primer of the pair comprises a first  
 CC sequence that is substantially identical to a portion of the circular  
 CC oligonucleotide probe, a second sequence that is complementary to the  
 CC second primer of the pair, and a signal generating moiety, the second  
 CC primer of the pair comprises a sequence that is complementary to the  
 CC first primer and a moiety capable of quenching, masking or inhibiting the  
 CC activity of the signal generating moiety, and when the first primer and  
 CC the second primer are bound to one another, the signal is inhibited,  
 CC adding at least one reverse primer comprising a sequence that is  
 CC substantially identical to a portion of the circular oligonucleotide  
 CC probe, adding a DNA polymerase, and amplifying the circular  
 CC oligonucleotide probe and separating the signal generating moiety and the  
 CC quenching, masking or inhibitory moiety to generate a signal, where  
 CC the detection of signal indicates the presence of the target nucleic acid in  
 CC the sample. Also included are a kit for (M1) and amplifying (M2) a  
 CC circular nucleic acid sequence. In (M1), the circular oligonucleotide  
 CC probe is formed by ligating the 3' and 5' ends of linear oligonucleotide  
 CC sequences in the target nucleic acid under conditions that allow  
 CC hybridisation between complementary sequences in the target nucleic acid  
 CC and the linear oligonucleotide probe. The circular probe is amplified  
 CC using an amplification method chosen from polymerase chain reaction,  
 CC strand displacement amplification, transcription mediated amplification,  
 CC ramification-extension amplification method (RAM) and primer extension.  
 CC (M1) is useful for detecting a target nucleic acid in a sample. (M2) is  
 CC useful for amplification of genomic DNA and total mRNAs expressed in  
 CC cells and for analysing differential mRNA expression. (M1) is useful for  
 CC detecting genetic variations in nucleic acids in sample from patients  
 CC with genetic diseases or neoplasia. The DNA and/or mRNA amplified by (M2)  
 CC is used in techniques developed for detection of infectious agents, and  
 CC to detect and monitor pathogenic microorganisms in a test sample, as well  
 CC as to detect abnormal genes in an individual. (M1) is useful for routine  
 CC diagnostic testing in a clinical laboratory setting. The present sequence  
 CC is an amplification probe used to demonstrate the above methods.

SQ Sequence 108 BP; 28 A; 34 C; 21 G; 25 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 0.056;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTCTC 20  
 |||||  
 DB 4 TTGGGACCCCACTACTCTC 23

RESULT 68  
 ADC54054/C

ID . ADC54054 standard; cDNA; 126 BP.

AC ADC54054;

DT 18-DEC-2003 (first entry)

XX Genotype 3 HCV 5' non-coding region fragment, SEQ ID NO:5.

KW HCV; hepatitis C virus; classification; interferon therapy; genotype 3;  
 MW MHG3C; MHG3C'; 5' non-coding region; ss.

OS Hepatitis C virus.

XX JP2002345467-A.

PD 03-DEC-2002.

PF 17-APR-2001; 2001JP-00118810.

PR 23-OCT-2000; 2000JP-00322567.

XX (SRUS-) SRL KK.

DR WPI; 2003-460879/44.

PT Probe and method for classification of hepatitis C virus (HCV) types used  
 PT for forecast of therapeutic effect of interferon administration.

PS Claim 10; SEQ ID NO 5; 15bp; Japanese.

CC The invention relates to a nucleic acid probe for the classification of  
 CC hepatitis C virus (HCV) into 3 genotypes. The 3 HCV genotypes are MH1am1  
 CC (type 1), MH2am1 (type 2) and MHG3C+MHG3C' (type 3). The probe can be  
 CC used to classify HCV type to enable prediction of the success or  
 CC otherwise of interferon therapy in a patient. The present sequence  
 CC represents a specifically claimed HCV genotype 3 5' non-coding region  
 CC fragment.

SQ Sequence 126 BP; 26 A; 34 C; 40 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 126;  
 Best Local Similarity 100.0%; Pred. No. 0.056;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTCTC 20  
 |||||  
 DB 115 TTGGGACCCCACTACTCTC 96

RESULT 69

AAS10487/C

ID AAS10487 standard; RNA; 163 BP.

XX AAS10487;

DT 24-OCT-2001 (first entry)

DE HCV 5'-UTR domain IIRdel1 EMSA RNA probe.

KW HCV 5'-UTR; minimal IRES; MIRS; internal ribosome entry site; eIF3;  
 KM eukaryotic initiation factor 3; HCV translation initiation; antiviral;

OS Hepatitis C virus; strain Ia M67463.

XX Synthetic.

EH Key

FT misc\_binding Location/Qualifiers  
 FT 1..5  
 FT /tag= a  
 FT /bound\_moiety= "Forms double stranded region with bases  
 FT 159-163"

FT misc\_binding  
 FT 7..10  
 FT /tag= b  
 FT /bound\_moiety= "Forms double stranded region with bases  
 FT 157-159"

FT misc\_binding  
 FT 11..19  
 FT /tag= c  
 FT /bound\_moiety= "Forms double stranded region with bases  
 FT 122-114"

FT misc\_binding  
 FT 20..23  
 FT /tag= d  
 FT /bound\_moiety= "Forms double stranded region with bases  
 FT 112-109"

FT misc\_binding  
 FT 26..41  
 FT /tag= e  
 FT /note= "Designated as IIRa"

FT stem\_loop  
 FT 42..51  
 FT /tag= f  
 FT /bound\_moiety= "Forms double stranded region with bases  
 FT 97-88"

FT misc\_binding  
 FT 54..55  
 FT /tag= g

FT		/bound_moiety= "Forms double stranded region with bases
FT		83-82"
FT	stem_loop	57.. .80
FT		/*tag= h
FT		/note= "Designated as IIIB"
FT	misc_binding	82.. .83
FT		/*tag= i
FT		/bound_moiety= "Forms double stranded region with bases
FT		55-54"
FT	misc_binding	88.. .97
FT		/*tag= j
FT		/bound_moiety= "Forms double stranded region with bases
FT		51-42"
FT	stem_loop	99.. .108
FT		/*tag= k
FT		/note= "Designated as IIIC"
FT	misc_binding	109.. .112
FT		/*tag= l
FT		/bound_moiety= "Forms double stranded region with bases
FT		23-20"
FT	misc_binding	114.. .122
FT		/*tag= m
FT		/bound_moiety= "Forms double stranded region with bases
FT		19-11"
FT	misc_binding	123.. .126
FT		/*tag= n
FT		/bound_moiety= "Forms double stranded region with bases
FT		149-146"
FT	stem_loop	129.. .144
FT		/*tag= o
FT		/note= "Designated as IIID"
FT	misc_binding	146.. .149
FT		/*tag= p
FT		/bound_moiety= "Forms double stranded region with bases
FT		126-123"
FT	misc_binding	154.. .157
FT		/*tag= q
FT		/bound_moiety= "Forms double stranded region with bases
FT		10-7"
FT	misc_binding	159.. .163
FT		/*tag= r
FT		/bound_moiety= "Forms double stranded region with bases 5
FT		-1"
PN		
XX	WO200144266-A2.	
PD		
XX	21-UUN-2001.	
PF		
XX	18-DEC-2000; 2000MO-GB004862.	
XX		
PR	16-DEC-1999; 99GB-00029820.	
XX	22-DEC-1999; 99US-0171804P.	
PA	(RIBO-) RIBOTARGETS LTD.	
P1	Karn J, Walker S;	
DR	WPI, 2001-465050/50.	
XX		
PT	Nucleotide sequences derived from Hepatitis C virus, useful for	
PT	identifying candidate viral compounds.	
PS		
CC	Disclosure; Fig 5B; 48pp; English.	
CC		
CC	The present sequence represents Hepatitis C virus (HCV) 5'-UTR domain	
CC	III deletion RNA probe used in a RNA electrophoretic gel mobility shift	
CC	assay (EMSA). The present sequence is described in an invention relating	
CC	to a novel compound comprising nucleotide sequences capable of annealing	
CC	and which is derived from a 5'-untranslated region (UTR) of HCV which is	
CC	essential for binding of eIF3 (eukaryotic initiation factor 3). The	
CC	invention particularly relates to a sub-region of the HCV 5'-UTR referred	
CC	to as the minimal internal ribosome entry site (MRES) which can be used	
CC	to identify drugs which inhibit HCV translation initiation. The compounds	

Query Match	Best Local Similarity	Score 20;	DB 4;	Length 163;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	100.0%; Pred. No. 0.055;			
1 TTGGGACCCCAACTACTC 20				
145 TTGGGACCCCAACTACTC 126				
Sequence 163 BP; 32 A; 43 C; 54 G; 0 T; 34 U; 0 Other;				
AAQ43061/C				
AAQ43061 standard; cDNA; 184 BP.				
AAQ43061;				
25-MAR-2003 (revised)				
23-SEP-1993 (first entry)				
-255 to -62 portion of 5' non-coding region of HCV from donors E-B8.				
Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV;				
NS-5; phylogeny; differentiation; NS-3; core region; type 3; ss.				
Hepatitis C virus.				
WO9310239-A2.				
27-MAY-1993.				
20-NOV-1992; 92MO-GB002143.				
21-NOV-1991; 91GB-00024696.				
24-JUN-1992; 92GB-00013362.				
(COMM-) COMMON SERVICES AGENCY.				
Simmonds P, Chan S, Yap PL;				
WPI; 1993-182554/22.				
DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for				
diagnosing and treating HCV infection, screening blood samples and				
identifying different HCV types.				
Disclosure; Fig 1; 120pp; English.				
The sequences given in AAQ43058-75 show the -255 to -62 non-coding region				
of hepatitis C virus (HCV) samples from 18 blood donors and other HCV				
variants. Analysis of this region revealed the existence of three				
distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of				
the groups identified were similar to those of HCV variants termed type 1				
and 2, while the third appeared to represent a novel virus type.				
Comparison of other regions of the genome, eg. the NS-5 region (see also				
AA937923-26), showed a high degree of sequence diversity with type 3				
being phylogenetically different to type 1 and 2. The same degree				
differentiation was noted in the NS-3 (see AA937927-30) and core region				
(see AA937931) between type 3 and type 1 sequences. (Updated on 25-MAR-				
2003 to correct PN field.)				
Sequence 184 BP; 36 A; 57 C; 58 G; 33 T; 0 U; 0 Other;				
Query Match	100.0%; Score 20; DB 2; Length 184;			
Best Local Similarity 100.0%; Pred. No. 0.055;				
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
1 TTGGGACCCCAACTACTC 20				

Db 179 TTGCGACCCCAACTACTC 160

RESULT 71

AAQ43068/c  
ID AAQ43068 standard; CDNA; 184 BP.

XX AC AAQ43068;

XX DT 25-MAR-2003 (revised)  
XX DT 23-SEP-1993 (first entry)

XX DE -255 to -62 region of 5' non-coding region of HCV from donor E-b17.

XX KM Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV;  
XX NS-5; phylogeny; differentiation; NS-3; core region; type 3; ss.

XX OS Hepatitis C virus.

XX PN WO9310239-A2.

XX PD 27-MAY-1993.

XX PF 20-NOV-1992; 92MO-GB002143.

XX PR 21-NOV-1991; 91GB-00024696.

XX PR 24-JUN-1992; 92GB-00013362.

XX PS (COMM-) COMMON SERVICES AGENCY.

XX PI Simmonds P, Chan S, Yap PL;

XX DR WPI; 1993-182554/22.

XX PT DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for  
XX PT diagnosing and treating HCV infection, screening blood samples and  
XX PT identifying different HCV types.

XX PS Disclosure; Fig 1; 120pp; English.

XX CC The sequences given in AAQ43058-75 show the -255 to -62 non-coding region  
XX CC of hepatitis C virus (HCV) samples from 18 blood donors and other HCV  
XX CC variants. Analysis of this region revealed the existence of three  
XX CC distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of  
XX CC the groups identified were similar to those of HCV variants termed type 1  
XX CC and 2, whilst the third appeared to represent a novel virus type.  
XX CC Comparison of other regions of the genome, eg. the NS-5 region (see also  
XX CC AAR37923-26), showed a high degree of sequence diversity with type 3  
XX CC being phylogenetically different to type 1 and 2. The same degree  
XX CC of differentiation was noted in the NS-3 (see AAR37927-30) and core region  
XX CC (see AAR37931) between type 3 and type 1 sequences. (Updated on 25-MAR-  
XX CC 2003 to correct PN field.)

XX SQ Sequence 184 BP; 34 A; 55 C; 59 G; 36 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 20; DB 2; Length 184;  
XX Best Local Similarity 100.0%; Pred. No. 0.055;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 179 TTGCGACCCCAACTACTC 160

RESULT 72

AAQ43060/c  
ID AAQ43060 standard; CDNA; 184 BP.

XX AC AAQ43060;

XX DT 25-MAR-2003 (revised)  
XX DT 23-SEP-1993 (first entry)

XX DE -255 to -62 portion of 5' non-coding region of HCV from donors E-b7.

XX KM Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV;  
XX NS-5; phylogeny; differentiation; NS-3; core region; type 3; ss.

XX OS Hepatitis C virus.

XX PN WO9310239-A2.

XX PD 27-MAY-1993.

XX PF 20-NOV-1992; 92MO-GB002143.

XX PR 21-NOV-1991; 91GB-00024696.

XX PR 24-JUN-1992; 92GB-00013362.

XX PS (COMM-) COMMON SERVICES AGENCY.

XX PI Simmonds P, Chan S, Yap PL;

XX DR WPI; 1993-182554/22.

XX PT DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for  
XX PT diagnosing and treating HCV infection, screening blood samples and  
XX PT identifying different HCV types.

XX PS Disclosure; Fig 1; 120pp; English.

XX CC The sequences given in AAQ43058-75 show the -255 to -62 non-coding region  
XX CC of hepatitis C virus (HCV) samples from 18 blood donors and other HCV  
XX CC variants. Analysis of this region revealed the existence of three  
XX CC distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of  
XX CC the groups identified were similar to those of HCV variants termed type 1  
XX CC and 2, whilst the third appeared to represent a novel virus type.  
XX CC Comparison of other regions of the genome, eg. the NS-5 region (see also  
XX CC AAR37923-26), showed a high degree of sequence diversity with type 3  
XX CC being phylogenetically different to type 1 and 2. The same degree  
XX CC of differentiation was noted in the NS-3 (see AAR37927-30) and core region  
XX CC (see AAR37931) between type 3 and type 1 sequences. (Updated on 25-MAR-  
XX CC 2003 to correct PN field.)

XX SQ Sequence 184 BP; 35 A; 59 C; 58 G; 32 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 20; DB 2; Length 184;  
XX Best Local Similarity 100.0%; Pred. No. 0.055;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 179 TTGCGACCCCAACTACTC 160

RESULT 73

AAQ43067/c  
ID AAQ43067 standard; CDNA; 184 BP.

XX AC AAQ43067;

XX DT 25-MAR-2003 (revised)  
XX DT 23-SEP-1993 (first entry)

XX DE -255 to -62 region of 5' non-coding region of HCV from donor E-b16.

XX KM Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV;  
XX NS-5; phylogeny; differentiation; NS-3; core region; type 3; ss.

XX OS Hepatitis C virus.

XX PN WO9310239-A2.

XX PD 27-MAY-1993.



```

PF 20-NOV-1992; 92WO-GB002143.
XX
XX 21-NOV-1991; 91GB-00024696.
PR 24-JUN-1992; 92GB-00013362.
XX
XX (COMM-) COMMON SERVICES AGENCY.
XX
XX Simmonds P, Chan S, Yap PL;
XX
XX WPI, 1993-182554/22.
XX
XX DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for
XX diagnosing and treating HCV infection, screening blood samples and
XX identifying different HCV types.
XX
XX Disclosure; Fig 1; 120pp; English.
XX
XX The sequences given in AAQ43058-75 show the -255 to -62 non-coding region
XX of hepatitis C virus (HCV) samples from 18 blood donors and other HCV
XX variants. Analysis of this region revealed the existence of three
XX distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of
XX the groups identified were similar to those of HCV variants termed type 1
XX and 2, whilst the third appeared to represent a novel virus type.
XX Comparison of other regions of the genome, eg. the NS-5 region (see also
XX AAR37923-26), showed a high degree of sequence diversity with type 3
XX being phylogenetically different to type 1 and 2. The same degree
XX of differentiation was noted in the NS-3 (see AAR37927-30) and core region
XX (see AAR37931) between type 3 and type 1 sequences. (Updated on 25-MAR-
XX 2003 to correct PN field.)
XX
XX Sequence 184 BP; 34 A; 55 C; 59 G; 36 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 184;
XX Best Local Similarity 100.0%; Pred. No. 0.055;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 TTCCGCGACCAACTACTC 20
DB 179 TTCCGCGACCAACTACTC 160
XX
XX RESULT 74
XX AAT11272
XX ID AAT11272 standard; RNA; 186 BP.
XX
XX AAT11272;
XX
XX 26-JUN-1996 (first entry)
XX
XX Hepatitis C virus partial 5'-UTR antisense RNA AS15.
XX
XX Antisense; therapy; complementary; HCV; 5'-untranslated region;
XX hepatitis C virus; inhibition; infection; treatment; stem-loop;
XX clone 2-1; ss.
XX
XX Hepatitis C virus.
XX
XX JP07303485-A.
XX
XX 21-NOV-1995.
XX
XX 13-MAY-1994; 94JP-00124609.
XX
XX 13-MAY-1994; 94JP-00124609.
XX
XX (TOFU) TONEN CORP.
XX
XX WPI, 1996-035187/04.
XX
XX Hepatitis C virus (HCV) anti-sense RNA - inhibits HCV structural gene
XX expression in vivo for treatment of HCV infection.
XX
XX Claim 2; Page 10; 12pp; Japanese.

```

```

XX
XX The present sequence is a specifically claimed example of RNA that is
XX complementary (i.e. antisense) to part of the 5'-untranslated region of
XX the hepatitis C virus genome sequence contained in clone 2-1. The 5'-UTR
XX includes several stem-loop sequences. The antisense RNA is useful for
XX inhibiting expression of HCV structural genes and thereby inhibiting
XX viral replication in vivo. The antisense therapy can be used in addition
XX to conventional interferon treatment of HCV infections
XX
XX Sequence 186 BP; 41 A; 65 C; 48 G; 0 T; 32 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 186;
XX Best Local Similarity 80.0%; Pred. No. 0.055;
XX Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 TTCCGCGACCAACTACTC 20
DB 43 TTCCGCGACCAACTACTC 62
XX
XX RESULT 75
XX AAQ43059/C
XX ID AAQ43059 standard; cDNA; 187 BP.
XX
XX AAQ43059;
XX
XX 25-MAR-2003 (revised)
XX 23-SEP-1993 (first entry)
XX
XX -255 to -62 portion of 5' non-coding region of HCV from donors E-b2-6.
XX
XX Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV;
XX NS-5; phylogeny; differentiation; NS-3; core region; type 3; ss.
XX
XX Hepatitis C virus.
XX
XX WO9310239-A2.
XX
XX 27-MAY-1993.
XX
XX 20-NOV-1992; 92WO-GB002143.
XX
XX 21-NOV-1991; 91GB-00024696.
XX 24-JUN-1992; 92GB-00013362.
XX
XX (COMM-) COMMON SERVICES AGENCY.
XX
XX Simmonds P, Chan S, Yap PL;
XX
XX WPI, 1993-182554/22.
XX
XX DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for
XX diagnosing and treating HCV infection, screening blood samples and
XX identifying different HCV types.
XX
XX Disclosure; Fig 1; 120pp; English.
XX
XX The sequences given in AAQ43058-75 show the -255 to -62 non-coding region
XX of hepatitis C virus (HCV) samples from 18 blood donors and other HCV
XX variants. Analysis of this region revealed the existence of three
XX distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of
XX the groups identified were similar to those of HCV variants termed type 1
XX and 2, whilst the third appeared to represent a novel virus type.
XX Comparison of other regions of the genome, eg. the NS-5 region (see also
XX AAR37923-26), showed a high degree of sequence diversity with type 3
XX being phylogenetically different to type 1 and 2. The same degree
XX of differentiation was noted in the NS-3 (see AAR37927-30) and core region
XX (see AAR37931) between type 3 and type 1 sequences. (Updated on 25-MAR-
XX 2003 to correct PN field.)
XX
XX Sequence 187 BP; 36 A; 57 C; 60 G; 34 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 187;

```

Best Local Similarity 100.0%; Pred. No. 0.055;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGAGCCCACTACTC 20  
182 TTCCGAGCCCACTACTC 163

RESULT 76

AA10486/C  
ID AA10486 standard; RNA; 187 BP.

AA10486;

11-SEP-2003 (revised)  
24-OCT-2001 (first entry)

HCV 5'-UTR domain III EMSA RNA probe.

HCV 5'-UTR; minimal IRES; MIREs; internal ribosome entry site; eIF3,  
eukaryotic initiation factor 3; HCV translation initiation; antiviral;  
RNA electrophoretic gel mobility shift assay; EMSA; ss.

Hepatitis C virus; strain Ia M67463.

Location/Qualifiers

Key

misc\_binding

1. .3

/\*tag= a

/bound\_moiety= "Forms double stranded region with bases

187-185"

4. .5

/\*tag= b

/bound\_moiety= "Forms double stranded region with bases

160-159"

7. .10

/\*tag= c

/bound\_moiety= "Forms double stranded region with bases

157-154"

11. .19

/\*tag= d

/bound\_moiety= "Forms double stranded region with bases

122-114"

20. .23

/\*tag= e

/bound\_moiety= "Forms double stranded region with bases

112-109"

26. .41

/\*tag= f

/note= "Designated as IIIa"

42. .51

/\*tag= g

/bound\_moiety= "Forms double stranded region with bases

97-88"

54. .55

/\*tag= h

/bound\_moiety= "Forms double stranded region with bases

83-82"

57. .80

/\*tag= i

/note= "Designated as IIIB"

82. .83

/\*tag= j

/bound\_moiety= "Forms double stranded region with bases

55-54"

88. .97

/\*tag= k

/bound\_moiety= "Forms double stranded region with bases

51-42"

99. .108

/\*tag= l

/note= "Designated as IIIC"

109. .112

/\*tag= m

misc\_binding

misc\_binding

stem\_loop

stem\_loop

misc\_binding

misc\_binding

stem\_loop

stem\_loop

misc\_binding

misc\_binding

misc\_binding

misc\_binding

FT /bound\_moiety= "Forms double stranded region with bases

23-20"

112. .114

/\*tag= n

/note= "eIF3 toeprint"

114. .122

/\*tag= o

/bound\_moiety= "Forms double stranded region with bases

19-11"

123. .126

/\*tag= p

/bound\_moiety= "Forms double stranded region with bases

149-146"

129. .144

/\*tag= q

/note= "Designated as IIId"

146. .149

/\*tag= r

/bound\_moiety= "Forms double stranded region with bases

126-123"

154. .157

/\*tag= s

/bound\_moiety= "Forms double stranded region with bases

10-7"

159. .160

/\*tag= t

/bound\_moiety= "Forms double stranded region with bases

161. .172

/\*tag= u

/note= "Designated as IIIE"

173. .184

/\*tag= v

185. .187

/\*tag= w

/bound\_moiety= "Forms double stranded region with bases

3

stem\_loop

stem\_loop

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

misc\_binding

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misc\_binding



```
XX OS Hepatitis C virus.
XX PN W09310239-A2.
XX PD 27-MAY-1993.
XX PF 20-NOV-1992; 92WO-GB002143.
XX PR 21-NOV-1991; 91GB-00024696.
XX PR 24-JUN-1992; 92GB-00013362.
XX PA (COMM-) COMMON SERVICES AGENCY.
XX PI Simmonds P, Chan S, Yap PL;
XX DR WPI; 1993-182554/22.
XX PT DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for
XX PT diagnosing and treating HCV infection, screening blood samples and
XX PT identifying different HCV types.
XX PS Disclosure; Fig 1; 120pp; English.
XX SQ The sequences given in AAQ43058-75 show the -255 to -62 non-coding region
CC of hepatitis C virus (HCV) samples from 18 blood donors and other HCV
CC variants. Analysis of this region revealed the existence of three
CC distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of
CC the groups identified were similar to those of HCV variants termed type 1
CC and 2, whilst the third appeared to represent a novel virus type.
CC Comparison of other regions of the genome, eg. the NS-5 region (see also
CC AAR37923-26), showed a high degree of sequence diversity with type 3
CC being phylogenetically different to type 1 and 2. The same degree
CC of differentiation was noted in the NS-3 (see AAR37927-30) and core region
CC (see AAR37931) between type 3 and type 1 sequences. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX SQ Sequence 194 BP; 37 A; 56 C; 64 G; 37 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 20; DB 2; Length 194;
XX Best Local Similarity 100.0%; Pred. NO. 0.054;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTCGGACCCCAACTACTC 20
DB 189 TTTCGGACCCCAACTACTC 170
RESULT 80
AAQ43058/C
ID AAQ43058 standard; CDNA; 194 BP.
XX AC AAQ43058;
XX AC 25-MAR-2003 (revised)
XX DT 23-SEP-1993 (first entry)
XX DE -255 to -62 portion of 5' non-coding region of HCV from donor E-D1.
XX KW Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV;
XX KW NS-5; phylogeny; differentiation; NS-3; core region; type 3; ss.
XX OS Hepatitis C virus.
XX PN W09310239-A2.
XX PD 27-MAY-1993.
XX PF 20-NOV-1992; 92WO-GB002143.
XX PR 21-NOV-1991; 91GB-00024696.
XX PR 24-JUN-1992; 92GB-00013362.
XX
```

```
PA (COMM-) COMMON SERVICES AGENCY.
XX PI Simmonds P, Chan S, Yap PL;
XX DR WPI; 1993-182554/22.
XX PF DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for
XX PT diagnosing and treating HCV infection, screening blood samples and
XX PT identifying different HCV types.
XX PS Disclosure; Fig 1; 120pp; English.
XX SQ The sequences given in AAQ43058-75 show the -255 to -62 non-coding region
CC of hepatitis C virus (HCV) samples from 18 blood donors and other HCV
CC variants. Analysis of this region revealed the existence of three
CC distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of
CC the groups identified were similar to those of HCV variants termed type 1
CC and 2, whilst the third appeared to represent a novel virus type.
CC Comparison of other regions of the genome, eg. the NS-5 region (see also
CC AAR37923-26), showed a high degree of sequence diversity with type 3
CC being phylogenetically different to type 1 and 2. The same degree
CC of differentiation was noted in the NS-3 (see AAR37927-30) and core region
CC (see AAR37931) between type 3 and type 1 sequences. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX SQ Sequence 194 BP; 37 A; 57 C; 63 G; 37 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 20; DB 2; Length 194;
XX Best Local Similarity 100.0%; Pred. NO. 0.054;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTTCGGACCCCAACTACTC 20
DB 189 TTTCGGACCCCAACTACTC 170
RESULT 81
AAQ43070/C
ID AAQ43070 standard; CDNA; 194 BP.
XX AC AAQ43070;
XX AC 25-MAR-2003 (revised)
XX DT 23-SEP-1993 (first entry)
XX DE -255 to -62 region of 5' non-coding region of HCV H-90.
XX KW Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV;
XX KW NS-5; phylogeny; differentiation; NS-3; core region; type 3; ss.
XX OS Hepatitis C virus.
XX PN W09310239-A2.
XX PD 27-MAY-1993.
XX PF 20-NOV-1992; 92WO-GB002143.
XX PR 21-NOV-1991; 91GB-00024696.
XX PR 24-JUN-1992; 92GB-00013362.
XX PA (COMM-) COMMON SERVICES AGENCY.
XX PI Simmonds P, Chan S, Yap PL;
XX DR WPI; 1993-182554/22.
XX PT DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for
XX PT diagnosing and treating HCV infection, screening blood samples and
XX PT identifying different HCV types.
XX PS Disclosure; Fig 1; 120pp; English.
XX
```

CC The sequences given in AA043058-75 show the -255 to -62 non-coding region  
CC of hepatitis C virus (HCV) samples from 18 blood donors and other HCV  
CC variants. Analysis of this region revealed the existence of three  
CC distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of  
CC the groups identified were similar to those of HCV variants termed type 1  
CC and 2, whilst the third appeared to represent a novel virus type.  
CC Comparison of other regions of the genome, eg. the NS-5 region (see also  
CC AAR37923-26), showed a high degree of sequence diversity with type 3  
CC being phylogenetically different to type 1 and 2. The same degree  
CC of differentiation was noted in the NS-3 (see AAR37927-30) and core region  
CC (see AAR37931) between type 3 and type 1 sequences. (Updated on 25-MAR-  
CC 2003 to correct PN field.)  
XX  
SQ Sequence 194 BP; 38 A; 56 C; 62 G; 38 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 2; Length 194;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGGAGCCCACTACTC 20  
DB 189 TTCCGGAGCCCACTACTC 170  
RESULT 82  
AA043075/c  
ID AA043075 standard; cDNA; 194 BP.  
XX  
AC AA043075;  
XX  
DT 25-MAR-2003 (revised)  
DT 23-SEP-1993 (first entry)  
XX  
DE -255 to -62 region of 5' non-coding region of HCV HCV-J1.  
XX  
KM Non-coding region; hepatitis C virus; blood donor; type 2; type 1; HCV;  
KM NS-5; phylogeny; differentiation; NS-3; core region; type 3; 88.  
XX  
OS Hepatitis C virus.  
XX  
PN WO9310239-A2.  
XX  
PD 27-MAY-1993.  
XX  
PF 20-NOV-1992; 92MO-GB002143.  
XX  
PR 21-NOV-1991; 91GB-00024696.  
PR 24-JUN-1992; 92GB-00013362.  
XX  
PS (COMM-) COMMON SERVICES AGENCY.  
XX  
PI Simmonds P, Chan S, Yap PL;  
PI WPI, 1993-182554/22.  
XX  
PT DNA encoding antigenic peptide(s) of new types of hepatitis C virus - for  
PT diagnosing and treating HCV infection, screening blood samples and  
PT identifying different HCV types.  
XX  
PS Disclosure; Fig 1; 120pp; English.  
XX  
CC The sequences given in AA043058-75 show the -255 to -62 non-coding region  
CC of hepatitis C virus (HCV) samples from 18 blood donors and other HCV  
CC variants. Analysis of this region revealed the existence of three  
CC distinct groups of HCV differing by 9-14% in nucleotide sequence. Two of  
CC the groups identified were similar to those of HCV variants termed type 1  
CC and 2, whilst the third appeared to represent a novel virus type.  
CC Comparison of other regions of the genome, eg. the NS-5 region (see also  
CC AAR37923-26), showed a high degree of sequence diversity with type 3  
CC being phylogenetically different to type 1 and 2. The same degree  
CC of differentiation was noted in the NS-3 (see AAR37927-30) and core region  
CC (see AAR37931) between type 3 and type 1 sequences. (Updated on 25-MAR-  
CC 2003 to correct PN field.)

XX  
SQ Sequence 194 BP; 37 A; 57 C; 63 G; 37 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 2; Length 194;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGGAGCCCACTACTC 20  
DB 189 TTCCGGAGCCCACTACTC 170  
RESULT 83  
ADS34710/c  
ID ADS34710 standard; DNA; 197 BP.  
XX  
AC ADS34710;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE siRNA-7 PCR product, seq id 53.  
XX  
KM siRNA; anti-inflammatory; hepatotropic; hepatitis C virus; HCV;  
KM proliferation; siRNA; short interfering RNA; RNA interference;  
KM gene silencing; ds.  
XX  
OS Unidentified.  
XX  
PN WO2004078974-A1.  
XX  
PD 16-SEP-2004.  
XX  
PF 23-JAN-2004; 2004WO-JP000605.  
XX  
PR 24-JAN-2003; 2003JP-00016750.  
XX  
PA (TOKM-) TOKYO METROPOLITAN ORG MEDICAL RES.  
PA (CHUS) CHUGAI SEIYAKU KK.  
XX  
PI Kohara M, Watanabe T, Taira K, Miyagishi M, Sudo M;  
PI WPI, 2004-662428/64.  
XX  
DR  
XX  
PT New oligo ribonucleotide or peptide nucleic acid capable of sequence-  
PT specifically binding with RNA of hepatitis C virus, useful for inhibiting  
PT proliferation of hepatitis C virus and useful as hepatitis C virus  
PT therapeutic agent.  
XX  
PS Example 6; SEQ ID NO 53; 80pp; Japanese.  
XX  
CC The invention relates to an oligo ribonucleotide or peptide nucleic acid  
CC (I) capable of sequence-specifically binding with RNA of hepatitis C  
CC virus (HCV), and comprising a sequence hybridising under stringent  
CC conditions with RNA of HCV. The method of the invention relates to the  
CC inhibition of the proliferation of HCV. The oligo ribonucleotide or  
CC peptide nucleic acid of the invention is useful for inhibiting the  
CC proliferation of HCV which involves contacting (I) with RNA of HCV. (1)  
CC is useful as a therapeutic agent of hepatitis C. The current sequence  
CC represents a PCR product from an example of the invention.  
XX  
SQ Sequence 197 BP; 48 A; 57 C; 56 G; 36 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 13; Length 197;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGGAGCCCACTACTC 20  
DB 77 TTCCGGAGCCCACTACTC 58  
RESULT 84  
ABL41919/c



PT which is amplified and detected, is more sensitive than a comparable  
PT ELISA and is useful to detect prion protein or lectin.  
XX  
PS Example 2; Page 35; 44pp; German.  
XX  
CC This invention describes a novel method of detecting a substance in a  
CC test sample. The method comprises forming a detector complex, in which  
CC the substance is bound to a connection agent conjugated to a detector  
CC nucleic acid which is replicated with a replication agent. A competitor  
CC nucleic acid which competes for the replication agent is also added and  
CC replication of the detector and competitor nucleic acids is determined.  
CC Preferably two or more binding reagents and/or two or more detector  
CC nucleic acids are used. The detected substance is preferably immobilised  
CC on a solid surface. Preferably the substance is bound to an immobilised  
CC binding reagent connected to a first immobilised nucleic acid, which is  
CC hybridised to a second nucleic acid bound to a solid surface. A negative  
CC control is preferably also performed using the detector and competitor  
CC nucleic acids in the absence of the substance and the mix of replicated  
CC detector and competitor nucleic acids in the sample test compared to the  
CC negative control test. The method is useful for detecting a substance,  
CC particularly a prion protein or a lectin in a liquid and is more  
CC sensitive than a comparable ELISA. This sequence represents  
CC polynucleotide fragment KF-2 which is a competitive inhibitor of murine  
CC IGG designated DNA-169, used in an assay described in the invention.  
XX  
SQ Sequence 209 BP; 36 A; 60 C; 69 G; 44 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 8; Length 209;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGGACCCCAACTACTC 20  
DB 170 TTGGGACCCCAACTACTC 151  
RESULT 86  
AD005658/C  
ID AD005658 standard; DNA; 226 BP.  
XX  
AC AD005658;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE HCV template DNA fragment.  
XX  
KW Nucleic acid amplification; mutation detection; cytosstatic;  
XX antiinflammatory; hepatotropic; viroicide; cancer; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2004035832-A1.  
XX  
PD 29-APR-2004.  
XX  
PF 17-OCT-2003; 2003WO-KR002179.  
XX  
PR 18-OCT-2002; 2002KR-00063832.  
XX  
PR 02-SEP-2003; 2003KR-00061066.  
XX  
PA (GENE-) GENEMATRIX INC.  
XX  
PI Kim N, Kim S, Kim S, Kim E, Moon M, Yoo W, Lee C, Chung H;  
XX Jee M, Hwang S, Hong S;  
XX  
DR WPI; 2004-348478/32.  
XX  
PT Detecting a mutation, useful in diagnosing and treating e.g. cancer or  
PT hepatitis, comprises generating fragments of polynucleotides using  
PT specific primers and measuring molecular weight of cleaved fragments.  
XX  
PS Example 4; SEQ ID NO 19; 58pp; English.  
XX

CC The invention relates to detecting a mutation. The method involves  
CC amplifying a target polynucleotide using a forward primer and a reverse  
CC primer; generating fragments of two or more single-stranded  
CC polynucleotides including one or more mutations sequence having the size  
CC of 2-32 bases by cleaving the amplified target polynucleotide with  
CC restriction enzymes, where the second restriction enzyme does not react  
CC while a first restriction enzyme is reacted with the amplified  
CC polynucleotide; and measuring the molecular weight of the cleaved  
CC fragments. The polynucleotide is cleaved to include one mutation among  
CC two or more different mutations in only one single stranded  
CC polynucleotide fragment and all mutations in the other single stranded  
CC nucleotide fragment. Restrictions enzyme treatment step is performed  
CC using restriction enzymes having different optimum temperatures. The  
CC method is useful in detecting a mutation. The method and primer are  
CC useful in diagnosing, prognosing, treating and preventing a disease, e.g.  
CC cancer or hepatitis B or C virus. The present sequence represents a HCV  
CC template DNA sequence.  
XX  
SQ Sequence 226 BP; 41 A; 64 C; 73 G; 48 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 226;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGGACCCCAACTACTC 20  
DB 200 TTGGGACCCCAACTACTC 181  
RESULT 87  
AD005662  
ID AD005662 standard; DNA; 230 BP.  
XX  
AC AD005662;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE PCR amplified HCV DNA fragment.  
XX  
KW Nucleic acid amplification; mutation detection; cytosstatic;  
XX antiinflammatory; hepatotropic; viroicide; cancer; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2004035832-A1.  
XX  
PD 29-APR-2004.  
XX  
PF 17-OCT-2003; 2003WO-KR002179.  
XX  
PR 18-OCT-2002; 2002KR-00063832.  
XX  
PR 02-SEP-2003; 2003KR-00061066.  
XX  
PA (GENE-) GENEMATRIX INC.  
XX  
PI Kim N, Kim S, Kim S, Kim E, Moon M, Yoo W, Lee C, Chung H;  
XX Jee M, Hwang S, Hong S;  
XX  
DR WPI; 2004-348478/32.  
XX  
PT Detecting a mutation, useful in diagnosing and treating e.g. cancer or  
PT hepatitis, comprises generating fragments of polynucleotides using  
PT specific primers and measuring molecular weight of cleaved fragments.  
XX  
PS Example 4; SEQ ID NO 23; 58pp; English.  
XX  
CC The invention relates to detecting a mutation. The method involves  
CC amplifying a target polynucleotide using a forward primer and a reverse  
CC primer; generating fragments of two or more single-stranded  
CC polynucleotides including one or more mutations sequence having the size  
CC of 2-32 bases by cleaving the amplified target polynucleotide with  
CC restriction enzymes, where the second restriction enzyme does not react  
CC while a first restriction enzyme is reacted with the amplified

CC polynucleotide; and measuring the molecular weight of the cleaved  
 CC fragments. The polynucleotide is cleaved to include one mutation among  
 CC two or more different mutations in only one single stranded  
 CC polynucleotide fragment and all mutations in the other single stranded  
 CC nucleotide fragment. Restrictions enzyme treatment step is performed  
 CC using restriction enzymes having different optimum temperatures. The  
 CC method is useful in detecting a mutation. The method and primer are  
 CC useful in diagnosing, prognosing, treating and preventing a disease, e.g.  
 CC cancer or hepatitis B or C virus. The present sequence represents a PCR  
 CC amplified HCV DNA fragment.

XX Sequence 230 BP; 48 A; 76 C; 64 G; 42 T; 0 U; 0 Other;

Query Match Best Local Similarity 100.0%; Score 20; DB 12; Length 230;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCACTACTC 20  
 DB 27 TTGCGAGCCCACTACTC 46

#### RESULT 88

AD005661/c ADO05661 standard; DNA; 230 BP.

AC ADO05661;

DT 15-JUL-2004 (first entry)

DE PCR amplified HCV DNA fragment.

XX Nucleic acid amplification; mutation detection; cytostratic;

KW antiinflammatory; hepatotropic; virucide; cancer; ds.

XX Hepatitis C virus.

PN WO2004035832-A1.

PD 29-APR-2004.

PF 17-OCT-2003; 2003WO-KR002179.

PR 18-OCT-2002; 2002KR-00063832.

PR 02-SEP-2003; 2003KR-00061066.

PA (GENE-) GENEMATRIX INC.

PI Kim N, Kim S, Kim S, Kim E, Moon M, Yoo W, Lee C, Chung H;

PI Jee M, Hwang S, Hong S;

DR WPI; 2004-348478/32.

PT Detecting a mutation, useful in diagnosing and treating e.g. cancer or  
 PT hepatitis, comprises generating fragments of polynucleotides using  
 PT specific primers and measuring molecular weight of cleaved fragments.

PS Example 4; SEQ ID NO 22; 58pp; English.

CC The invention relates to detecting a mutation. The method involves  
 CC amplifying a target polynucleotide using a forward primer and a reverse  
 CC primer; generating fragments of two or more single-stranded  
 CC polynucleotides including one or more mutations sequence having the size  
 CC of 2-32 bases by cleaving the amplified target polynucleotide with  
 CC restriction enzymes, where the second restriction enzyme does not react  
 CC while a first restriction enzyme is reacted with the amplified  
 CC polynucleotide; and measuring the molecular weight of the cleaved  
 CC fragments. The polynucleotide is cleaved to include one mutation among  
 CC two or more different mutations in only one single stranded  
 CC polynucleotide fragment and all mutations in the other single stranded  
 CC nucleotide fragment. Restrictions enzyme treatment step is performed  
 CC using restriction enzymes having different optimum temperatures. The  
 CC method is useful in detecting a mutation. The method and primer are

CC useful in diagnosing, prognosing, treating and preventing a disease, e.g.  
 CC cancer or hepatitis B or C virus. The present sequence represents a PCR  
 CC amplified HCV DNA fragment.

XX Sequence 230 BP; 42 A; 64 C; 76 G; 48 T; 0 U; 0 Other;

Query Match Best Local Similarity 100.0%; Score 20; DB 12; Length 230;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCACTACTC 20  
 DB 204 TTGCGAGCCCACTACTC 185

#### RESULT 89

AAV70460/c AAV70460 standard; DNA; 232 BP.

AC AAV70460;

DT 08-APR-1999 (first entry)

DE Partial sequence of HCV subtype 1b amplicon #86.

XX Nucleic acid detection; nucleic acid characterisation; hybridisation;

KW infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.

XX Hepatitis C virus.

PN WO9850403-A1.

PD 12-NOV-1998.

PF 05-MAY-1998; 98WO-US003194.

PR 05-MAY-1997; 97US-00851588.

PR 19-SEP-1997; 97US-00934097.

PR 03-MAR-1998; 98US-00034205.

PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;

PI Anderson TA, Dahlberg JE;

DR WPI; 1998-610317/51.

PT Detection and characterisation of nucleic acid sequences - by mixing a  
 PT folded target and one or more probes to form a probe/folded target  
 PT complex and detecting and characterising the complexes.

PS Example 5; Page 172-173; 279pp; English.

CC The invention relates to methods and compositions of detection and  
 CC characterisation of nucleic acid sequences and sequence changes. One  
 CC method of detection and characterisation comprises: (a) providing: (i) a  
 CC folded target having a DNA sequence comprising at least 1 double stranded  
 CC region and at least 1 single stranded region; and (ii) at least 1 probe  
 CC complementary to at least a portion of the folded target; and (b) mixing  
 CC the target and probes so that the probe hybridises to form a probe  
 CC /folded target complex. Also provided are methods for determination of  
 CC structure formation in nucleic acid targets; for analysing folded nucleic  
 CC acids targets; and for analysis of nucleic acid structures. The methods  
 CC can be used for the detection and characterisation of nucleic acid  
 CC sequences to detect the presence of pathogenic nucleic acid sequences  
 CC indicative of an infection, the presence of variants or alleles of  
 CC mammalian genes associated with disease and cancers, and the  
 CC identification of the source of nucleic acids found in forensic samples,  
 CC as well as in paternity determinations. The methods allow simultaneous  
 CC analysis of both strands (e.g. the sense and antisense strands) and are  
 CC ideal for high-level multiplexing. The products produced are amenable to  
 CC qualitative, quantitative and positional analysis. The methods may be  
 CC performed in solution or in the solid phase (e.g. on a solid support).



CC The methods are powerful in that they allow for analysis of longer  
 CC fragments of nucleic acid than current methodologies. Sequences AAV70453-  
 CC 61 represent partial sequences of different amplicons of hepatitis C  
 CC virus (HCV) subtypes 1a, 1b, 2c and 3a. These partial sequences are used  
 CC for identifying the HCV subtypes

XX  
 SQ Sequence 232 BP; 40 A; 65 C; 76 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 232;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
 Db 199 TTGGGACCCCAACTACTC 180

RESULT 90  
 ABL46070/C  
 ID ABL46070 standard; DNA; 232 BP.

XX ABL46070;  
 AC  
 DT 26-APR-2002 (first entry)

XX Hepatitis C virus partial sequence #86 SEQ ID NO:37.

XX Nucleic acid accessible hybridisation site; detection; hybridisation;  
 KW characterisation; identification; nucleic acid structure; diagnosis;  
 KW PCR primer; probe; ss.

OS Hepatitis C virus.  
 OS Synthetic.

XX WO200198537-A2.

XX 27-DEC-2001.

XX 15-JUN-2001; 2001WO-US019401.

XX 17-JUN-2000; 2000US-0212308P.

XX 15-JUN-2001; 2001US-00212308.

XX (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX Lyamichev V, Alawi H, Dong F, Neri BP, Vener IT;

XX WPI, 2002-049698/06.

XX Identifying oligonucleotides hybridizing to nucleic acids containing  
 PT secondary structure, useful in clinical diagnosis, comprises identifying  
 PT primers that interact with the target to form an extension product under  
 PT amplification conditions.

XX Example 5; Page 366; 409pp; English.

XX The present invention describes a method for identifying oligonucleotides  
 CC with desired hybridisation properties to nucleic acid targets containing  
 CC secondary structure. The method comprises amplifying a target nucleic  
 CC acid having at least one accessible and one inaccessible site. Primers  
 CC that form an extension product are identified as the oligonucleotides  
 CC which can interact with the folded target nucleic acid. Oligonucleotides  
 CC from the present invention can be used in novel detection methods for  
 CC clinical diagnostic purposes, including the detection and identification  
 CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
 CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
 CC sequences used in the exemplification of the present invention

XX Sequence 232 BP; 40 A; 65 C; 76 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 232;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
 Db 199 TTGGGACCCCAACTACTC 180

RESULT 91  
 ADK82260/C  
 ID ADK82260 standard; DNA; 232 BP.

XX ADK82260;

XX 03-JUN-2004 (first entry)

XX Hepatitis C virus polynucleotide seqid 37.

XX nucleic acid analysis; hepatitis C virus;  
 KW non-contiguous single-stranded region; NCSR; cleavage structure;  
 KW clinical; diagnostic; microorganism detection;  
 KW microorganism identification; hepatitis C virus; HCV; ds.

XX Hepatitis C virus.

XX US6709815-B1.

XX 23-MAR-2004.

XX 18-JUL-2000; 2000US-00402618.

XX 05-MAY-1997; 97US-00861588.

XX 19-SEP-1997; 97US-00934097.

XX 03-MAR-1998; 98US-00034205.

XX (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;

XX Anderson TA, Dahlberg JE;

XX WPI, 2004-256067/24.

XX Analyzing nucleic acids, comprises mixing target nucleic acid such as

XX hepatitis C virus nucleic acid, bridging oligonucleotide, second

XX oligonucleotide and cleavage agent to form cleavage structure.

XX Example 5; SEQ ID NO 37; 143pp; English.

XX The invention describes a method of analysing nucleic acids comprising  
 CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
 CC having non-contiguous single-stranded regions (NCSR) separated by an  
 CC intervening region, a bridging oligonucleotide capable of binding to the  
 CC first and second NCSR; a second oligonucleotide binding to a portion of  
 CC the first NCSR and a cleavage agent, and mixing the contents to form a  
 CC cleavage structure. The method is useful for analysing nucleic acids,  
 CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
 CC purposes and detection and identification of pathogenic microorganisms  
 CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
 CC polynucleotide that is sufficient for identification of HCV subtypes  
 CC using the analysis methods of the invention.

XX Sequence 232 BP; 40 A; 65 C; 76 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 232;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
 Db 199 TTGGGACCCCAACTACTC 180

RESULT 92  
 AAV70459/C  
 ID AAV70459 standard; DNA; 239 BP.

XX AC AAV70459;  
XX XX  
DT DT 08-APR-1999 (first entry)  
DE DE Partial sequence of HCV subtype 1a amplicon #85.  
KW KW Nucleic acid detection; nucleic acid characterisation; hybridisation;  
KM KM infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.  
XX XX  
OS OS Hepatitis C virus.  
PN PN MO9850403-A1.  
PD PD 12-NOV-1998.  
PE PE 05-MAY-1998; 98WO-US003194.  
PR PR 05-MAY-1997; 97US-00851588.  
PR PR 19-SEP-1997; 97US-00934097.  
PA PA 03-MAR-1998; 98US-00034205.  
PA PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XX XX  
PI PI Dong F., Lyamichev VI, Prudent JR, Fors L, Neiri BP, Brow MAD;  
PT PT Anderson TA, Dahlberg JE;  
DR DR MPI; 1998-610317/51.  
XX XX  
XX XX Detection and characterisation of nucleic acid sequences - by mixing a  
PT PT folded target and one or more probes to form a probe/folded target  
PT PT complex and detecting and characterising the complexes.  
XX XX  
PS PS Example 5; Page 172; 279pp; English.

The invention relates to methods and compositions of detection and  
characterisation of nucleic acid sequences and sequence changes. One  
method of detection and characterisation comprises: (a) providing: (i) a  
folded target having a DNA sequence comprising at least 1 double stranded  
region and at least 1 single stranded region; and (ii) at least 1 probe  
complementary to at least a portion of the folded target; and (b) mixing  
the target and probes so that the probe hybridises to form a probe  
/folded target complex. Also provided are methods for determination of  
structure formation in nucleic acid targets; for analysing folded nucleic  
acid targets; and for analysis of nucleic acid structures. The methods  
can be used for the detection and characterisation of nucleic acid  
sequences to detect the presence of pathogenic nucleic acid sequences  
indicative of an infection, the presence of variants or alleles of  
mammalian genes associated with disease and cancers, and the  
identification of the source of nucleic acids found in forensic samples,  
as well as in paternally determinations. The methods allow simultaneous  
analysis of both strands (e.g. the sense and antisense strands) and are  
ideal for high-level multiplexing. The products produced are amenable to  
qualitative, quantitative and positional analysis. The methods may be  
performed in solution or in the solid phase (e.g. on a solid support).  
The methods are powerful in that they allow for analysis of longer  
fragments of nucleic acid than current methodologies. Sequences AAV70453-  
61 represent partial sequences of different amplicons of hepatitis C  
virus (HCV) subtypes 1a, 1b, 2c and 3a. These partial sequences are used  
for identifying the HCV subtypes

Sequence 239 BP; 45 A; 64 C; 77 G; 53 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 TTGCGACCCCACTACTC 20  
|||||  
Ddb TTGCGACCCCACTACTC 187

RESULT 93

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AAV70455/c ID AAV70455 standard; DNA; 239 BP.  
AC AAV70455;  
DT 08-APR-1999 (first entry)  
DE Partial sequence of HCV subtype 1a amplicon #72.  
KM Nucleic acid detection; nucleic acid characterisation; hybridisation;  
KW infection; disease; cancer; forensic; paternity; multiplexing; HCV; de  
XX Hepatitis C virus.  
OS MO850403-A1.  
PN 12-NOV-1998.  
PD 05-MAY-1998; 96WO-US003194.  
PF 05-MAY-1997; 97US-00851588,  
PR 19-SEP-1997; 97US-00934097,  
PR 03-MAR-1998; 98US-00034205.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
PI Dong F, Lyamachev VI, Prudent JR, Fors LJ, Neri BP, Brow MAD;  
PI Anderson TA, Dahlberg JE;  
DX MPI, 1998-610317/51.  
XX  
PT Detection and characterisation of nucleic acid sequences - by mixing a  
PT folded target and one or more probes to form a probe/folded target  
PT complex and detecting and characterising the complexes.  
PS Example 5; Page 171; 279pp; English.  
XX  
CC The invention relates to methods and compositions of detection and  
CC characterisation of nucleic acid sequences and sequence changes. One  
CC method of detection and characterisation comprises: (a) providing: (1) a  
CC folded target having a DNA sequence comprising at least 1 double stranded  
CC region and at least 1 single stranded region; and (ii) at least 1 probe  
CC complementary to at least a portion of the folded target; and (b) mixing  
CC the target and probes so that the probe hybridises to form a probe  
CC /folded target complex. Also provided are methods for determination of  
CC structure formation in nucleic acid targets; for analysing folded nucleic  
CC acids targets; and for analysis of nucleic acid structures. The methods  
CC can be used for the detection and characterisation of nucleic acid  
CC sequences to detect the presence of pathogenic nucleic acid sequences  
CC indicative of an infection, the presence of variants or alleles of  
CC mammalian genes associated with disease and cancers, and the  
CC identification of the source of nucleic acids found in forensic samples,  
CC as well as in patently determinations. The methods allow simultaneous  
CC analysis of both strands (e.g. the sense and antisense strand) and are  
CC ideal for high-level multiplexing. The products produced are amenable to  
CC qualitative, quantitative and positional analysis. The methods may be  
CC performed in solution or in the solid phase (e.g. on a solid support).  
CC The methods are powerful in that they allow for analysis of longer  
CC fragments of nucleic acid than current methodologies. Sequences AAV70453-  
CC 61 represent partial sequences of different amplicons of hepatitis C  
CC virus (HCV) subtypes 1a, 1b, 2c and 3a. These partial sequences are used  
CC for identifying the HCV subtypes
```

```
SQ Sequence 239 BP; 45 A; 63 C; 78 G; 53 T; 0 U; 0 Other;
```

```
Query Match      100.0%; Score 20; DB 2; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches    20; Conservative   0; Mismatches     0; Indels       0; Gaps        0.
```

```
1 TTGGGAGCCCAACTATCTC 20  
|||||  
db TTGGGAGCCCAACTACTTC 187
```

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RESULT 94
ABLA6065/C
ID ABLA6065 standard; DNA; 239 BP.
XX
AC ABLA6065;
XX
DT 26-APR-2002 (first entry)
XX
DE Hepatitis C virus partial sequence #72 SEQ ID NO:32.
XX
KM Nucleic acid accessible hybridisation site; detection; hybridisation;
KM characterisation; identification; nucleic acid structure; diagnosis;
KM PCR primer; probe; ss.
XX
OS Hepatitis C virus.
OS Synthetic.
XX
PN WO200198537-A2.
XX
PD 27-DEC-2001.
XX
PF 15-JUN-2001; 2001WO-US019401.
XX
PR 17-JUN-2000; 2000US-0212308P.
PR 15-JUN-2001; 2001US-00212308.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;
XX
DR WPI; 2002-049698/06.
XX
PT Identifying oligonucleotides hybridizing to nucleic acids containing
PT secondary structure, useful in clinical diagnosis, comprises identifying
PT primers that interact with the target to form an extension product under
PT amplification conditions.
XX
PS Example 5; Page 365; 409pp; English.
XX
CC The present invention describes a method for identifying oligonucleotides
CC with desired hybridisation properties to nucleic acid targets containing
CC secondary structure. The method comprises amplifying a target nucleic
CC acid having at least one accessible and one inaccessible site. Primers
CC that form an extension product are identified as the oligonucleotides
CC which can interact with the folded target nucleic acid. Oligonucleotides
CC from the present invention can be used in novel detection methods for
CC clinical diagnostic purposes, including the detection and identification
CC of pathogenic organisms (e.g. HIV). The method allows the ability to
CC rapidly analyse nucleic acid structures. ABLA6034 to ABLA6367 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 239 BP; 45 A; 63 C; 78 G; 53 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 6; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TTGGGAGCCCAACTACTC 20
DB 206 TTGGGAGCCCAACTACTC 187
XX
RESULT 95
ABLA6069/C
ID ABLA6069 standard; DNA; 239 BP.
XX
AC ABLA6069;
XX
DT 26-APR-2002 (first entry)
XX
DE Hepatitis C virus partial sequence #85 SEQ ID NO:36.
XX
```

```
KM Nucleic acid accessible hybridisation site; detection; hybridisation;
KM characterisation; identification; nucleic acid structure; diagnosis;
KM PCR primer; probe; ss.
XX
OS Hepatitis C virus.
OS Synthetic.
XX
PN WO200198537-A2.
XX
PD 27-DEC-2001.
XX
PF 15-JUN-2001; 2001WO-US019401.
XX
PR 17-JUN-2000; 2000US-0212308P.
PR 15-JUN-2001; 2001US-00212308.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;
XX
DR WPI; 2002-049698/06.
XX
PT Identifying oligonucleotides hybridizing to nucleic acids containing
PT secondary structure, useful in clinical diagnosis, comprises identifying
PT primers that interact with the target to form an extension product under
PT amplification conditions.
XX
PS Example 5; Page 366; 409pp; English.
XX
CC The present invention describes a method for identifying oligonucleotides
CC with desired hybridisation properties to nucleic acid targets containing
CC secondary structure. The method comprises amplifying a target nucleic
CC acid having at least one accessible and one inaccessible site. Primers
CC that form an extension product are identified as the oligonucleotides
CC which can interact with the folded target nucleic acid. Oligonucleotides
CC from the present invention can be used in novel detection methods for
CC clinical diagnostic purposes, including the detection and identification
CC of pathogenic organisms (e.g. HIV). The method allows the ability to
CC rapidly analyse nucleic acid structures. ABLA6034 to ABLA6367 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 239 BP; 45 A; 64 C; 77 G; 53 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 6; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TTGGGAGCCCAACTACTC 20
DB 206 TTGGGAGCCCAACTACTC 187
XX
RESULT 96
ADK82255/C
ID ADK82255 standard; DNA; 239 BP.
XX
AC ADK82255;
XX
DT 03-JUN-2004 (first entry)
XX
DE Hepatitis C virus polynucleotide seqid 32.
XX
KM nucleic acid analysis; hepatitis C virus;
KM non-contiguous single-stranded region; NCSR; cleavage structure;
KM clinical; diagnostic; microorganism detection;
KM microorganism identification; hepatitis C virus; HCV; ds.
XX
OS Hepatitis C virus.
XX
PN US6709815-B1.
XX
PD 23-MAR-2004.
XX
```

PF 18-JUL-2000; 2000US-00402618.  
 XX  
 PR 05-MAY-1997; 97US-00851588.  
 PR 19-SEP-1997; 97US-00934097.  
 PR 03-MAR-1998; 98US-00034205.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;  
 XX  
 DR WPI; 2004-256067/24.  
 XX  
 PT Analyzing nucleic acids, comprises mixing target nucleic acid such as  
 PT hepatitis C virus nucleic acid, bridging oligonucleotide, second  
 PT oligonucleotide and cleavage agent to form cleavage structure.  
 XX  
 PS Example 5; SEQ ID NO 32; 143bp; English.  
 XX  
 CC The invention describes a method of analyzing nucleic acids comprising  
 CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
 CC having non-contiguous single-stranded regions (NCSR) separated by an  
 CC intervening region, a bridging oligonucleotide capable of binding to the  
 CC first and second NCSR, a second oligonucleotide binding to a portion of  
 CC the first NCSR and a cleavage agent, and mixing the contents to form a  
 CC cleavage structure. The method is useful for analyzing nucleic acids,  
 CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
 CC purposes and detection and identification of pathogenic microorganisms  
 CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
 CC polynucleotide that is sufficient for identification of HCV subtypes  
 CC using the analysis methods of the invention.  
 XX  
 SQ Sequence 239 BP; 45 A; 63 C; 78 G; 53 T; 0 U; 0 Other;  
 XX  
 QY Query Match 100.0%; Score 20; DB 12; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 DB 1 TTGGCGACCCCAACTACTC 20  
 206 TTGGCGACCCCAACTACTC 187  
 XX  
 RESULT 97  
 ADR82259/C  
 ID ADR82259 standard; DNA; 239 BP.  
 AC ADR82259;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Hepatitis C virus polynucleotide seqid 36.  
 XX  
 KW nucleic acid analysis; hepatitis C virus;  
 KW non-contiguous single-stranded region; NCSR; cleavage structure;  
 KW clinical; diagnostic; microorganism detection;  
 KW microorganism identification; hepatitis C virus; HCV; ds.  
 XX  
 OS Hepatitis C virus.  
 OS  
 PN US6709815-B1.  
 XX  
 PD 23-MAR-2004.  
 XX  
 PF 18-JUL-2000; 2000US-00402618.  
 XX  
 PR 05-MAY-1997; 97US-00851588.  
 PR 19-SEP-1997; 97US-00934097.  
 PR 03-MAR-1998; 98US-00034205.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI

PI Anderson TA, Dahlberg JE;  
 XX  
 DR WPI; 2004-256067/24.  
 XX  
 PT Analyzing nucleic acids, comprises mixing target nucleic acid such as  
 PT hepatitis C virus nucleic acid, bridging oligonucleotide, second  
 PT oligonucleotide and cleavage agent to form cleavage structure.  
 XX  
 PS Example 5; SEQ ID NO 36; 143bp; English.  
 XX  
 CC The invention describes a method of analyzing nucleic acids comprising  
 CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
 CC having non-contiguous single-stranded regions (NCSR) separated by an  
 CC intervening region, a bridging oligonucleotide capable of binding to the  
 CC first and second NCSR, a second oligonucleotide binding to a portion of  
 CC the first NCSR and a cleavage agent, and mixing the contents to form a  
 CC cleavage structure. The method is useful for analyzing nucleic acids,  
 CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
 CC purposes and detection and identification of pathogenic microorganisms  
 CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
 CC polynucleotide that is sufficient for identification of HCV subtypes  
 CC using the analysis methods of the invention.  
 XX  
 SQ Sequence 239 BP; 45 A; 64 C; 77 G; 53 T; 0 U; 0 Other;  
 XX  
 QY Query Match 100.0%; Score 20; DB 12; Length 239;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 DB 1 TTGGCGACCCCAACTACTC 20  
 206 TTGGCGACCCCAACTACTC 187  
 XX  
 RESULT 98  
 AAV70458/C  
 ID AAV70458 standard; DNA; 240 BP.  
 AC AAV70458;  
 XX  
 DT 08-APR-1999 (first entry)  
 XX  
 DE Partial sequence of HCV subtype 3a amplicon #81.  
 XX  
 KW Nucleic acid detection; nucleic acid characterisation; hybridisation;  
 KW infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.  
 XX  
 OS Hepatitis C virus.  
 OS  
 PN WO9850403-A1.  
 XX  
 PD 12-NOV-1998.  
 XX  
 PF 05-MAY-1998; 98WO-US003194.  
 XX  
 PR 05-MAY-1997; 97US-00851588.  
 PR 19-SEP-1997; 97US-00934097.  
 PR 03-MAR-1998; 98US-00034205.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;  
 XX  
 DR WPI; 1998-610317/51.  
 XX  
 PT Detection and characterisation of nucleic acid sequences - by mixing a  
 PT folded target and one or more probes to form a probe/folded target  
 PT complex and detecting and characterising the complexes.  
 XX  
 PS Example 5; Page 172; 279pp; English.  
 XX  
 CC The invention relates to methods and compositions of detection and

CC characterisation of nucleic acid sequences and sequence changes. One  
 CC method of detection and characterisation comprises: (a) providing: (i) a  
 CC folded target having a DNA sequence comprising at least 1 double stranded  
 CC region and at least 1 single stranded region; and (ii) at least 1 probe  
 CC complementary to at least a portion of the folded target; and (b) mixing  
 CC the target and probes so that the probe hybridises to form a probe  
 CC /folded target complex. Also provided are methods for determination of  
 CC structure formation in nucleic acid targets; for analysing folded nucleic  
 CC acids targets; and for analysis of nucleic acid structures. The methods  
 CC can be used for the detection and characterisation of nucleic acid  
 CC sequences to detect the presence of pathogenic nucleic acid sequences  
 CC indicative of an infection, the presence of variants or alleles of  
 CC mammalian genes associated with disease and cancers, and the  
 CC identification of the source of nucleic acids found in forensic samples,  
 CC as well as in paternity determinations. The methods allow simultaneous  
 CC analysis of both strands (e.g. the sense and antisense strands) and are  
 CC ideal for high-level multiplexing. The products produced are amenable to  
 CC qualitative, quantitative and positional analysis. The methods may be  
 CC performed in solution or in the solid phase (e.g. on a solid support).  
 CC The methods are powerful in that they allow for analysis of longer  
 CC fragments of nucleic acid than current methodologies. Sequences AAV70453-  
 CC 61 represent partial sequences of different amplicons of hepatitis C  
 CC virus (HCV) subtypes 1a, 1b, 2c and 3a. These partial sequences are used  
 CC for identifying the HCV subtypes

Sequence 240 BP; 45 A; 66 C; 79 G; 50 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 240;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCCGACCCCAACTACTC 20  
 |||||  
 Db 207 TTCCGACCCCAACTACTC 188

RESULT 99  
 AAV70456/C  
 ID AAV70456 standard; DNA; 240 BP.

XX AAV70456;  
 AC  
 XX  
 DT 08-APR-1999 (first entry)  
 XX  
 DE Partial sequence of HCV subtype 1a amplicon #73.

XX Nucleic acid detection; nucleic acid characterisation; hybridisation;  
 KW infection; disease; cancer; forensic; paternity; multiplexing; HCV; de.  
 XX Hepatitis C virus.

OS Hepatitis C virus.

PN WO9850403-A1.

PD 12-NOV-1998.

PN 05-MAY-1998; 98WO-US003194.

PF 05-MAY-1997; 97US-00851588.

PR 19-SEP-1997; 97US-00934097.

PR 03-MAR-1998; 98US-00034205.

XX (THIR-) THIRD WAVE TECHNOLOGIES INC.

PA

PI Dong F, Lyamichov VI, Prudent JR, Fors L, Neri BP, Brow MAD;

PI Anderson TA, Dahlberg JE;

XX WPI; 1998-610317/51.

DR Detection and characterisation of nucleic acid sequences - by mixing a  
 PT folded target and one or more probes to form a probe/folded target  
 PT complex and detecting and characterising the complexes.  
 PS Example 5; Page 171; 279pp; English.

XX The invention relates to methods and compositions of detection and  
 CC characterisation of nucleic acid sequences and sequence changes. One  
 CC method of detection and characterisation comprises: (a) providing: (i) a  
 CC folded target having a DNA sequence comprising at least 1 double stranded  
 CC region and at least 1 single stranded region; and (ii) at least 1 probe  
 CC complementary to at least a portion of the folded target; and (b) mixing  
 CC the target and probes so that the probe hybridises to form a probe  
 CC /folded target complex. Also provided are methods for determination of  
 CC structure formation in nucleic acid targets; for analysing folded nucleic  
 CC acids targets; and for analysis of nucleic acid structures. The methods  
 CC can be used for the detection and characterisation of nucleic acid  
 CC sequences to detect the presence of pathogenic nucleic acid sequences  
 CC indicative of an infection, the presence of variants or alleles of  
 CC mammalian genes associated with disease and cancers, and the  
 CC identification of the source of nucleic acids found in forensic samples,  
 CC as well as in paternity determinations. The methods allow simultaneous  
 CC analysis of both strands (e.g. the sense and antisense strands) and are  
 CC ideal for high-level multiplexing. The products produced are amenable to  
 CC qualitative, quantitative and positional analysis. The methods may be  
 CC performed in solution or in the solid phase (e.g. on a solid support).  
 CC The methods are powerful in that they allow for analysis of longer  
 CC fragments of nucleic acid than current methodologies. Sequences AAV70453-  
 CC 61 represent partial sequences of different amplicons of hepatitis C  
 CC virus (HCV) subtypes 1a, 1b, 2c and 3a. These partial sequences are used  
 CC for identifying the HCV subtypes

Sequence 240 BP; 47 A; 63 C; 78 G; 52 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 240;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCCGACCCCAACTACTC 20  
 |||||  
 Db 207 TTCCGACCCCAACTACTC 188

RESULT 100  
 AAV70461/C  
 ID AAV70461 standard; DNA; 240 BP.

XX AAV70461;  
 AC  
 XX  
 DT 08-APR-1999 (first entry)  
 XX  
 DE Partial sequence of HCV subtype 3a amplicon #91.

XX Nucleic acid detection; nucleic acid characterisation; hybridisation;  
 KW infection; disease; cancer; forensic; paternity; multiplexing; HCV; de.  
 XX Hepatitis C virus.

OS Hepatitis C virus.

PN WO9850403-A1.

PD 12-NOV-1998.

PN 05-MAY-1998; 98WO-US003194.

PF 05-MAY-1997; 97US-00851588.

PR 19-SEP-1997; 97US-00934097.

PR 03-MAR-1998; 98US-00034205.

XX (THIR-) THIRD WAVE TECHNOLOGIES INC.

PA

PI Dong F, Lyamichov VI, Prudent JR, Fors L, Neri BP, Brow MAD;

PI Anderson TA, Dahlberg JE;

XX WPI; 1998-610317/51.

DR Detection and characterisation of nucleic acid sequences - by mixing a  
 PT folded target and one or more probes to form a probe/folded target  
 PT complex and detecting and characterising the complexes.  
 PS Example 5; Page 171; 279pp; English.

XX Example 5; Page 173; 279pp; English.

PS The invention relates to methods and compositions of detection and

CC characterisation of nucleic acid sequences and sequence changes. One

CC method of detection and characterisation comprises: (a) providing: (1) a

CC folded target and at least a DNA sequence comprising at least 1 double stranded

CC complementary to at least 1 single stranded region; and (11) at least 1 probe

CC /folded target and probes so that the probe hybridises to form a probe

CC structure formation in nucleic acid targets; for analysing folded nucleic

CC acids targets; and for analysis of nucleic acid structures. The methods

CC can be used for the detection and characterisation of nucleic acid

CC sequences to detect the presence of pathogenic nucleic acid sequences

CC indicative of an infection, the presence of variants or alleles of

CC mammalian genes associated with disease and cancers, and the

CC identification of the source of nucleic acids found in forensic samples,

CC as well as in paternity determinations. The methods allow simultaneous

CC analysis of both strands (e.g. the sense and antisense strands) and are

CC ideal for high-level multiplexing. The products produced are amenable to

CC qualitative, quantitative and positional analysis. The methods may be

CC performed in solution or in the solid phase (e.g. on a solid support).

CC The methods are powerful in that they allow for analysis of longer

CC fragments of nucleic acid than current methodologies. Sequences AAV70453-

CC 61 represent partial sequences of different amplicons of hepatitis C

CC virus (HCV) subtypes 1a, 1b, 2c and 3a. These partial sequences are used

CC for identifying the HCV subtypes

XX

SQ Sequence 240 BP; 47 A; 66 C; 77 G; 50 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 240;

Best Local Similarity 100.0%; Pred. No. 0.054;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGAGCCGACACTACTC 20

DB 208 TTGGGAGCCGACACTACTC 189

RESULT 101

ABL46066/C

ID ABL46066 standard; DNA; 240 BP.

AC ABL46066;

XX

DT 26-APR-2002 (first entry)

XX

DE Hepatitis C virus partial sequence #73 SEQ ID NO:33.

XX

KW Nucleic acid accessible hybridisation site; detection; hybridisation;

KW characterisation; identification; nucleic acid structure; diagnosis;

KW PCR primer; probe; ss.

XX

OS Hepatitis C virus.

OS Synthetic.

XX

WO200198537-A2.

XX

PN 27-DEC-2001.

XX

PD 15-JUN-2001; 2001WO-US019401.

XX

PF 17-JUN-2000; 2000US-0212308P.

XX

PR 15-JUN-2001; 2001US-00212308.

XX

PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;

XX

DR WPI; 2002-049698/06.

XX

PT Identifying oligonucleotides hybridizing to nucleic acids containing

PT secondary structure, useful in clinical diagnosis, comprises identifying

PT primers that interact with the target to form an extension product under

PT amplification conditions.

XX

PS Example 5; Page 366; 409pp; English.

XX

CC The present invention describes a method for identifying oligonucleotides

CC with desired hybridisation properties to nucleic acid targets containing

CC secondary structure. The method comprises amplifying a target nucleic

CC acid having at least one accessible and one inaccessible site. Primers

CC that form an extension product are identified as the oligonucleotides

CC from the present invention can be used in novel detection methods for

CC clinical diagnostic purposes, including the detection and identification

CC of pathogenic organisms (e.g. HIV). The method allows the ability to

CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent

CC sequences used in the exemplification of the present invention

XX

SQ Sequence 240 BP; 47 A; 63 C; 78 G; 52 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 240;

Best Local Similarity 100.0%; Pred. No. 0.054;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGAGCCGACACTACTC 20

DB 207 TTGGGAGCCGACACTACTC 188

RESULT 102

ABL46068/C

ID ABL46068 standard; DNA; 240 BP.

AC ABL46068;

XX

DT 26-APR-2002 (first entry)

XX

DE Hepatitis C virus partial sequence #81 SEQ ID NO:35.

XX

KW Nucleic acid accessible hybridisation site; detection; hybridisation;

KW characterisation; identification; nucleic acid structure; diagnosis;

KW PCR primer; probe; ss.

XX

OS Hepatitis C virus.

OS Synthetic.

XX

WO200198537-A2.

XX

PN 27-DEC-2001.

XX

PD 15-JUN-2001; 2001WO-US019401.

XX

PF 17-JUN-2000; 2000US-0212308P.

XX

PR 15-JUN-2001; 2001US-00212308.

XX

PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;

XX

DR WPI; 2002-049698/06.

XX

PT Identifying oligonucleotides hybridizing to nucleic acids containing

PT secondary structure, useful in clinical diagnosis, comprises identifying

PT primers that interact with the target to form an extension product under

PT amplification conditions.

XX

PS Example 5; Page 366; 409pp; English.

XX

CC The present invention describes a method for identifying oligonucleotides

CC with desired hybridisation properties to nucleic acid targets containing

CC secondary structure. The method comprises amplifying a target nucleic

CC acid having at least one accessible and one inaccessible site. Primers

CC that form an extension product are identified as the oligonucleotides

CC which can interact with the folded target nucleic acid. Oligonucleotides  
CC from the present invention can be used in novel detection methods for  
CC clinical diagnostic purposes, including the detection and identification  
CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
CC sequences used in the exemplification of the present invention  
XX

SO Sequence 240 BP; 45 A; 66 C; 79 G; 50 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGACCCCAACTACTC 20  
DB 207 TTCCGGACCCCAACTACTC 188

RESULT 103  
ABL46071/C  
ID ABL46071 standard; DNA; 240 BP.

AC ABL46071;  
DT 26-APR-2002 (first entry)

DE Hepatitis C virus partial sequence #91 SEQ ID NO:38.

KM Nucleic acid accessible hybridisation site; detection; hybridisation;  
KW characterisation; identification; nucleic acid structure; diagnosis;  
OS PCR primer; probe; seq.

OS Hepatitis C virus.  
OS Synthetic.

PN WO200198537-A2.

PD 27-DEC-2001.

PE 15-JUN-2001; 2001WO-US019401.

PR 17-JUN-2000; 2000US-0212308P.

PR 15-JUN-2001; 2001US-00212308.

PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;

PP WPI; 2002-049698/06.

PT Identifying oligonucleotides hybridizing to nucleic acids containing  
PT secondary structure, useful in clinical diagnosis, comprises identifying  
PT primers that interact with the target to form an extension product under  
PT amplification conditions.  
XX

PS Example 5; Page 367; 403pp; English.

XX The present invention describes a method for identifying oligonucleotides  
CC with desired hybridisation properties to nucleic acid targets containing  
CC secondary structure. The method comprises amplifying a target nucleic  
CC acid having at least one accessible and one inaccessible site. Primers  
CC that form an extension product are identified as the oligonucleotides  
CC which can interact with the folded target nucleic acid. Oligonucleotides  
CC from the present invention can be used in novel detection methods for  
CC clinical diagnostic purposes, including the detection and identification  
CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
CC sequences used in the exemplification of the present invention  
XX

SO Sequence 240 BP; 47 A; 66 C; 77 G; 50 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.054;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGACCCCAACTACTC 20  
DB 208 TTCCGGACCCCAACTACTC 189

RESULT 104  
ADK82261/C  
ID ADK82261 standard; DNA; 240 BP.

AC ADK82261;

DT 03-JUN-2004 (first entry)

DE Hepatitis C virus polynucleotide seqid 38.

KM nucleic acid analysis; hepatitis C virus;  
KW non-contiguous single-stranded region; NCSR; cleavage structure;  
KW clinical; diagnostic; microorganism detection;  
KW microorganism identification; hepatitis C virus; HCV, ds.

OS Hepatitis C virus.

XX US6709815-B1.

PD 23-MAR-2004.

PE 18-JUL-2000; 2000US-00402618.

PR 05-MAY-1997; 97US-00851588.

PR 19-SEP-1997; 97US-00934097.

PR 03-MAR-1998; 98US-00034205.

PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MMD;

PP WPI; 2004-256067/24.

PT Analyzing nucleic acids, comprises mixing target nucleic acid such as  
PT hepatitis C virus nucleic acid, bridging oligonucleotide, second  
PT oligonucleotide and cleavage agent to form cleavage structure.  
XX

PS Example 5; SEQ ID NO 38; 143pp; English.

XX The invention describes a method of analysing nucleic acids comprising  
CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
CC having non-contiguous single-stranded regions (NCSR) separated by an  
CC intervening region, a bridging oligonucleotide capable of binding to the  
CC first and second NCSR; a second oligonucleotide binding to a portion of  
CC the first NCSR and a cleavage agent, and mixing the contents to form a  
CC cleavage structure. The method is useful for analysing nucleic acids,  
CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
CC purposes and detection and identification of pathogenic microorganisms  
CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
CC polynucleotide that is sufficient for identification of HCV subtypes  
CC using the analysis methods of the invention.  
XX

SO Sequence 240 BP; 47 A; 66 C; 77 G; 50 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGGACCCCAACTACTC 20  
DB 208 TTCCGGACCCCAACTACTC 189

RESULT 105  
ADK82258/C

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ID      ADK82258 standard; DNA; 240 BP.
XX
XX      ADK82258;
AC
XX      03-JUN-2004 (first entry)
DT
XX      Hepatitis C virus polynucleotide seqid 35.
XX
XX      nucleic acid analysis; hepatitis C virus;
XX      non-contiguous single-stranded region; NCSR; cleavage structure;
XX      clinical; diagnostic; microorganism detection;
XX      microorganism identification; hepatitis C virus; HCV; ds.
OS
XX      Hepatitis C virus.
XX
XX      US6709815-B1.
XX
XX      23-MAR-2004.
XX
XX      18-JUL-2000; 2000US-00402618.
XX
XX      05-MAY-1997; 97US-00851588.
XX      19-SEP-1997; 97US-00934097.
XX      03-MAR-1998; 98US-00034205.
XX
XX      (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX      Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;
XX      Anderson TA, Dahlberg JE;
XX
XX      WPI; 2004-256067/24.
XX
XX      Analyzing nucleic acids, comprises mixing target nucleic acid such as
XX      hepatitis C virus nucleic acid, bridging oligonucleotide, second
XX      oligonucleotide and cleavage agent to form cleavage structure.
XX
XX      Example 5; SEQ ID NO 35; 143bp; English.
XX
XX      The invention describes a method of analysing nucleic acids comprising
XX      providing a target nucleic acid, e.g. hepatitis C virus nucleic acid
XX      having non-contiguous single-stranded regions (NCSR) separated by an
XX      intervening region, a bridging oligonucleotide capable of binding to the
XX      first and second NCSR, a second oligonucleotide binding to a portion of
XX      the first NCSR and a cleavage agent, and mixing the contents to form a
XX      cleavage structure. The method is useful for analysing nucleic acids,
XX      e.g. hepatitis C virus nucleic acid useful for clinical diagnostic
XX      purposes and detection and identification of pathogenic microorganisms
XX      such as hepatitis C virus. This sequence represents a hepatitis C virus
XX      polynucleotide that is sufficient for identification of HCV subtypes
XX      using the analysis methods of the invention.
XX
XX      Sequence 240 BP; 45 A; 66 C; 79 G; 50 T; 0 U; 0 Other;
SQ
Query Match          100.0%; Score 20; DB 12; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTCCGACCCCAACTACTC 20
       207 TTCCGACCCCAACTACTC 188
Db
RESULT 106
ADK82256/c
ID      ADK82256 standard; DNA; 240 BP.
AC
XX      ADK82256;
XX
XX      03-JUN-2004 (first entry)
DT
XX      Hepatitis C virus polynucleotide seqid 33.
XX
XX      nucleic acid analysis; hepatitis C virus;

```

```

KW      non-contiguous single-stranded region; NCSR; cleavage structure;
KW      clinical; diagnostic; microorganism detection;
KW      microorganism identification; hepatitis C virus; HCV; ds.
XX
XX      Hepatitis C virus.
XX
XX      US6709815-B1.
XX
XX      23-MAR-2004.
XX
XX      18-JUL-2000; 2000US-00402618.
XX
XX      05-MAY-1997; 97US-00851588.
XX      19-SEP-1997; 97US-00934097.
XX      03-MAR-1998; 98US-00034205.
XX
XX      (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX      Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;
XX      Anderson TA, Dahlberg JE;
XX
XX      WPI; 2004-256067/24.
XX
XX      Analyzing nucleic acids, comprises mixing target nucleic acid such as
XX      hepatitis C virus nucleic acid, bridging oligonucleotide, second
XX      oligonucleotide and cleavage agent to form cleavage structure.
XX
XX      Example 5; SEQ ID NO 33; 143bp; English.
XX
XX      The invention describes a method of analysing nucleic acids comprising
XX      providing a target nucleic acid, e.g. hepatitis C virus nucleic acid
XX      having non-contiguous single-stranded regions (NCSR) separated by an
XX      intervening region, a bridging oligonucleotide capable of binding to the
XX      first and second NCSR, a second oligonucleotide binding to a portion of
XX      the first NCSR and a cleavage agent, and mixing the contents to form a
XX      cleavage structure. The method is useful for analysing nucleic acids,
XX      e.g. hepatitis C virus nucleic acid useful for clinical diagnostic
XX      purposes and detection and identification of pathogenic microorganisms
XX      such as hepatitis C virus. This sequence represents a hepatitis C virus
XX      polynucleotide that is sufficient for identification of HCV subtypes
XX      using the analysis methods of the invention.
XX
XX      Sequence 240 BP; 47 A; 63 C; 78 G; 52 T; 0 U; 0 Other;
SQ
Query Match          100.0%; Score 20; DB 12; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTCCGACCCCAACTACTC 20
       207 TTCCGACCCCAACTACTC 188
Db
RESULT 107
AAD43290/c
ID      AAD43290 standard; DNA; 241 BP.
AC
XX      AAD43290;
XX
XX      14-NOV-2002 (first entry)
DT
XX      HCV target DNA.
XX
XX      Amplification; target nucleic acid; ds.
XX
XX      Hepatitis C virus.
XX
XX      EPI236805-A1.
XX
XX      04-SEP-2002.
XX
XX      27-FEB-2002; 2002EP-00004483.
XX

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PR 02-MAR-2001; 2001EP-00105172.  
 XX (HOFF) ROCHE DIAGNOSTICS GMBH.  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 XX  
 PI Jaeger S;  
 XX  
 DR WPI; 2002-610695/66.  
 XX  
 PT Amplification of a target nucleic acid region using a specific control  
 sequence.  
 PS Example 1; Page 18; 28pp; English.  
 XX  
 CC The invention relates to a method for amplification of a target nucleic  
 CC acid region in a sample using a specific control sequence. The invention  
 CC is also directed to a method of determination of a target nucleic acid  
 CC using a special control nucleic acid. Nucleic acids of the invention are  
 CC used as a control in a reaction for amplifying target nucleic acids and  
 CC as a control in a hybridisation reaction for determination of target  
 CC nucleic acids. The present sequence is HCV (Hepatitis C virus) type I  
 CC target DNA. This sequence is used to illustrate the methods of the  
 CC invention  
 CC  
 SQ Sequence 241 BP; 44 A; 67 C; 79 G; 51 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 TTGGGACCCCAACTACTC 20  
 DB 208 TTGGGACCCCAACTACTC 189  
 RESULT 108  
 AAD43742/C  
 ID AAD43742 standard; DNA; 241 BP.  
 AC AAD43742;  
 XX  
 DT 07-AUG-2003 (revised)  
 DT 14-NOV-2002 (first entry)  
 XX  
 DE HCV amplicon.  
 XX  
 KW Amplification; target nucleic acid; control nucleic acid; ds.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN EP1236804-A1.  
 XX  
 PD 04-SEP-2002.  
 XX  
 PF 02-MAR-2001; 2001EP-00105172.  
 XX  
 PR 02-MAR-2001; 2001EP-00105172.  
 XX  
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 XX  
 PI Jaeger S;  
 XX  
 DR WPI; 2002-610694/66.  
 XX  
 PT Amplification of a target nucleic acid region using control sequences.  
 PS Example 1; Page 18; 29pp; English.  
 XX  
 CC The invention relates to a method for amplification of a target nucleic  
 CC acid region. The method is useful for amplification of a nucleic acid  
 CC molecule using control nucleic acid sequences. The control nucleic acid  
 CC sequences are at least in part parallel-complementary to the sequence of

CC the target nucleic acid. The present sequence is HCV amplicon used to  
 CC illustrate the method of the invention. (Updated on 07-AUG-2003 to  
 CC correct OS field.)  
 XX  
 SQ Sequence 241 BP; 44 A; 67 C; 79 G; 51 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 TTGGGACCCCAACTACTC 20  
 DB 208 TTGGGACCCCAACTACTC 189  
 RESULT 109  
 AAV70454/C  
 ID AAV70454 standard; DNA; 244 BP.  
 AC AAV70454;  
 XX  
 DT 08-APR-1999 (first entry)  
 XX  
 DE Partial sequence of HCV subtype 1a amplicon #69.  
 XX  
 KW Nucleic acid detection; nucleic acid characterisation; hybridisation;  
 KW infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.  
 OS Hepatitis C virus.  
 XX  
 PN WO9850403-A1.  
 XX  
 PD 12-NOV-1998.  
 XX  
 PF 05-MAY-1998; 98WO-US003194.  
 XX  
 PR 05-MAY-1997; 97US-00851588.  
 PR 19-SEP-1997; 97US-00934097.  
 PR 03-MAR-1998; 98US-00034205.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MMD;  
 PI Anderson TA, Dahlberg JE;  
 XX  
 DR WPI; 1998-610317/51.  
 XX  
 PT Detection and characterisation of nucleic acid sequences - by mixing a  
 PT folded target and one or more probes to form a probe/folded target  
 PT complex and detecting and characterising the complexes.  
 PS Example 5; Page 170-171; 279pp; English.  
 XX  
 CC The invention relates to methods and compositions of detection and  
 CC characterisation of nucleic acid sequences and sequence changes. One  
 CC method of detection and characterisation comprises: (a) providing: (i) a  
 CC folded target having a DNA sequence comprising at least 1 double stranded  
 CC region and at least 1 single stranded region; and (ii) at least 1 probe  
 CC complementary to at least a portion of the folded target; and (b) mixing  
 CC the target and probes so that the probe hybridises to form a probe  
 CC /folded target complex. Also provided are methods for determination of  
 CC structure formation in nucleic acid targets; for analysing folded nucleic  
 CC acids targets; and for analysis of nucleic acid structures. The methods  
 CC can be used for the detection and characterisation of nucleic acid  
 CC sequences to detect the presence of pathogenic nucleic acid sequences  
 CC indicative of an infection, the presence of variants or alleles of  
 CC mammalian genes associated with disease and cancers, and the  
 CC identification of the source of nucleic acids found in forensic samples,  
 CC as well as in paternity determinations. The methods allow simultaneous  
 CC analysis of both strands (e.g. the sense and antisense strands) and are  
 CC ideal for high-level multiplexing. The products produced are amenable to  
 CC qualitative, quantitative and positional analysis. The methods may be  
 CC performed in solution or in the solid phase (e.g. on a solid support).

CC The methods are powerful in that they allow for analysis of longer  
 CC fragments of nucleic acid than current methodologies. Sequences AAV70453-  
 CC 61 represent partial sequences of different amplicons of hepatitis C  
 CC virus (HCV) subtypes 1a, 1b, 2c and 3a. These partial sequences are used  
 CC for identifying the HCV subtypes  
 CC XX

SO Sequence 244 BP; 49 A; 64 C; 79 G; 52 T; 0 U; 0 Other;

Query Match Best Local Similarity 100.0%; Score 20; DB 2; Length 244;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCGACACTACTC 20  
 Db 208 TTGCGACCCGACACTACTC 189

RESULT 110  
 ID AAV70450 standard; DNA; 244 BP.

XX AAV70450;

DT 08-APR-1999 (first entry)

DE HCV subtype 1b PCR fragment.

XX Nucleic acid detection; nucleic acid characterisation; hybridisation;  
 KM infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.

OS Hepatitis C virus.

XX WO9850403-A1.

PN 12-NOV-1998.

PF 05-MAY-1998; 98WO-US003194.

PR 05-MAY-1997; 97US-00851588.

PR 19-SEP-1997; 97US-00934097.

PR 03-MAR-1998; 98US-00034205.

(THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;

DR WPI; 1998-610317/51.

XX Detection and characterisation of nucleic acid sequences - by mixing a  
 PT folded target and one or more probes to form a probe/folded target  
 PT complex and detecting and characterising the complexes.

XX Example 3; Page 169; 279pp; English.

CC The invention relates to methods and compositions of detection and  
 CC characterisation of nucleic acid sequences and sequence changes. One  
 CC method of detection and characterisation comprises: (a) providing: (i) a  
 CC folded target having a DNA sequence comprising at least 1 double stranded  
 CC region and at least 1 single stranded region; and (ii) at least 1 probe  
 CC complementary to at least a portion of the folded target; and (b) mixing  
 CC the target and probes so that the probe hybridises to form a probe  
 CC /folded target complex. Also provided are methods for determination of  
 CC structure formation in nucleic acid targets; for analysing folded nucleic  
 CC acids targets; and for analysis of nucleic acid structures. The methods  
 CC can be used for the detection and characterisation of nucleic acid  
 CC sequences to detect the presence of pathogenic nucleic acid sequences  
 CC indicative of an infection, the presence of variants or alleles of  
 CC mammalian genes associated with disease and cancers, and the  
 CC identification of the source of nucleic acids found in forensic samples,  
 CC as well as in paternity determinations. The methods allow simultaneous  
 CC analysis of both strands (e.g. the sense and antisense strands) and are  
 CC ideal for high-level multiplexing. The products produced are amenable to

CC qualitative, quantitative and positional analysis. The methods may be  
 CC performed in solution or in the solid phase (e.g. on a solid support).  
 CC The methods are powerful in that they allow for analysis of longer  
 CC fragments of nucleic acid than current methodologies. Sequences AAV70449-  
 CC 52 represent a hepatitis C virus (HCV) subtype sequences produced by PCR.  
 CC These PCR products can be used in hybridisation analysis using multiple  
 CC capture probes for HCV genotyping  
 CC XX

SO Sequence 244 BP; 44 A; 67 C; 81 G; 52 T; 0 U; 0 Other;

Query Match Best Local Similarity 100.0%; Score 20; DB 2; Length 244;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCGACACTACTC 20  
 Db 208 TTGCGACCCGACACTACTC 189

RESULT 111

ID AAV70449 standard; DNA; 244 BP.

XX AAV70449;

DT 08-APR-1999 (first entry)

DE HCV subtype 1a PCR fragment.

XX Nucleic acid detection; nucleic acid characterisation; hybridisation;  
 KM infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.

OS Hepatitis C virus.

XX WO9850403-A1.

PN 12-NOV-1998.

PF 05-MAY-1998; 98WO-US003194.

PR 05-MAY-1997; 97US-00851588.

PR 19-SEP-1997; 97US-00934097.

PR 03-MAR-1998; 98US-00034205.

(THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;

DR WPI; 1998-610317/51.

XX Detection and characterisation of nucleic acid sequences - by mixing a  
 PT folded target and one or more probes to form a probe/folded target  
 PT complex and detecting and characterising the complexes.

XX Example 3; Page 169; 279pp; English.

CC The invention relates to methods and compositions of detection and  
 CC characterisation of nucleic acid sequences and sequence changes. One  
 CC method of detection and characterisation comprises: (a) providing: (i) a  
 CC folded target having a DNA sequence comprising at least 1 double stranded  
 CC region and at least 1 single stranded region; and (ii) at least 1 probe  
 CC complementary to at least a portion of the folded target; and (b) mixing  
 CC the target and probes so that the probe hybridises to form a probe  
 CC /folded target complex. Also provided are methods for determination of  
 CC structure formation in nucleic acid targets; for analysing folded nucleic  
 CC acids targets; and for analysis of nucleic acid structures. The methods  
 CC can be used for the detection and characterisation of nucleic acid  
 CC sequences to detect the presence of pathogenic nucleic acid sequences  
 CC indicative of an infection, the presence of variants or alleles of  
 CC mammalian genes associated with disease and cancers, and the  
 CC identification of the source of nucleic acids found in forensic samples,  
 CC as well as in paternity determinations. The methods allow simultaneous

CC analysis of both strands (e.g. the sense and antisense strands) and are  
 CC ideal for high-level multiplexing. The products produced are amenable to  
 CC qualitative, quantitative and positional analysis. The methods may be  
 CC performed in solution or in the solid phase (e.g. on a solid support).  
 CC The methods are powerful in that they allow for analysis of longer  
 CC fragments of nucleic acid than current methodologies. Sequences AAV70449-  
 CC 52 represent a hepatitis C virus (HCV) subtype sequences produced by PCR.  
 CC These PCR products can be used in hybridisation analysis using multiple  
 CC capture probes for HCV genotyping  
 CC  
 SQ Sequence 244 BP; 46 A; 67 C; 80 G; 51 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 2; Length 244;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTCCGACCCCAACTACTC 20  
 DB 208 TTCCGACCCCAACTACTC 189  
 RESULT 112  
 AAV70452/C  
 ID AAV70452 standard; DNA; 244 BP.  
 XX  
 AC AAV70452;  
 XX  
 DT 08-APR-1999 (first entry)  
 XX  
 DE HCV subtype 3a PCR fragment.  
 XX  
 KW Nucleic acid detection; nucleic acid characterisation; hybridisation;  
 KM infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN MO9850403-A1.  
 XX  
 PD 12-NOV-1998.  
 XX  
 PF 05-MAY-1998; 98WO-US003194.  
 XX  
 PR 05-MAY-1997; 97US-00851588.  
 PR 19-SEP-1997; 97US-00934087.  
 PR 03-MAR-1998; 98US-00034205.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD,  
 PI Anderson TA, Dahlberg JE;  
 XX  
 DR WPI; 1998-610317/51.  
 XX  
 PT Detection and characterisation of nucleic acid sequences - by mixing a  
 PT folded target and one or more probes to form a probe/folded target  
 PT complex and detecting and characterising the complexes.  
 XX  
 PS Example 3; Page 170; 279pp; English.  
 XX  
 CC The invention relates to methods and compositions of detection and  
 CC characterisation of nucleic acid sequences and sequence changes. One  
 CC method of detection and characterisation comprises: (a) providing: (i) a  
 CC folded target having a DNA sequence comprising at least 1 double stranded  
 CC region and at least 1 single stranded region; and (ii) at least 1 probe  
 CC complementary to at least a portion of the folded target; and (b) mixing  
 CC the target and probes so that the probe hybridises to form a probe  
 CC /folded target complex. Also provided are methods for determination of  
 CC structure formation in nucleic acid targets; for analysing folded nucleic  
 CC acids targets; and for analysis of nucleic acid structures. The methods  
 CC can be used for the detection and characterisation of nucleic acid  
 CC sequences to detect the presence of pathogenic nucleic acid sequences  
 CC indicative of an infection, the presence of variants or alleles of  
 CC mammalian genes associated with disease and cancers, and the

CC identification of the source of nucleic acids found in forensic samples,  
 CC as well as in paternity determinations. The methods allow simultaneous  
 CC analysis of both strands (e.g. the sense and antisense strands) and are  
 CC ideal for high-level multiplexing. The products produced are amenable to  
 CC qualitative, quantitative and positional analysis. The methods may be  
 CC performed in solution or in the solid phase (e.g. on a solid support).  
 CC The methods are powerful in that they allow for analysis of longer  
 CC fragments of nucleic acid than current methodologies. Sequences AAV70449-  
 CC 52 represent a hepatitis C virus (HCV) subtype sequences produced by PCR.  
 CC These PCR products can be used in hybridisation analysis using multiple  
 CC capture probes for HCV genotyping  
 CC  
 SQ Sequence 244 BP; 48 A; 69 C; 79 G; 48 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 2; Length 244;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTCCGACCCCAACTACTC 20  
 DB 208 TTCCGACCCCAACTACTC 189  
 RESULT 113  
 ABL46062/C  
 ID ABL46062 standard; DNA; 244 BP.  
 XX  
 AC ABL46062;  
 XX  
 DT 26-APR-2002 (first entry)  
 XX  
 DE Hepatitis C virus subtype 3a target DNA PCR product SEQ ID NO:29.  
 XX  
 KW Nucleic acid accessible hybridisation site; detection; hybridisation;  
 KM characterisation; identification; nucleic acid structure; diagnosis;  
 KW PCR primer; probe; ss.  
 XX  
 OS Hepatitis C virus.  
 OS Synthetic.  
 XX  
 PN WO200198537-A2.  
 XX  
 PD 27-DEC-2001.  
 XX  
 PF 15-JUN-2001; 2001WO-US019401.  
 XX  
 PR 17-JUN-2000; 2000US-0212308P.  
 PR 15-JUN-2001; 2001US-00212308.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;  
 XX  
 DR WPI; 2002-049698/06.  
 XX  
 PT Identifying oligonucleotides hybridizing to nucleic acids containing  
 PT secondary structure, useful in clinical diagnosis, comprises identifying  
 PT primers that interact with the target to form an extension product under  
 PT amplification conditions.  
 XX  
 PS Example 3; Page 365; 409pp; English.  
 XX  
 CC The present invention describes a method for identifying oligonucleotides  
 CC with desired hybridisation properties to nucleic acid targets containing  
 CC secondary structure. The method comprises amplifying a target nucleic  
 CC acid having at least one accessible and one inaccessible site. Primers  
 CC that form an extension product are identified as the oligonucleotides  
 CC which can interact with the folded target nucleic acid. Oligonucleotides  
 CC from the present invention can be used in novel detection methods for  
 CC clinical diagnostic purposes, including the detection and identification  
 CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
 CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
 CC sequences used in the exemplification of the present invention

XX Sequence 244 BP; 48 A; 69 C; 79 G; 48 T; 0 U; 0 Other;  
SQ

Query Match 100.0%; Score 20; DB 6; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACACTACTC 20  
DB 208 TTGCGACCCCAACACTACTC 189

RESULT 114  
ABL46059/c  
ID ABL46059 standard; DNA; 244 BP.

AC ABL46059;  
XX  
XX 26-APR-2002 (first entry)

DE Hepatitis C virus subtype 1a target DNA PCR product SEQ ID NO:26.

KM Nucleic acid accessible hybridisation site; detection; hybridisation;  
KW characterisation; identification; nucleic acid structure; diagnosis;  
XX PCR primer; probe; ss.

OS Hepatitis C virus.  
XX Synthetic.

PN MO200198537-A2.

XX  
XX 27-DEC-2001.

PF 15-JUN-2001; 2001MO-US019401.

XX  
XX 17-JUN-2000; 2000US-0212308P.

PR 15-JUN-2001; 2001US-00212308.

XX  
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;

XX  
XX WPI; 2002-049698/06.

PT Identifying oligonucleotides hybridizing to nucleic acids containing  
PT secondary structure, useful in clinical diagnosis, comprises identifying  
PT primers that interact with the target to form an extension product under  
PT amplification conditions.

XX  
XX Example 3; Page 364; 409pp; English.

CC The present invention describes a method for identifying oligonucleotides  
CC with desired hybridisation properties to nucleic acid targets containing  
CC secondary structure. The method comprises amplifying a target nucleic  
CC acid having at least one accessible and one inaccessible site. Primers  
CC that form an extension product are identified as the oligonucleotides  
CC which can interact with the folded target nucleic acid. Oligonucleotides  
CC from the present invention can be used in novel detection methods for  
CC clinical diagnostic purposes, including the detection and identification  
CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
CC sequences used in the exemplification of the present invention

SQ Sequence 244 BP; 46 A; 67 C; 80 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACACTACTC 20  
DB 208 TTGCGACCCCAACACTACTC 189

RESULT 115  
ABL46060/c  
ID ABL46060 standard; DNA; 244 BP.

AC ABL46060;  
XX  
XX 26-APR-2002 (first entry)

DE Hepatitis C virus subtype 1b target DNA PCR product SEQ ID NO:27.

KM Nucleic acid accessible hybridisation site; detection; hybridisation;  
KW characterisation; identification; nucleic acid structure; diagnosis;  
XX PCR primer; probe; ss.

OS Hepatitis C virus.  
XX Synthetic.

PN MO200198537-A2.

XX  
XX 27-DEC-2001.

PF 15-JUN-2001; 2001MO-US019401.

XX  
XX 17-JUN-2000; 2000US-0212308P.

PR 15-JUN-2001; 2001US-00212308.

XX  
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;

XX  
XX WPI; 2002-049698/06.

PT Identifying oligonucleotides hybridizing to nucleic acids containing  
PT secondary structure, useful in clinical diagnosis, comprises identifying  
PT primers that interact with the target to form an extension product under  
PT amplification conditions.

XX  
XX Example 3; Page 364; 409pp; English.

CC The present invention describes a method for identifying oligonucleotides  
CC with desired hybridisation properties to nucleic acid targets containing  
CC secondary structure. The method comprises amplifying a target nucleic  
CC acid having at least one accessible and one inaccessible site. Primers  
CC that form an extension product are identified as the oligonucleotides  
CC which can interact with the folded target nucleic acid. Oligonucleotides  
CC from the present invention can be used in novel detection methods for  
CC clinical diagnostic purposes, including the detection and identification  
CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
CC sequences used in the exemplification of the present invention

SQ Sequence 244 BP; 44 A; 67 C; 81 G; 52 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACACTACTC 20  
DB 208 TTGCGACCCCAACACTACTC 189

RESULT 116

ABL46064/c  
ID ABL46064 standard; DNA; 244 BP.

XX  
XX ABL46064;

XX  
XX 26-APR-2002 (first entry)

DE Hepatitis C virus partial sequence #69 SEQ ID NO:31.

```

XX      Nucleic acid accessible hybridisation site; detection; hybridisation;
KW      characterisation; identification; nucleic acid structure; diagnosis;
KM      PCR primer; probe; ss.
XX
XX      Hepatitis C virus.
OS      Synthetic.
XX
XX      WO2001098537-A2.
PN
XX      27-DEC-2001.
PD
XX      15-JUN-2001; 2001WO-US019401.
PP
XX      17-JUN-2000; 2000US--0212308P.
PR
XX      15-JUN-2001; 2001US--00212308.
XX
XX      (THIR-) THIRD WAVE TECHNOLOGIES INC.
PA
XX      Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;
PI      WPI; 2002-049698/06.
XX
XX      The present invention describes a method for identifying oligonucleotides
CC      with desired hybridisation properties to nucleic acid targets containing
CC      secondary structure. The method comprises amplifying a target nucleic
CC      acid having at least one accessible and one inaccessible site. Primers
CC      that form an extension product are identified as the oligonucleotides
CC      which can interact with the folded target nucleic acid. Oligonucleotides
CC      from the present invention can be used in novel detection methods for
CC      clinical diagnostic purposes, including the detection and identification
CC      of pathogenic organisms (e.g. HIV). The method allows the ability to
CC      rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
CC      sequences used in the exemplification of the present invention
XX
SO      Sequence 244 BP; 49 A; 64 C; 79 G; 52 T; 0 U; 0 Other;
XX
XX      Query Match      100.0%; Score 20; DB 6; Length 244;
XX      Best Local Similarity 100.0%; Pred. No. 0.054;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX      1 TTTCGACCCCAACTACTC 20
XX      |||||
XX      208 TTTCGACCCCAACTACTC 189
XX
XX      RESULT 117
XX      ADK82254/C
XX      ID      ADK82254 standard; DNA; 244 BP.
XX      ADK82254;
XX
XX      03-JUN-2004 (first entry)
XX      DE      Hepatitis C virus polynucleotide seqid 31.
XX
XX      nucleic acid analysis; hepatitis C virus;
XX      non-contiguous single-stranded region; NCSR; cleavage structure;
KW      clinical; diagnostic; microorganism detection;
XX      microorganism identification; hepatitis C virus; HCV; ds.
XX
XX      Hepatitis C virus.
OS
XX      US6709815-B1.
XX      23-MAR-2004.
XX

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XX 18-JUL-2000; 2000US-00402618.
PR 05-MAY-1997; 97US-00851588.
PR 19-SEP-1997; 97US-00934097.
PR 03-MAR-1998; 98US-00034205.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX PA
XX PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;
XX PI Anderson TA, Dahlberg JE;
XX
XX WPI; 2004-256067/24.
XX
XX Analyzing nucleic acid, comprises mixing target nucleic acid such as
XX hepatitis C virus nucleic acid, bridging oligonucleotide, second
XX oligonucleotide and cleavage agent to form cleavage structure.
XX
XX Example 5; SEQ ID NO 31; 143pp; English.
XX
XX The invention describes a method of analysing nucleic acids comprising
XX providing a target nucleic acid, e.g. hepatitis C virus nucleic acid
XX having non-continuous single-stranded regions (NSR) separated by an
XX intervening region, a bridging oligonucleotide capable of binding to the
XX first and second NSR; a second oligonucleotide binding to a portion of
XX the first NSR and a cleavage agent, and mixing the contents to form a
XX cleavage structure. The method is useful for analysing nucleic acids,
XX e.g. hepatitis C virus nucleic acid useful for clinical diagnostic
XX purposes and detection and identification of pathogenic microorganisms
XX such as hepatitis C virus. This sequence represents a hepatitis C virus
XX polynucleotide that is sufficient for identification of HCV subtypes
XX using the analysis methods of the invention.
XX
XX Sequence 244 BP; 49 A; 64 C; 79 G; 52 T; 0 U; 0 Other;
XX
XX Query March 100.0%; Score 20; DB 12; Length 244;
XX Best Local Similarity 100.0%; Pred. No. 0.054;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TTGCGGACCCGACACTACTC 20
XX |||||
XX Db 208 TTGCGGACCCGACACTACTC 189
XX
XX RESULT 118
XX ADK82351
XX ID ADK82351 standard; RNA; 244 BP.
XX
XX ADK82351;
XX
XX DT 03-JUN-2004 (first entry)
XX
XX Hepatitis C virus subtype 1a 5'UTR RNA.
XX
XX nucleic acid analyses; hepatitis C virus;
XX non-continuous single-stranded region; NSR; cleavage structure;
XX clinical; diagnostic; microorganism detection;
XX microorganism identification; hepatitis C virus; HCV; subtype 1a; ds;
XX 5'UTR; 5' untranslated region.
XX
XX Hepatitis C virus.
XX
XX OS
XX US6709815-B1.
XX
XX PD 23-MAR-2004.
XX
XX PF 18-JUL-2000; 2000US-00402618.
XX
XX PR 05-MAY-1997; 97US-00851588.
XX PR 19-SEP-1997; 97US-00934097.
XX PR 03-MAR-1998; 98US-00034205.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX

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PI Dong F, Lyamichiev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
PI Anderson TA, Dahlberg JE;  
XX WPI; 2004-256067/24.  
XX  
XX Analyzing nucleic acids, comprises mixing target nucleic acid such as  
PT hepatitis C virus nucleic acid, bridging oligonucleotide, second  
PT oligonucleotide and cleavage agent to form cleavage structure.  
XX  
PS Example 8; SEQ ID NO 128, 143pp; English.  
XX  
XX The invention describes a method of analyzing nucleic acids comprising  
CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
CC having non-contiguous single-stranded regions (NCSR) separated by an  
CC intervening region, a bridging oligonucleotide capable of binding to the  
CC first and second NCSR, a second oligonucleotide binding to a portion of  
CC the first NCSR and a cleavage agent, and mixing the contents to form a  
CC cleavage structure. The method is useful for analyzing nucleic acids,  
CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
CC purposes and detection and identification of pathogenic microorganisms  
CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
CC subtype 1a 5'UTR that can be used in the analysis of folded structures  
CC using the method of the invention.  
SQ Sequence 244 BP; 51 A; 80 C; 67 G; 0 T; 46 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 244;  
Best Local Similarity 80.0%; Pred. No. 0.054;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGACCCCAACTACTC 20  
DB 37 TTGCGACCCCAACTACTC 56  
RESULT 119  
ADK82250/C  
ID ADK82250 standard; DNA; 244 BP.  
XX  
XX ADK82250;  
XX  
XX 03-JUN-2004 (first entry)  
XX  
XX Hepatitis C virus subtype 1b polynucleotide seqid 27.  
XX  
XX nucleic acid analysis; hepatitis C virus;  
KM non-contiguous single-stranded region; NCSR; cleavage structure;  
KW clinical; diagnostic; microorganism detection;  
KW microorganism identification; hepatitis C virus; HCV; subtype 1b; ds.  
XX  
OS Hepatitis C virus.  
XX  
XX US6709815-B1.  
XX  
XX 23-MAR-2004.  
XX  
XX 18-JUL-2000; 2000US-00402618.  
XX  
XX 05-MAY-1997; 97US-00851588.  
XX  
XX 19-SEP-1997; 97US-00934097.  
XX  
XX 03-MAR-1998; 98US-00034205.  
XX  
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XX  
XX Dong F, Lyamichiev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
PI Anderson TA, Dahlberg JE;  
XX  
XX WPI; 2004-256067/24.  
XX  
XX Analyzing nucleic acids, comprises mixing target nucleic acid such as  
PT hepatitis C virus nucleic acid, bridging oligonucleotide, second  
PT oligonucleotide and cleavage agent to form cleavage structure.

PS Example 3; SEQ ID NO 27; 143pp; English.  
XX  
XX The invention describes a method of analyzing nucleic acids comprising  
CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
CC having non-contiguous single-stranded regions (NCSR) separated by an  
CC intervening region, a bridging oligonucleotide capable of binding to the  
CC first and second NCSR, a second oligonucleotide binding to a portion of  
CC the first NCSR and a cleavage agent, and mixing the contents to form a  
CC cleavage structure. The method is useful for analyzing nucleic acids,  
CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
CC purposes and detection and identification of pathogenic microorganisms  
CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
CC subtype 1b polynucleotide identified using the analysis methods of the  
CC invention.  
SQ Sequence 244 BP; 44 A; 67 C; 81 G; 52 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGACCCCAACTACTC 20  
DB 208 TTGCGACCCCAACTACTC 189  
RESULT 120  
ADK82347  
ID ADK82347 standard; DNA; 244 BP.  
XX  
XX ADK82347;  
XX  
XX 03-JUN-2004 (first entry)  
XX  
XX Hepatitis C virus subtype 1a 5'UTR.  
XX  
XX nucleic acid analysis; hepatitis C virus;  
KM non-contiguous single-stranded region; NCSR; cleavage structure;  
KW clinical; diagnostic; microorganism detection;  
KW microorganism identification; hepatitis C virus; HCV; subtype 1a; ds.  
XX  
XX 5'UTR; 5' untranslated region.  
XX  
OS Hepatitis C virus.  
XX  
XX US6709815-B1.  
XX  
XX 23-MAR-2004.  
XX  
XX 18-JUL-2000; 2000US-00402618.  
XX  
XX 05-MAY-1997; 97US-00851588.  
XX  
XX 19-SEP-1997; 97US-00934097.  
XX  
XX 03-MAR-1998; 98US-00034205.  
XX  
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XX  
XX Dong F, Lyamichiev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
PI Anderson TA, Dahlberg JE;  
XX  
XX WPI; 2004-256067/24.  
XX  
XX Analyzing nucleic acids, comprises mixing target nucleic acid such as  
PT hepatitis C virus nucleic acid, bridging oligonucleotide, second  
PT oligonucleotide and cleavage agent to form cleavage structure.  
XX  
PS Example 8; SEQ ID NO 124, 143pp; English.  
XX  
XX The invention describes a method of analyzing nucleic acids comprising  
CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
CC having non-contiguous single-stranded regions (NCSR) separated by an  
CC intervening region, a bridging oligonucleotide capable of binding to the  
CC first and second NCSR, a second oligonucleotide binding to a portion of  
CC the first NCSR and a cleavage agent, and mixing the contents to form a

CC cleavage structure. The method is useful for analysing nucleic acids,  
 CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
 CC purposes and detection and identification of pathogenic microorganisms  
 CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
 CC subtype 1a 5'UTR that can be used in the analysis of folded structures  
 CC using the method of the invention.

XX Sequence 244 BP; 51 A; 80 C; 67 G; 46 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 244;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
 DB 37 TTGGGACCCCAACTACTC 56

RESULT 121  
 ADK82252/C  
 ID ADK82252 standard; DNA; 244 BP.

XX AC ADK82252;  
 XX DT 03-JUN-2004 (first entry)

XX DE Hepatitis C virus subtype 3a polynucleotide seqid 29.

XX KW nucleic acid analysis; hepatitis C virus;  
 KW non-contiguous single-stranded region; NCSR; cleavage structure;  
 KW clinical; diagnostic; microorganism detection;  
 KW microorganism identification; hepatitis C virus; HCV; subtype 3a; ds.

XX OS Hepatitis C virus.

XX XX US6709815-B1.

XX PD 23-MAR-2004.

XX PF 18-JUL-2000; 2000US-00402618.

XX PR 05-MAY-1997; 97US-00851588.

XX PR 19-SEP-1997; 97US-00934097.

XX PR 03-MAR-1998; 98US-00034205.

XX PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;

XX DR WPI; 2004-256067/24.

XX PT Analyzing nucleic acids, comprises mixing target nucleic acid such as  
 PT hepatitis C virus nucleic acid, bridging oligonucleotide, second  
 PT oligonucleotide and cleavage agent to form cleavage structure.

XX PS Example 3; SEQ ID NO 29; 143pp; English.

XX The invention describes a method of analysing nucleic acids comprising  
 CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
 CC having non-contiguous single-stranded regions (NCSR) separated by an  
 CC intervening region, a bridging oligonucleotide capable of binding to the  
 CC first and second NCSR; a second oligonucleotide binding to a portion of  
 CC the first NCSR and a cleavage agent, and mixing the contents to form a  
 CC cleavage structure. The method is useful for analysing nucleic acids,  
 CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
 CC purposes and detection and identification of pathogenic microorganisms  
 CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
 CC subtype 3a polynucleotide identified using the analysis methods of the  
 CC invention.

XX Sequence 244 BP; 48 A; 69 C; 79 G; 48 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 244;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
 DB 208 TTGGGACCCCAACTACTC 189

RESULT 122  
 ADK82350  
 ID ADK82350 standard; DNA; 244 BP.

XX AC ADK82350;  
 XX DT 03-JUN-2004 (first entry)

XX DE Hepatitis C virus subtype 3a 5'UTR.

XX KW nucleic acid analysis; hepatitis C virus;  
 KW non-contiguous single-stranded region; NCSR; cleavage structure;  
 KW clinical; diagnostic; microorganism detection;  
 KW microorganism identification; hepatitis C virus; HCV; subtype 3a; ds;  
 KW 5'UTR; 5' untranslated region.

XX OS Hepatitis C virus.

XX XX US6709815-B1.

XX PD 23-MAR-2004.

XX PF 18-JUL-2000; 2000US-00402618.

XX PR 05-MAY-1997; 97US-00851588.

XX PR 19-SEP-1997; 97US-00934097.

XX PR 03-MAR-1998; 98US-00034205.

XX PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;

XX DR WPI; 2004-256067/24.

XX PT Analyzing nucleic acids, comprises mixing target nucleic acid such as  
 PT hepatitis C virus nucleic acid, bridging oligonucleotide, second  
 PT oligonucleotide and cleavage agent to form cleavage structure.

XX PS Example 8; SEQ ID NO 127; 143pp; English.

XX The invention describes a method of analysing nucleic acids comprising  
 CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
 CC having non-contiguous single-stranded regions (NCSR) separated by an  
 CC intervening region, a bridging oligonucleotide capable of binding to the  
 CC first and second NCSR; a second oligonucleotide binding to a portion of  
 CC the first NCSR and a cleavage agent, and mixing the contents to form a  
 CC cleavage structure. The method is useful for analysing nucleic acids,  
 CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
 CC purposes and detection and identification of pathogenic microorganisms  
 CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
 CC subtype 3a 5'UTR that can be used in the analysis of folded structures  
 CC using the method of the invention.

XX Sequence 244 BP; 48 A; 79 C; 69 G; 48 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 244;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
 DB 37 TTGGGACCCCAACTACTC 56

```

RESULT 123
ADK82249/C
ID ADK82249 standard; DNA; 244 BP.
XX
XX ADK82249;
XX
XX 03-JUN-2004 (first entry)
XX
XX Hepatitis C virus subtype 1a polynucleotide segid 26.
DE
XX nucleic acid analysis; hepatitis C virus;
XX non-contiguous single-stranded region; NCSR; cleavage structure;
XX clinical; diagnostic; microorganism detection;
XX microorganism identification; hepatitis C virus; HCV; subtype 1a; ds.
OS
XX Hepatitis C virus.
XX
XX US6709815-B1.
XX
XX 23-MAR-2004.
XX
XX 18-JUL-2000; 2000US-00402618.
XX
XX 05-MAY-1997; 97US-00851588.
XX
XX 19-SEP-1997; 97US-00934097.
XX
XX 03-MAR-1998; 98US-00034205.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;
XX Anderson TA, Dahlberg JE;
XX
XX WPI; 2004-256067/24.
XX
XX Analyzing nucleic acids, comprises mixing target nucleic acid such as
XX hepatitis C virus nucleic acid, bridging oligonucleotide, second
XX oligonucleotide and cleavage agent to form cleavage structure.
XX
XX Example 3; SEQ ID NO 26; 143bp; English.
XX
XX The invention describes a method of analysing nucleic acids comprising
XX providing a target nucleic acid, e.g. hepatitis C virus nucleic acid
XX having non-contiguous single-stranded regions (NCSR) separated by an
XX intervening region, a bridging oligonucleotide capable of binding to the
XX first and second NCSR; a second oligonucleotide binding to a portion of
XX the first NCSR and a cleavage agent, and mixing the contents to form a
XX cleavage structure. The method is useful for analysing nucleic acids,
XX e.g. hepatitis C virus nucleic acid useful for clinical diagnostic
XX purposes and detection and identification of pathogenic microorganisms
XX such as hepatitis C virus. This sequence represents a hepatitis C virus
XX subtype 1a polynucleotide identified using the analysis methods of the
XX invention.
XX
XX Sequence 244 BP; 46 A; 67 C; 80 G; 51 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 12; Length 244;
Best Local Similarity 100.0%; Pred. NO. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGCGACCCCAACTACTC 20
Db 208 TTGCGACCCCAACTACTC 189

```

```

DE Hepatitis C virus subtype 1b 5'UTR.
XX
XX nucleic acid analysis; hepatitis C virus;
XX non-contiguous single-stranded region; NCSR; cleavage structure;
XX clinical; diagnostic; microorganism detection;
XX microorganism identification; hepatitis C virus; HCV; subtype 1b; ds;
XX 5'UTR; 5' untranslated region.
OS
XX Hepatitis C virus.
XX
XX US6709815-B1.
XX
XX 23-MAR-2004.
XX
XX 18-JUL-2000; 2000US-00402618.
XX
XX 05-MAY-1997; 97US-00851588.
XX
XX 19-SEP-1997; 97US-00934097.
XX
XX 03-MAR-1998; 98US-00034205.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;
XX Anderson TA, Dahlberg JE;
XX
XX WPI; 2004-256067/24.
XX
XX Analyzing nucleic acids, comprises mixing target nucleic acid such as
XX hepatitis C virus nucleic acid, bridging oligonucleotide, second
XX oligonucleotide and cleavage agent to form cleavage structure.
XX
XX Example 8; SEQ ID NO 125; 143bp; English.
XX
XX The invention describes a method of analysing nucleic acids comprising
XX providing a target nucleic acid, e.g. hepatitis C virus nucleic acid
XX having non-contiguous single-stranded regions (NCSR) separated by an
XX intervening region, a bridging oligonucleotide capable of binding to the
XX first and second NCSR; a second oligonucleotide binding to a portion of
XX the first NCSR and a cleavage agent, and mixing the contents to form a
XX cleavage structure. The method is useful for analysing nucleic acids,
XX e.g. hepatitis C virus nucleic acid useful for clinical diagnostic
XX purposes and detection and identification of pathogenic microorganisms
XX such as hepatitis C virus. This sequence represents a hepatitis C virus
XX subtype 1b 5'UTR that can be used in the analysis of folded structures
XX using the method of the invention.
XX
XX Sequence 244 BP; 52 A; 81 C; 67 G; 44 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 12; Length 244;
Best Local Similarity 100.0%; Pred. NO. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGCGACCCCAACTACTC 20
Db 37 TTGCGACCCCAACTACTC 56

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RESULT 124
ADK82348
ID ADK82348 standard; DNA; 244 BP.
XX
XX ADK82348;
XX
XX 03-JUN-2004 (first entry)
XX
XX

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RESULT 125
AD005655/C
ID AD005655 standard; DNA; 244 BP.
XX
XX AD005655;
XX
XX 15-JUL-2004 (first entry)
XX
XX HCV 5' NCR (non coding region) template DNA.
XX
XX Nucleic acid amplification; mutation detection; cytosstatic;
XX antiinflammatory; hepatotropic; virucide; cancer; ds.
XX
XX Hepatitis C virus.
XX
XX WO2004035832-A1.
XX

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XX 29-APR-2004.
PD
XX
PF 17-OCT-2003; 2003WO-KR002179.
XX
XX 18-OCT-2002; 2002KR-00063832.
PR
XX 02-SEP-2003; 2003KR-00061066.
XX
XX (GENE-) GENEMATRIX INC.
XX
XX Kim N, Kim S, Kim S, Kim E, Moon M, Yoo W, Lee C, Chung H;
PI Jee M, Hwang S, Hong S;
XX
XX WPI; 2004-348478/32.
DR
XX Detecting a mutation, useful in diagnosing and creating e.g. cancer or
PT hepatitis, comprises generating fragments of polynucleotides using
PT specific primers and measuring molecular weight of cleaved fragments.
XX
XX Example 4; SEQ ID NO 16; 58bp; English.
PS
XX The invention relates to detecting a mutation. The method involves
CC amplifying a target polynucleotide using a forward primer and a reverse
CC primer; generating fragments of two or more single-stranded
CC polynucleotides including one or more mutations sequence having the size
CC of 2-33 bases by cleaving the amplified target polynucleotide with
CC restriction enzymes, where the second restriction enzyme does not react
CC while a first restriction enzyme is reacted with the amplified
CC polynucleotide; and measuring the molecular weight of the cleaved
CC fragments. The polynucleotide is cleaved to include one mutation among
CC two or more different mutations in only one single stranded
CC polynucleotide fragment and all mutations in the other single stranded
CC nucleotide fragment. Restrictions enzyme treatment step is performed
CC using restriction enzymes having different optimum temperatures. The
CC method is useful in detecting a mutation. The method and primer are
CC useful in diagnosing, prognosis, creating and preventing a disease, e.g.
CC cancer or hepatitis B or C virus. The present sequence represents a HCV
CC 5' NCR (non coding region) template DNA sequence.
XX
XX Sequence 244 BP; 46 A; 67 C; 80 G; 51 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 20; DB 12; Length 244;
XX Best Local Similarity 100.0%; Pred. No. 0.054;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTCGGAGCCCAACTACTC 20
Db 208 TTCGGAGCCCAACTACTC 189

```

```

XX (CHTR ) CHIRON CORP.
XX
XX Cha T, Beall E, Irvine B, Kolberg J, Urdea MS;
XX
XX WPI; 1992-398869/48.
XX
XX Compsn. comprising a non-hepatitis C virus-1 nucleotide sequence -
PT related to HCV-1, useful for treating and detecting HCV-1 infections and
PT as a vaccine.
XX
XX Claim 8; Page 85; 186pp; English.
PS
XX This is a non-HCV-1 sequence which corresponds to a nucleotide sequence
CC within the 5' untranslated region of HCV-1 of genotype G11. This sequence
CC (from isolate us4) is identical to that of isolates nac5, arg2, spl, ghl
CC and 115; it differs by one nucleotide from isolate jhl (AAQ31072). The
CC sequence is a preferred example of an oligonucleotide for use as a probe
CC in hybridisation assays, as a primer for synthesis of HCV genotype-
CC specific nucleic acid, as a binding partner for separating HCV nucleic
CC acid or as an antisense oligonucleotide to prevent expression of HCV
CC genes. Polypeptides encoded by oligonucleotides of the invention (no
CC sequences given in the specification) are useful in vaccines against HCV
CC and to produce antibodies to detect the virus. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX Sequence 252 BP; 43 A; 72 C; 84 G; 53 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 20; DB 2; Length 252;
XX Best Local Similarity 100.0%; Pred. No. 0.054;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTCGGAGCCCAACTACTC 20
Db 186 TTCGGAGCCCAACTACTC 167

```



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XX DE HCV-1 genotype GIV 5'UT region sequence gj61329.
XX XX Hepatitis C virus; non-A, non-B hepatitis; 5'UTR; untranslated region;
XX KM ss.
XX OS Synthetic.
XX PN WO9219743-A2.
XX PD 12-NOV-1992.
XX PF 08-MAY-1992; 92WO-US004036.
XX PR 08-MAY-1991; 91US-00697326.
XX PA (CHIR ) CHIRON CORP.
XX PI Cha T, Beall E, Irvine B, Kolberg J, Urdea MS;
XX DR WPI, 1992-398869/48.
XX PT Compsn. comprising a non-hepatitis C virus-1 nucleotide sequence -
XX PT related to HCV-1, useful for treating and detecting HCV-1 infections and
XX PT as a vaccine.
XX PS Claim 8; Page 93; 186pp; English.
XX CC This is a non-HCV-1 sequence which corresponds to a nucleotide sequence
XX CC within the 5'untranslated region of HCV-1 of genotype GIV. The sequence
XX CC is a preferred example of an oligonucleotide for use as a probe in
XX CC hybridisation assays, as a primer for synthesis of HCV genotype-specific
XX CC nucleic acid, as a binding partner for separating HCV nucleic acid or as
XX CC an antisense oligonucleotide to prevent expression of HCV genes.
XX CC Polypeptides encoded by oligonucleotides of the invention (no sequences
XX CC given in the specification) are useful in vaccines against HCV and to
XX CC produce antibodies to detect the virus. (Updated on 25-MAR-2003 to
XX CC correct PN field.)
XX SQ Sequence 252 BP; 46 A; 71 C; 83 G; 52 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 252;
XX Best Local Similarity 100.0%; Pred. No. 0.054;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGACCCCAACTACTC 20
Db 186 TTCCGACCCCAACTACTC 167

RESULT 131
AAQ31080/c
ID AAQ31080 standard; DNA; 252 BP.
XX
XX AC AAQ31080;
XX DT 25-MAR-2003 (revised)
XX DT 24-MAR-1993 (first entry)
XX
XX DE HCV-1 genotype GIV 5'UT region sequence s21.
XX KM Hepatitis C virus; non-A, non-B hepatitis; 5'UTR; untranslated region;
XX KM ss.
XX OS Synthetic.
XX OS WO9219743-A2.
XX PN 12-NOV-1992.
XX PD 08-MAY-1992; 92WO-US004036.
XX PF 08-MAY-1991; 91US-00697326.
XX PR 08-MAY-1991; 91US-00697326.

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XX PA (CHIR ) CHIRON CORP.
XX XX Cha T, Beall E, Irvine B, Kolberg J, Urdea MS;
XX XX WPI, 1992-398869/48.
XX PT Compsn. comprising a non-hepatitis C virus-1 nucleotide sequence -
XX PT related to HCV-1, useful for treating and detecting HCV-1 infections and
XX PT as a vaccine.
XX PS Claim 8; Page 92; 186pp; English.
XX CC This is a non-HCV-1 sequence which corresponds to a nucleotide sequence
XX CC within the 5'untranslated region of HCV-1 of genotype GIV. The sequence
XX CC is a preferred example of an oligonucleotide for use as a probe in
XX CC hybridisation assays, as a primer for synthesis of HCV genotype-specific
XX CC nucleic acid, as a binding partner for separating HCV nucleic acid or as
XX CC an antisense oligonucleotide to prevent expression of HCV genes.
XX CC Polypeptides encoded by oligonucleotides of the invention (no sequences
XX CC given in the specification) are useful in vaccines against HCV and to
XX CC produce antibodies to detect the virus. (Updated on 25-MAR-2003 to
XX CC correct PN field.)
XX SQ Sequence 252 BP; 46 A; 71 C; 83 G; 52 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 252;
XX Best Local Similarity 100.0%; Pred. No. 0.054;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGACCCCAACTACTC 20
Db 186 TTCCGACCCCAACTACTC 167

RESULT 132
AAQ31067/c
ID AAQ31067 standard; DNA; 252 BP.
XX
XX AC AAQ31067;
XX DT 25-MAR-2003 (revised)
XX DT 24-MAR-1993 (first entry)
XX
XX DE HCV-1 genotype GI 5'UT region sequence ams.
XX KM Hepatitis C virus; non-A, non-B hepatitis; 5'UTR; untranslated region;
XX KM ss.
XX OS Synthetic.
XX OS WO9219743-A2.
XX PN 12-NOV-1992.
XX PD 08-MAY-1992; 92WO-US004036.
XX PF 08-MAY-1991; 91US-00697326.
XX PR 08-MAY-1991; 91US-00697326.
XX PA (CHIR ) CHIRON CORP.
XX PI Cha T, Beall E, Irvine B, Kolberg J, Urdea MS;
XX DR WPI, 1992-398869/48.
XX PT Compsn. comprising a non-hepatitis C virus-1 nucleotide sequence -
XX PT related to HCV-1, useful for treating and detecting HCV-1 infections and
XX PT as a vaccine.
XX PS Claim 8; Page 82; 186pp; English.
XX CC This is a non-HCV-1 sequence which corresponds to a nucleotide sequence
XX CC within the 5'untranslated region of HCV-1 of genotype GI. The sequence is

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CC a preferred example of a oligonucleotide for use as a probe in  
 CC hybridisation assays, as a primer for synthesis of HCV genotype-specific  
 CC nucleic acid, as a binding partner for separating HCV nucleic acid or as  
 CC an antisense oligonucleotide to prevent expression of HCV genes.  
 CC Polypeptides encoded by oligonucleotides of the invention (no sequences  
 CC given in the specification) are useful in vaccines against HCV and to  
 CC produce antibodies to detect the virus. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX

XX Sequence 252 BP; 46 A; 73 C; 81 G; 52 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCAACTACTC 20  
 DB 186 TTGCGACCCAACTACTC 167

RESULT 133

ID AAQ31066 standard; DNA; 252 BP.

AC AAQ31066;

DT 25-MAR-2003 (revised)

DT 24-MAR-1993 (first entry)

DE HCV-1 genotype GI 5'UT region sequence us5.

KW Hepatitis C virus; non-A, non-B hepatitis; 5'UTR; untranslated region;  
 ss.

XX Synthetic.

PN WO9219743-A2.

PD 12-NOV-1992.

PF 08-MAY-1992; 92WO-US004036.

PR 08-MAY-1991; 91US-00697326.

PA (CHIR) CHIRON CORP.

PI Cha T, Beall E, Irvine B, Kolberg J, Urdea MS;

DR WPI; 1992-398869/48.

PT Compsn. comprising a non-hepatitis C virus-1 nucleotide sequence -  
 PT related to HCV-1, useful for treating and detecting HCV-1 infections and  
 PT as a vaccine.

PS Claim 8; Page 81; 186pp; English.

XX This is a non-HCV-1 sequence which corresponds to a nucleotide sequence  
 CC within the 5'untranslated region of HCV-1 of genotype GI. The sequence is  
 CC a preferred example of a oligonucleotide for use as a probe in  
 CC hybridisation assays, as a primer for synthesis of HCV genotype-specific  
 CC nucleic acid, as a binding partner for separating HCV nucleic acid or as  
 CC an antisense oligonucleotide to prevent expression of HCV genes.  
 CC Polypeptides encoded by oligonucleotides of the invention (no sequences  
 CC given in the specification) are useful in vaccines against HCV and to  
 CC produce antibodies to detect the virus. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX

XX Sequence 252 BP; 44 A; 72 C; 83 G; 53 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCAACTACTC 20  
 DB 186 TTGCGACCCAACTACTC 167

RESULT 134

ID AAQ31072 standard; DNA; 252 BP.

AC AAQ31072;

DT 25-MAR-2003 (revised)

DT 24-MAR-1993 (first entry)

DE HCV-1 genotype GI 5'UT region sequence jhl.

KW Hepatitis C virus; non-A, non-B hepatitis; 5'UTR; untranslated region;  
 ss.

XX Synthetic.

PN WO9219743-A2.

PD 12-NOV-1992.

PF 08-MAY-1992; 92WO-US004036.

PR 08-MAY-1991; 91US-00697326.

PA (CHIR) CHIRON CORP.

PI Cha T, Beall E, Irvine B, Kolberg J, Urdea MS;

DR WPI; 1992-398869/48.

PT Compsn. comprising a non-hepatitis C virus-1 nucleotide sequence -  
 PT related to HCV-1, useful for treating and detecting HCV-1 infections and  
 PT as a vaccine.

PS Claim 8; Page 86; 186pp; English.

XX This is a non-HCV-1 sequence which corresponds to a nucleotide sequence  
 CC within the 5'untranslated region of HCV-1 of genotype GI. The sequence  
 CC is a preferred example of a oligonucleotide for use as a probe in  
 CC hybridisation assays, as a primer for synthesis of HCV genotype-specific  
 CC nucleic acid, as a binding partner for separating HCV nucleic acid or as  
 CC an antisense oligonucleotide to prevent expression of HCV genes.  
 CC Polypeptides encoded by oligonucleotides of the invention (no sequences  
 CC given in the specification) are useful in vaccines against HCV and to  
 CC produce antibodies to detect the virus. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX

XX Sequence 252 BP; 43 A; 71 C; 84 G; 54 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 252;  
 Best Local Similarity 100.0%; Pred. No. 0.054;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCAACTACTC 20  
 DB 186 TTGCGACCCAACTACTC 167

RESULT 135

ID AAQ32981 standard; DNA; 256 BP.

AC AAQ32981;

DT 24-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 14-MAY-1993 (first entry)

```

DE HCV EI 5' non-coding region.
XX
XX PCR; amplification; prototype; HCV pt; ss.
KM Hepatitis C virus; HCVel.
OS
XX WO9221759-A1.
PN
XX 10-DEC-1992.
PD
XX
XX 04-JUN-1992; 92WO-FR000501.
PF
XX 06-JUN-1991; 91FR-00006882.
PR
XX (INSP ) INST PASTEUR.
PA
XX Brechot C, Kremendorf D, Porchon C;
PI
XX WPI; 1992-433657/52.
DR
XX
XX New nucleotide and peptide sequences - specific for French isolate of
PT hepatitis C virus and useful in diagnosing and treating related
PT infections.
PS
XX Disclosure; Fig 2; 50pp; French.
XX
XX RNA was extracted from the serum of an HCV-positive blood donor, subjected
CC to reverse transcription and the cDNA formed amplified by PCR.
CC Amplification prods. were cloned, screened with a probe derived from the
CC HCV prototype and inserts sequenced. The results showed marked
CC conservation in the non-coding region, significant variability in the
CC structural region (encoding envelope proteins) and reduced variability in
CC the non-structural region. The non-coding region corresponds to positions
CC -259 to -4 of HCV prototype (HCV pt) (WO-A-90/14436). (Updated on 25-MAR-
CC 2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 256 BP; 44 A; 73 C; 85 G; 54 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTCCGACCCCAACTACTC 20
DB 193 TTCCGACCCCAACTACTC 174

```

```

XX
XX Porchon C, Brechot C, Kremendorf D;
PI
XX WPI; 1999-394595/33.
DR
XX
XX Nucleotides and peptides from hepatitis C virus isolate for detecting EI-
PT specific antigens.
PT
XX
XX Disclosure; Col 9-10; 45pp; English.
PS
XX
XX This sequence is the hepatitis C virus (HCV) EI 5' non-coding region. The
CC invention relates to human or murine monoclonal antibodies directed
CC against a HCV EI protein sequence. The monoclonal antibodies and their
CC fragments are useful for the in vitro diagnosis of HCV EI-specific
CC antigens. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 256 BP; 44 A; 73 C; 85 G; 54 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTCCGACCCCAACTACTC 20
DB 193 TTCCGACCCCAACTACTC 174

```

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RESULT 136
AAx84004/c
ID AAx84004 standard; cDNA; 256 BP.
XX
XX AAx84004;
AC
XX
XX 27-AUG-2003 (revised)
DT 26-AUG-1999 (first entry)
XX
XX HCV EI 5' non-coding region.
DE
XX
XX HCV EI region; monoclonal antibody; diagnosis; HCV EI-specific antigen;
KM ss.
XX
XX Hepatitis C virus.
OS
XX US5919454-A.
PN
XX 06-JUN-1999.
PD
XX
XX 07-JUN-1995; 95US-00487231.
PF
XX 18-MAR-1993; 93US-00965285.
PR
XX (INSP ) INST PASTEUR.
PA

```

```

RESULT 137
AAx16761/c
ID AAx16761 standard; cDNA to mRNA; 256 BP.
XX
XX AAx16761;
AC
XX 27-APR-1999 (first entry)
DT
XX
XX Hepatitis C virus EI non-coding region.
DE
XX
XX EI region; French Hepatitis C virus; HCV; immunogen; antibody; detection;
KM immunosassay; ss.
XX
XX Hepatitis C virus.
OS
XX US5866139-A.
PN
XX
XX 02-FEB-1999.
PD
XX
XX 07-JUN-1995; 95US-00483695.
PF
XX 18-MAR-1993; 93US-00965285.
PR
XX (INSP ) INST PASTEUR.
PA
XX
XX Porchon C, Kremendorf D, Brechot C;
PI
XX
XX WPI; 1999-141865/12.
DR
XX
XX New isolated and purified Hepatitis C virus EI peptides - useful for
PT vaccine production or diagnostic purposes.
PT
XX
XX Disclosure; Col 9-10; 45pp; English.
PS
XX
XX The sequence represents the EI non-coding region from a French Hepatitis
CC C virus (HCV) isolate. HCV encoded protein or peptides derived from them
CC can be: (1) conjugated to a carrier protein and used as immunogens for
CC eliciting protective antibodies; or (ii) labelled, and used as
CC immunoassay reagents for detecting antibodies specific for HCV EI
XX
SQ Sequence 256 BP; 44 A; 73 C; 85 G; 54 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 TTGGGAGCCCACTACTC 20  
 DB 193 TTGGGAGCCCACTACTC 174

RESULT 138  
 ADF08496/c  
 ID ADF08496 standard; DNA, 263 BP.

AC ADF08496;

DT 12-FEB-2004 (first entry)

DE Hepatitis C virus (HCV) genomic DNA 5'UTR region.

KM Hepatitis C virus; HCV; inducible promoter; HCV infection; ds; 5'UTR.

OS Hepatitis C virus.

PN US2003148267-A1.

PD 07-AUG-2003.

PF 08-NOV-2002; 2002US-00292129.

PR 09-NOV-2001; 2001US-0345405P.

PA (SCHM/) SCHMIDT E V.

PA (CHUN/) CHUNG R T.

PI Schmidt EV, Chung RT;

DR WPI; 2003-897533/82.

PT Identifying a compound that increases the mutation rate of hepatitis C virus (HCV) comprises detecting an increase in HCV quasispecies produced by the cell in the presence of the candidate compound.

PS Example 13; SEQ ID NO 13; 35pp; English.

XX The invention relates to a method for identifying a compound that  
 CC increases the mutation rate of hepatitis C virus (HCV), comprising  
 CC detecting an increase in HCV quasispecies produced by the cell in the  
 CC presence of the candidate compound by e.g. sequencing HCV nucleic acid  
 CC molecules isolated from the test cell. The method involves providing a  
 CC test cell containing a nucleic acid molecule comprising a first  
 CC nucleotide sequence consisting of an infectious hepatitis C viral genome  
 CC copy and an inducible promoter operably linked to the first and second  
 CC nucleotide sequences, where the ribozyme is configured to remove a 3'  
 CC sequence unnecessary for replication of the hepatitis C viral genome from  
 CC a transcript initiated by the promoter, inducing the inducible promoter,  
 CC contacting the test cell with a candidate compound and detecting an  
 CC increase in HCV quasispecies produced by the cell in the presence of the  
 CC candidate compound compared to that in the absence of the compound, where  
 CC an increase in the HCV quasispecies indicates that the compound increases  
 CC the mutation rate of HCV. The method is useful in identifying compounds  
 CC that may be used for treating HCV infection. This sequence represents an  
 CC HCV genomic DNA 5'UTR region used in the method of the invention.

SQ Sequence 263 BP; 51 A; 72 C; 86 G; 54 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 263;

Best Local Similarity 100.0%; Pred. No. 0.054;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGAGCCCACTACTC 20

DB 217 TTGGGAGCCCACTACTC 198

RESULT 139

ABN79973/c

ID ABN79973 standard; DNA; 278 BP.

XX ABN79973;

DT 15-JUL-2002 (first entry)

DE Hepatitis C virus 5' untranslated region genotype 3a.

KM Single nucleotide polymorphism; nucleic acid typing; hepatitis C virus; tissue typing; untranslated region; UTR; ds; HCV.

OS Hepatitis C virus.

PN WO200220837-A2.

PD 14-MAR-2002.

PF 10-SEP-2001; 2001WO-GB004042.

PR 08-SEP-2000; 2000GB-00022069.

PA (PYRO-) PYROSEQUENCING AB.

PA (STRD) UNIV LEIAND STANFORD JUNIOR.

PI (GARD/) GARDNER R.

PI Ronaghi M, Ekstroem B, Pourmand N;

DR WPI; 2002-393849/42.

PT Typing nucleic acid for obtaining information about several variable sites involves simultaneously or sequentially performing two or more primer extension reactions, and determining the pattern of nucleotide incorporation.

PS Example 1; Fig 2; 86pp; English.

XX The invention relates to a novel method for obtaining typing information  
 CC about several variable sites within target nucleic acid, or typing one or  
 CC more nucleic acid molecules. The methods of the invention are useful for  
 CC typing one or more nucleic acid molecules containing two or more variable  
 CC sites, preferably nucleic acid molecules containing three or more  
 CC variable sites are typed, where three or more primer extension reactions  
 CC are performed. The method is also useful for diagnosis of pathological  
 CC conditions characterized by the presence of specific nucleic acid  
 CC molecule(s). The methods are particularly suited for identifying  
 CC microbial species or their subtypes, and in typing procedures e.g. typing  
 CC of polymorphisms, tissue typing or in clinical applications. The sequence  
 CC represents the 5' untranslated region (UTR) of a hepatitis C virus (HCV)  
 CC genotype, amplified in the invention to type HCV-positive sera

SQ Sequence 278 BP; 51 A; 81 C; 89 G; 57 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 278;

Best Local Similarity 100.0%; Pred. No. 0.053;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGAGCCCACTACTC 20

DB 233 TTGGGAGCCCACTACTC 214

RESULT 140

AAT29118/c

AC AAT29118;

DT 02-DEC-1996 (first entry)

DE Hepatitis C virus genome fragment (Clone HCV3.1).

KM p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus; Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;

```

KW Staphylococcus; identification; detection; ds.
XX
OS Hepatitis C virus.
XX
PN W09615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US014673.
XX
PR 09-NOV-1994; 94US-00337164.
PR 09-MAR-1995; 95US-00402601.
PR 07-JUN-1995; 95US-00484956.
PR 30-AUG-1995; 95US-00520946.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Dahlberg JE, Lyamichev VI, Brow MAD, Oldenburg MC, Heisler LM;
PI Fors L, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection esp.
PT in human p53 gene, to identify strains of microorganisms and viruses.
XX
PS Example 32; Page 301; 43pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease selected
CC from the group consisting of Cleavase (RTM) BN enzyme, Thermus aquaticus
CC DNA polymerase, Thermus thermophilus DNA polymerase, Escherichia coli
CC ExoIII and the Saccharomyces cerevisiae Rad1/Rad10 complex. The nucleic
CC acid substrate is preferably an oligonucleotide containing a human p53
CC gene sequence or alternatively, microbial gene sequences. Cleavage
CC products are compared to the cleavage products of reference gene
CC sequences. The method is used for detecting mutation in the human p53
CC gene; for identifying strains of microorganisms, especially bacteria
CC selected from the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The
CC method may also be used for the identification of viruses, especially
CC hepatitis C virus (HCV) and simian immunodeficiency virus (SIV). Four
CC primers (AAT29110-113) were used to generate six DNA HCV fragments by RT-
CC PCR. The sequence described in AAT29110 is an external antisense primer.
CC The sequence described in AAT29111 is a sense primer used after
CC termination of the reverse transcription reaction. The remaining two
CC primers (AAT29112, AAT29113) were used in a second round of amplification
CC reactions which produced a 281 bp product which corresponds to a
CC conserved 5' noncoding region of HCV between positions -284 and -4 of the
CC HCV genome. The amplified sequences are described in AAT29116-121
XX
SQ Sequence 281 BP; 48 A; 80 C; 92 G; 61 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTTCGGACCCCAACTACTC 20
Db 218 TTTCGGACCCCAACTACTC 199

```

```

XX
OS Hepatitis C virus.
XX
PN W09615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US014673.
XX
PR 09-NOV-1994; 94US-00337164.
PR 09-MAR-1995; 95US-00402601.
PR 07-JUN-1995; 95US-00484956.
PR 30-AUG-1995; 95US-00520946.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Dahlberg JE, Lyamichev VI, Brow MAD, Oldenburg MC, Heisler LM;
PI Fors L, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection esp.
PT in human p53 gene, to identify strains of microorganisms and viruses.
XX
PS Example 32; Page 302; 43pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease selected
CC from the group consisting of Cleavase (RTM) BN enzyme, Thermus aquaticus
CC DNA polymerase, Thermus thermophilus DNA polymerase, Escherichia coli
CC ExoIII and the Saccharomyces cerevisiae Rad1/Rad10 complex. The nucleic
CC acid substrate is preferably an oligonucleotide containing a human p53
CC gene sequence or alternatively, microbial gene sequences. Cleavage
CC products are compared to the cleavage products of reference gene
CC sequences. The method is used for detecting mutation in the human p53
CC gene; for identifying strains of microorganisms, especially bacteria
CC selected from the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The
CC method may also be used for the identification of viruses, especially
CC hepatitis C virus (HCV) and simian immunodeficiency virus (SIV). Four
CC primers (AAT29110-113) were used to generate six DNA HCV fragments by RT-
CC PCR. The sequence described in AAT29110 is an external antisense primer.
CC The sequence described in AAT29111 is a sense primer used after
CC termination of the reverse transcription reaction. The remaining two
CC primers (AAT29112, AAT29113) were used in a second round of amplification
CC reactions which produced a 281 bp product which corresponds to a
CC conserved 5' noncoding region of HCV between positions -284 and -4 of the
CC HCV genome. The amplified sequences are described in AAT29116-121
XX
SQ Sequence 281 BP; 51 A; 82 C; 91 G; 57 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTTCGGACCCCAACTACTC 20
Db 218 TTTCGGACCCCAACTACTC 199

```

```

RESULT 141
AAT29121/c
ID AAT29121 standard; DNA; 281 BP.
XX
AC AAT29121;
XX
DT 02-DEC-1996 (first entry)
DE Hepatitis C virus genome fragment (Clone HCV7.1).
XX
p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
Staphylococcus; identification; detection; ds.

```

```

RESULT 142
AAT29116/c
ID AAT29116 standard; DNA; 281 BP.
XX
AC AAT29116;
XX
DT 20-NOV-1996 (first entry)
DE Hepatitis C virus genome fragment (Clone HCV1.1).
XX
p53; mutant; mutation; cleavage; nuclease; cleavase; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
Staphylococcus; identification; detection; ds.

```

```

OS Hepatitis C virus.
XX
XX MO9615267-A1.
XX
XX 23-MAY-1996.
XX
XX
XX 09-NOV-1995; 95WO-US014673.
XX
XX PR 09-NOV-1994; 94US-00337164.
XX PR 09-MAR-1995; 95US-00402601.
XX PR 07-JUN-1995; 95US-00484956.
XX PR 30-AUG-1995; 95US-00520946.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX Dahlberg JE, Lyamichev VI, Brow MAD, Oldenburg MC, Heisler IM,
XX Fors L, Olive DM;
XX
XX WPI; 1996-259862/26.
XX
XX
XX Cleavage of nucleic acids to detect mutation(s) - allows detection esp.
XX in human p53 gene, to identify strains of microorganisms and viruses.
XX
XX Example 32; Page 300; 433p; English.
XX
XX Cleavage of nucleic acids using an enzyme, especially a nuclease selected
XX from the group consisting of Cleavase (RTM) BN enzyme, Thermus aquaticus
XX DNA polymerase, Thermus thermophilus DNA polymerase, Escherichia coli
XX EcoRI and the Saccharomyces cerevisiae Rad1/Rad10 complex. The nucleic
XX acid substrate is preferably an oligonucleotide containing a human p53
XX gene sequence or alternatively, microbial gene sequences. Cleavage
XX products are compared to the cleavage products of reference gene
XX sequences. The method is used for detecting mutation in the human p53
XX gene; for identifying strains of microorganisms, especially bacteria
XX selected from the group of members of the genera Campylobacter,
XX Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The
XX method may also be used for the identification of viruses, especially
XX hepatitis C virus (HCV) and simian immunodeficiency virus (SIV). Four
XX primers (AAT29110-115) were used to generate six DNA HCV fragments by RT-
XX PCR. The sequence described in AAT29110 is an external antisense primer.
XX The sequence described in AAT29111 is a sense primer used after
XX termination of the reverse transcription reaction. The remaining two
XX primers (AAT29112, AAT29113) were used in a second round of amplification
XX reactions which produced a 281 bp product which corresponds to a
XX conserved 5' noncoding region of HCV between positions -284 and -4 of the
XX HCV genome. The amplified sequences are described in AAT29116-121
XX
XX Sequence 281 BP; 50 A; 80 C; 92 G; 59 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 0.053;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TTCCGACCCCAACTACTC 20
XX 218 TTCCGACCCCAACTACTC 199
XX
XX RESULT 143
XX ADB16264/c
XX ID ADB16264 standard; DNA; 281 BP.
XX
XX ADB16264;
XX
XX 20-NOV-2003 (first entry)
XX
XX Cleavase BN DNA substrate #41.
XX
XX ds; DNA polymerase; microorganism strain identification; bacteria;
XX Campylobacter; Escherichia; Mycobacterium; Salmonella; Shigella;
XX Staphylococcus; virus; hepatitis C virus; simian immunodeficiency virus;
XX Mycobacterium tuberculosis.
XX

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OS Hepatitis C virus.
XX
XX US2003054338-A1.
XX
XX
XX 20-MAR-2003.
XX
XX
XX 28-AUG-2001; 2001US-00940925.
XX
XX PR 07-DEC-1992; 92US-00986330.
XX PR 04-JUN-1993; 93US-00073384.
XX PR 06-JUN-1994; 94US-00254359.
XX PR 09-NOV-1994; 94US-00337164.
XX PR 09-MAR-1995; 95US-00402601.
XX PR 07-JUN-1995; 95US-00484956.
XX PR 30-AUG-1995; 95US-00520946.
XX PR 06-FEB-1997; 97US-00789079.
XX PR 19-FEB-1997; 97US-00802233.
XX PR 05-SEP-2000; 2000US-00655378.
XX
XX (DAHL/) DAHLBERG J E.
XX (BROW/) BROW M A D.
XX (LYAM/) LYAMICHEV V I.
XX
XX Dahlberg JE, Brow MAD, Lyamichev VI;
XX
XX WPI; 2003-615811/58.
XX
XX
XX Identification of strains of microorganisms, by treating nucleic acid
XX cleavage structure(s) derived from microorganisms with nuclease to form
XX cleavage products(s) and detecting the product(s).
XX
XX Example 34; Fig 82; 303p; English.
XX
XX The invention relates to a method of detecting and identifying strains of
XX microorganisms by providing a nuclease and a nucleic acid substrate
XX containing sequences derived from microorganism(s), treating the nucleic
XX acid substrate to form cleavage structure(s) and reacting the nucleic
XX with the cleavage structures so that cleavage product(s) are produced.
XX The method is used for the identification of strains of microorganisms.
XX The microorganism comprises bacteria including Campylobacter,
XX Escherichia, Mycobacterium, Salmonella, Shigella or Staphylococcus or a
XX virus comprising hepatitis C virus or simian immunodeficiency virus.
XX Mycobacterium comprises strains of multi-drug resistant Mycobacterium
XX tuberculosis. The method is less sensitive to size so that entire genes,
XX rather than gene fragments, may be analysed. It facilitates the use of
XX internal standards for subsequent analysis and data comparison, and
XX increases the productivity of personnel and equipment. The present
XX sequence represents a Cleavase BN substrate DNA.
XX
XX Sequence 281 BP; 48 A; 80 C; 92 G; 61 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 9; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 0.053;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TTCCGACCCCAACTACTC 20
XX 218 TTCCGACCCCAACTACTC 199
XX
XX RESULT 144
XX ADB16262/c
XX ID ADB16262 standard; DNA; 281 BP.
XX
XX ADB16262;
XX
XX 20-NOV-2003 (first entry)
XX
XX Cleavase BN DNA substrate #39.
XX
XX ds; DNA polymerase; microorganism strain identification; bacteria;
XX Campylobacter; Escherichia; Mycobacterium; Salmonella; Shigella;
XX Staphylococcus; virus; hepatitis C virus; simian immunodeficiency virus;
XX

```



KM Mycobacterium tuberculosis.  
 XX  
 OS Hepatitis C virus.  
 XX  
 FN US2003054338-A1.  
 XX  
 PD 20-MAR-2003.  
 XX  
 PF 28-AUG-2001; 2001US-00940925.  
 XX  
 PR 07-DEC-1992; 92US-00986330.  
 PR 04-JUN-1993; 93US-00073384.  
 PR 06-JUN-1994; 94US-00254359.  
 PR 09-NOV-1994; 94US-00337164.  
 PR 09-MAR-1995; 95US-00402601.  
 PR 07-JUN-1995; 95US-00464956.  
 PR 30-AUG-1995; 95US-00520946.  
 PR 06-FEB-1997; 97US-00789079.  
 PR 19-FEB-1997; 97US-00802233.  
 PR 05-SEP-2000; 2000US-00655378.  
 XX  
 PA (DAHL/) DAHLBERG J E.  
 PA (BROW/) BROW M A D.  
 PA (LYAM/) LYAMICHEV V I.  
 XX  
 PI Dahlberg JE, Brow MAD, Lyamichev VI;  
 DR WPI; 2003-615811/58.  
 XX  
 PT Identification of strains of microorganisms, by treating nucleic acid  
 PT cleavage structure(s) derived from microorganisms with nuclease to form  
 PT cleavage products(s) and detecting the product(s).  
 XX  
 PS Example 34; Fig 82; 303pp; English.  
 XX  
 CC The invention relates to a method of detecting and identifying strains of  
 CC microorganisms by providing a nuclease and a nucleic acid substrate  
 CC containing sequences derived from microorganism(s), treating the nucleic  
 CC acid substrate to form cleavage structure(s) and reacting the nuclease  
 CC with the cleavage structures so that cleavage product(s) are produced.  
 CC The method is used for the identification of strains of microorganisms.  
 CC The microorganism comprises bacteria including Campylobacter,  
 CC Escherichia, Mycobacterium, Salmonella, Shigella or Staphylococcus or a  
 CC virus comprising hepatitis C virus or simian immunodeficiency virus. The  
 CC Mycobacterium comprises strains of multi-drug resistant Mycobacterium  
 CC tuberculosis. The method is less sensitive to size so that entire genes,  
 CC rather than gene fragments, may be analysed. It facilitates the use of  
 CC internal standards for subsequent analysis and data comparison, and  
 CC increases the productivity of personnel and equipment. The present  
 CC sequence represents a Cleavage BN substrate DNA.  
 XX  
 SQ Sequence 281 BP; 50 A; 80 C; 92 G; 59 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 9; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 218 TTGCGACCCCAACTACTC 199  
 RESULT 145  
 ADB16267/C  
 ID ADB16267 standard; DNA; 281 BP.  
 XX  
 AC ADB16267;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Cleavage BN DNA substrate #44.  
 XX  
 DB; DNA polymerase; microorganism strain identification; bacteria;

KM Campylobacter; Escherichia; Mycobacterium; Salmonella; Shigella;  
 KM Staphylococcus; virus; hepatitis C virus; simian immunodeficiency virus;  
 KM Mycobacterium tuberculosis.  
 XX  
 OS Hepatitis C virus.  
 XX  
 FN US2003054338-A1.  
 XX  
 PD 20-MAR-2003.  
 XX  
 PF 28-AUG-2001; 2001US-00940925.  
 XX  
 PR 07-DEC-1992; 92US-00986330.  
 PR 04-JUN-1993; 93US-00073384.  
 PR 06-JUN-1994; 94US-00254359.  
 PR 09-NOV-1994; 94US-00337164.  
 PR 09-MAR-1995; 95US-00402601.  
 PR 07-JUN-1995; 95US-00464956.  
 PR 30-AUG-1995; 95US-00520946.  
 PR 06-FEB-1997; 97US-00789079.  
 PR 19-FEB-1997; 97US-00802233.  
 PR 05-SEP-2000; 2000US-00655378.  
 XX  
 PA (DAHL/) DAHLBERG J E.  
 PA (BROW/) BROW M A D.  
 PA (LYAM/) LYAMICHEV V I.  
 XX  
 PI Dahlberg JE, Brow MAD, Lyamichev VI;  
 DR WPI; 2003-615811/58.  
 XX  
 PT Identification of strains of microorganisms, by treating nucleic acid  
 PT cleavage structure(s) derived from microorganisms with nuclease to form  
 PT cleavage products(s) and detecting the product(s).  
 XX  
 PS Example 34; Fig 82; 303pp; English.  
 XX  
 CC The invention relates to a method of detecting and identifying strains of  
 CC microorganisms by providing a nuclease and a nucleic acid substrate  
 CC containing sequences derived from microorganism(s), treating the nucleic  
 CC acid substrate to form cleavage structure(s) and reacting the nuclease  
 CC with the cleavage structures so that cleavage product(s) are produced.  
 CC The method is used for the identification of strains of microorganisms.  
 CC The microorganism comprises bacteria including Campylobacter,  
 CC Escherichia, Mycobacterium, Salmonella, Shigella or Staphylococcus or a  
 CC virus comprising hepatitis C virus or simian immunodeficiency virus. The  
 CC Mycobacterium comprises strains of multi-drug resistant Mycobacterium  
 CC tuberculosis. The method is less sensitive to size so that entire genes,  
 CC rather than gene fragments, may be analysed. It facilitates the use of  
 CC internal standards for subsequent analysis and data comparison, and  
 CC increases the productivity of personnel and equipment. The present  
 CC sequence represents a Cleavage BN substrate DNA.  
 XX  
 SQ Sequence 281 BP; 51 A; 82 C; 91 G; 57 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 9; Length 281;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 218 TTGCGACCCCAACTACTC 199  
 RESULT 146  
 ADB16268  
 ID ADB16268 standard; DNA; 281 BP.  
 XX  
 AC ADB16268;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Cleavage BN DNA substrate #45.

```

XX de; DNA polymerase; microorganism strain identification; bacteria;
KW Campylobacter; Escherichia; Mycobacterium; Salmonella; Shigella;
KW Staphylococcus; virus; hepatitis C virus; simian immunodeficiency virus;
XX Mycobacterium tuberculosis.
OS Hepatitis C virus.
XX US2003054338-A1.
XX
XX 20-MAR-2003.
XX
XX 28-AUG-2001; 2001US-00940925.
XX
XX 07-DEC-1992; 92US-00986330.
XX 04-JUN-1993; 93US-00073384.
XX 06-JUN-1994; 94US-00254359.
XX 09-NOV-1994; 94US-00337164.
XX 09-MAR-1995; 95US-00402601.
XX 07-JUN-1995; 95US-00484956.
XX 30-AUG-1995; 95US-00520946.
XX 06-FEB-1997; 97US-00789079.
XX 19-FEB-1997; 97US-00802233.
XX 05-SEP-2000; 2000US-00655378.
XX
XX (DAHL/) DAHLBERG J E.
XX (BROW/) BROW M A D.
XX (LYAM/) LYAMICHEV V I.
XX
XX Dahlberg JE, Brow MAD, Lyamichev VI;
XX
XX WPI; 2003-615811/58.
XX
XX Identification of strains of microorganisms, by treating nucleic acid
XX cleavage structure(s) derived from microorganisms with nuclease to form
XX cleavage products(s) and detecting the product(s).
XX
XX Example 34; Page 163; 303pp; English.
XX
XX The invention relates to a method of detecting and identifying strains of
XX microorganisms by providing a nuclease and a nucleic acid substrate
XX containing sequences derived from microorganism(s), treating the nucleic
XX acid substrate to form cleavage structure(s) and reacting the nuclease
XX with the cleavage structures so that cleavage product(s) are produced.
XX The method is used for the identification of strains of microorganisms.
XX The microorganism comprises bacteria including Campylobacter,
XX Escherichia, Mycobacterium, Salmonella, Shigella or Staphylococcus or a
XX virus comprising hepatitis C virus or simian immunodeficiency virus. The
XX Mycobacterium comprises strains of multi-drug resistant Mycobacterium
XX tuberculosis. The method is less sensitive to size so that entire genes,
XX rather than gene fragments, may be analysed. It facilitates the use of
XX internal standards for subsequent analysis and data comparison, and
XX increases the productivity of personnel and equipment. The present
XX sequence represents a Cleavage BN substrate DNA.
XX
XX Sequence 281 BP; 59 A; 92 C; 80 G; 50 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 9; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 0.053;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TTGCGACCCCAACTACTC 20
XX |||||
XX DB 64 TTGCGACCCCAACTACTC 83
XX
XX RESULT 147
XX ID ADB16273 standard; DNA; 281 BP.
XX AC ADB16273;
XX XX
XX DT 20-NOV-2003 (first entry)

```

```

XX XX Cleavage BN DNA substrate #50.
XX DE
XX XX
XX KW de; DNA polymerase; microorganism strain identification; bacteria;
XX KW Campylobacter; Escherichia; Mycobacterium; Salmonella; Shigella;
XX KW Staphylococcus; virus; hepatitis C virus; simian immunodeficiency virus;
XX KW Mycobacterium tuberculosis.
XX
XX OS Hepatitis C virus.
XX
XX US2003054338-A1.
XX
XX 20-MAR-2003.
XX
XX 28-AUG-2001; 2001US-00940925.
XX
XX 07-DEC-1992; 92US-00986330.
XX 04-JUN-1993; 93US-00073384.
XX 06-JUN-1994; 94US-00254359.
XX 09-NOV-1994; 94US-00337164.
XX 09-MAR-1995; 95US-00402601.
XX 07-JUN-1995; 95US-00484956.
XX 30-AUG-1995; 95US-00520946.
XX 06-FEB-1997; 97US-00789079.
XX 19-FEB-1997; 97US-00802233.
XX 05-SEP-2000; 2000US-00655378.
XX
XX (DAHL/) DAHLBERG J E.
XX (BROW/) BROW M A D.
XX (LYAM/) LYAMICHEV V I.
XX
XX Dahlberg JE, Brow MAD, Lyamichev VI;
XX
XX WPI; 2003-615811/58.
XX
XX Identification of strains of microorganisms, by treating nucleic acid
XX cleavage structure(s) derived from microorganisms with nuclease to form
XX cleavage products(s) and detecting the product(s).
XX
XX Example 34; Page 164; 303pp; English.
XX
XX The invention relates to a method of detecting and identifying strains of
XX microorganisms by providing a nuclease and a nucleic acid substrate
XX containing sequences derived from microorganism(s), treating the nucleic
XX acid substrate to form cleavage structure(s) and reacting the nuclease
XX with the cleavage structures so that cleavage product(s) are produced.
XX The method is used for the identification of strains of microorganisms.
XX The microorganism comprises bacteria including Campylobacter,
XX Escherichia, Mycobacterium, Salmonella, Shigella or Staphylococcus or a
XX virus comprising hepatitis C virus or simian immunodeficiency virus. The
XX Mycobacterium comprises strains of multi-drug resistant Mycobacterium
XX tuberculosis. The method is less sensitive to size so that entire genes,
XX rather than gene fragments, may be analysed. It facilitates the use of
XX internal standards for subsequent analysis and data comparison, and
XX increases the productivity of personnel and equipment. The present
XX sequence represents a Cleavage BN substrate DNA.
XX
XX Sequence 281 BP; 57 A; 91 C; 82 G; 51 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 9; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 0.053;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TTGCGACCCCAACTACTC 20
XX |||||
XX DB 64 TTGCGACCCCAACTACTC 83
XX
XX RESULT 148
XX ID ADB16269 standard; DNA; 281 BP.
XX AC ADB16269;
XX XX
XX DT 20-NOV-2003 (first entry)

```

```

XX 20-NOV-2003 (first entry)
DT
XX
DE Cleavage BN DNA substrate #46.
XX
KM ds; DNA polymerase; microorganism strain identification; bacteria;
KW Campylobacter; Escherichia; Mycobacterium; Salmonella; Shigella;
KM Staphylococcus; virus; hepatitis C virus; simian immunodeficiency virus;
XX Mycobacterium tuberculosis.
OS Hepatitis C virus.
XX
XX US2003054338-A1.
XX
XX 20-MAR-2003.
XX
XX 28-AUG-2001; 2001US-00940925.
XX
XX 07-DEC-1992; 92US-00986330.
XX 04-JUN-1993; 93US-00073384.
XX 06-JUN-1994; 94US-00254359.
XX 09-NOV-1994; 94US-00337164.
XX 09-MAR-1995; 95US-00402601.
XX 07-JUN-1995; 95US-00484956.
XX 30-AUG-1995; 95US-00520946.
XX 06-FEB-1997; 97US-00789079.
XX 19-FEB-1997; 97US-00802233.
XX 05-SEP-2000; 2000US-00655378.
XX
XX (DAHL/) DAHLBERG J E.
XX (BROW/) BROW M A D.
XX (LYAM/) LYAMICHEV V I.
XX
PI Dahlberg JE, Brow MAD, Lyamichev VI;
XX
XX WPI: 2003-615811/58.
XX
XX Identification of strains of microorganisms, by treating nucleic acid
PT cleavage structure(s) derived from microorganisms with nuclease to form
PT cleavage products(s) and detecting the product(s).
XX
XX Example 34; Page 163; 303pp; English.
XX
XX The invention relates to a method of detecting and identifying strains of
CC microorganisms by providing a nuclease and a nucleic acid substrate
CC containing sequences derived from microorganism(s), treating the nucleic
CC acid substrate to form cleavage structure(s) and reacting the nuclease
CC with the cleavage structures so that cleavage product(s) are produced.
CC The method is used for the identification of strains of microorganisms.
CC The microorganism comprises bacteria including Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella or Staphylococcus or a
CC virus comprising hepatitis C virus or simian immunodeficiency virus. The
CC Mycobacterium comprises strains of multi-drug resistant Mycobacterium
CC tuberculosis. The method is less sensitive to size so that entire genes,
CC rather than gene fragments, may be analysed. It facilitates the use of
CC internal standards for subsequent analysis and data comparison, and
CC increases the productivity of personnel and equipment. The present
CC sequence represents a Cleavage BN substrate DNA.
XX
XX Sequence 281 BP; 60 A; 91 C; 80 G; 50 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGACCCCAACTACTC 20
Db 64 TTCCGACCCCAACTACTC 83

```

```

XX ADB16270;
AC
XX 20-NOV-2003 (first entry)
DT
XX
DE Cleavage BN DNA substrate #47.
XX
KM ds; DNA polymerase; microorganism strain identification; bacteria;
KW Campylobacter; Escherichia; Mycobacterium; Salmonella; Shigella;
KM Staphylococcus; virus; hepatitis C virus; simian immunodeficiency virus;
XX Mycobacterium tuberculosis.
OS Hepatitis C virus.
XX
XX US2003054338-A1.
XX
XX 20-MAR-2003.
XX
XX 28-AUG-2001; 2001US-00940925.
XX
XX 07-DEC-1992; 92US-00986330.
XX 04-JUN-1993; 93US-00073384.
XX 06-JUN-1994; 94US-00254359.
XX 09-NOV-1994; 94US-00337164.
XX 09-MAR-1995; 95US-00402601.
XX 07-JUN-1995; 95US-00484956.
XX 30-AUG-1995; 95US-00520946.
XX 06-FEB-1997; 97US-00789079.
XX 19-FEB-1997; 97US-00802233.
XX 05-SEP-2000; 2000US-00655378.
XX
XX (DAHL/) DAHLBERG J E.
XX (BROW/) BROW M A D.
XX (LYAM/) LYAMICHEV V I.
XX
PI Dahlberg JE, Brow MAD, Lyamichev VI;
XX
XX WPI: 2003-615811/58.
XX
XX Identification of strains of microorganisms, by treating nucleic acid
PT cleavage structure(s) derived from microorganisms with nuclease to form
PT cleavage products(s) and detecting the product(s).
XX
XX Example 34; Page 163; 303pp; English.
XX
XX The invention relates to a method of detecting and identifying strains of
CC microorganisms by providing a nuclease and a nucleic acid substrate
CC containing sequences derived from microorganism(s), treating the nucleic
CC acid substrate to form cleavage structure(s) and reacting the nuclease
CC with the cleavage structures so that cleavage product(s) are produced.
CC The method is used for the identification of strains of microorganisms.
CC The microorganism comprises bacteria including Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella or Staphylococcus or a
CC virus comprising hepatitis C virus or simian immunodeficiency virus. The
CC Mycobacterium comprises strains of multi-drug resistant Mycobacterium
CC tuberculosis. The method is less sensitive to size so that entire genes,
CC rather than gene fragments, may be analysed. It facilitates the use of
CC internal standards for subsequent analysis and data comparison, and
CC increases the productivity of personnel and equipment. The present
CC sequence represents a Cleavage BN substrate DNA.
XX
XX Sequence 281 BP; 61 A; 92 C; 80 G; 48 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGACCCCAACTACTC 20
Db 64 TTCCGACCCCAACTACTC 83

```

RESULT 149  
ADB16270  
ID ADB16270 standard; DNA; 281 BP.

RESULT 150

```

AD02537/c
ID  ADC02537 standard; DNA; 281 BP.
XX
AC  ADC02537;
XX
DT  18-DEC-2003 (first entry)
XX
DE  HCV clone 3.1.
XX
KW  ds; nucleic acid treatment system; nucleic acid sequence detection;
KM  nucleic acid sequence characterisation; microbial gene sequence change;
XX  bacterial pathogen; viral pathogen.
XX
OS  Hepatitis C virus.
XX
PN  US2003108873-A1.
XX
PD  12-JUN-2003.
XX
PE  28-AUG-2001; 2001US-00941193.
XX
PR  07-DEC-1992; 92US-00986330.
PR  04-JUN-1993; 93US-00073384.
PR  06-JUN-1994; 94US-00254359.
PR  09-NOV-1994; 94US-00337164.
PR  09-MAR-1995; 95US-00402601.
PR  07-JUN-1995; 95US-00484956.
PR  30-AUG-1995; 95US-00520946.
PR  06-FEB-1997; 97US-00789079.
PR  19-FEB-1997; 97US-00802233.
PR  05-SEP-2000; 2000US-00655378.
XX
PA  (DAHL/) DAHLBERG J E.
PA  (BROW/) BROW M A D.
PA  (LYAM/) LYAMICHEV V I.
XX
PI  Dahlberg JE, Brow MAD, Lyamichev VI;
XX
DR  WPI; 2003-708773/67.
XX
PT  Treatment system for detection and characterization of nucleic acid
PT  sequences and sequence changes, comprises target nucleic acid, and three
XX  oligonucleotides.
XX
PS  Disclosure; SEQ ID NO 123; 165bp; English.
XX
CC  The invention relates to a nucleic acid treatment system which consists
CC  of a target nucleic acid having first and second regions; a first
CC  oligonucleotide having a 3' portion complementary to the first region,
CC  and a 5' portion; a second oligonucleotide having a portion complementary
CC  to the second region; and a third oligonucleotide having a portion
CC  complementary to 5' portion of first oligonucleotide. The system is
CC  useful for detection and characterization of nucleic acid sequences and
CC  sequence changes in microbial gene sequences. The inventive system is
CC  robust. The system allows detection of and identification of bacterial
CC  and viral pathogens in a sample. The present sequence represents a HCV
CC  clone.
XX
SQ  Sequence 281 BP; 48 A; 80 C; 93 G; 60 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  1 TTGCGACCCCAACTACTC 20
    |||||
DB  218 TTGCGACCCCAACTACTC 199

```

```

AC  AD02535;
XX
DT  18-DEC-2003 (first entry)
XX
DE  HCV clone 1.1.
XX
KW  ds; nucleic acid treatment system; nucleic acid sequence detection;
KM  nucleic acid sequence characterisation; microbial gene sequence change;
XX  bacterial pathogen; viral pathogen.
XX
OS  Hepatitis C virus.
XX
PN  US2003108873-A1.
XX
PD  12-JUN-2003.
XX
PE  28-AUG-2001; 2001US-00941193.
XX
PR  07-DEC-1992; 92US-00986330.
PR  04-JUN-1993; 93US-00073384.
PR  06-JUN-1994; 94US-00254359.
PR  09-NOV-1994; 94US-00337164.
PR  09-MAR-1995; 95US-00402601.
PR  07-JUN-1995; 95US-00484956.
PR  30-AUG-1995; 95US-00520946.
PR  06-FEB-1997; 97US-00789079.
PR  19-FEB-1997; 97US-00802233.
PR  05-SEP-2000; 2000US-00655378.
XX
PA  (DAHL/) DAHLBERG J E.
PA  (BROW/) BROW M A D.
PA  (LYAM/) LYAMICHEV V I.
XX
PI  Dahlberg JE, Brow MAD, Lyamichev VI;
XX
DR  WPI; 2003-708773/67.
XX
PT  Treatment system for detection and characterization of nucleic acid
PT  sequences and sequence changes, comprises target nucleic acid, and three
XX  oligonucleotides.
XX
PS  Disclosure; SEQ ID NO 121; 165bp; English.
XX
CC  The invention relates to a nucleic acid treatment system which consists
CC  of a target nucleic acid having first and second regions; a first
CC  oligonucleotide having a 3' portion complementary to the first region,
CC  and a 5' portion; a second oligonucleotide having a portion complementary
CC  to the second region; and a third oligonucleotide having a portion
CC  complementary to 5' portion of first oligonucleotide. The system is
CC  useful for detection and characterization of nucleic acid sequences and
CC  sequence changes in microbial gene sequences. The inventive system is
CC  robust. The system allows detection of and identification of bacterial
CC  and viral pathogens in a sample. The present sequence represents a HCV
CC  clone.
XX
SQ  Sequence 281 BP; 50 A; 80 C; 92 G; 59 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  1 TTGCGACCCCAACTACTC 20
    |||||
DB  218 TTGCGACCCCAACTACTC 199

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RESULT 151
AD02535/c
ID  ADC02535 standard; DNA; 281 BP.
XX
DT  18-DEC-2003 (first entry)

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RESULT 152
AD02536/c
ID  ADC02536 standard; DNA; 261 BP.
XX
AC  AD02536;
XX
DT  18-DEC-2003 (first entry)

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```
XX HCv clone 2.1.
DE
XX ds; nucleic acid treatment system; nucleic acid sequence detection;
KW nucleic acid sequence characterisation; microbial gene sequence change;
KW bacterial pathogen; viral pathogen.
XX
XX Hepatitis C virus.
OS
XX US2003108873-A1.
PN
XX 12-JUN-2003.
PD
XX 28-AUG-2001; 2001US-00941193.
PF
XX 07-DEC-1992; 92US-00986330.
PR
XX 04-JUN-1993; 93US-00073384.
PR 06-JUN-1994; 94US-00254359.
PR 09-NOV-1994; 94US-00337164.
PR 09-MAR-1995; 95US-00402601.
PR 07-JUN-1995; 95US-00484956.
PR 30-AUG-1995; 95US-00520946.
PR 06-FEB-1997; 97US-00789079.
PR 19-FEB-1997; 97US-00802233.
PR 05-SEP-2000; 2000US-00655378.
XX
XX (DAHL/) DAHLBERG J E.
PA (BROW/) BROW M A D.
PA (LYAM/) LYAMICHEV V I.
XX
XX Dahlberg JE, Brow MAD, Lyamichev VI;
PI WPI; 2003-708773/67.
DR
XX Treatment system for detection and characterization of nucleic acid
PT sequences and sequence changes, comprises target nucleic acid, and three
PT oligonucleotides.
XX
XX Disclosure; SEQ ID NO 122; 165bp; English.
PS
XX The invention relates to a nucleic acid treatment system which consists
CC of a target nucleic acid having first and second regions; a first
CC oligonucleotide having a 3' portion complementary to the first region,
CC and a 5' portion; a second oligonucleotide having a portion complementary
CC to the second region; and a third oligonucleotide having a portion
CC complementary to 5' portion of first oligonucleotide. The system is
CC useful for detection and characterisation of nucleic acid sequences and
CC sequence changes in microbial gene sequences. The inventive system is
CC robust. The system allows detection of and identification of bacterial
CC and viral pathogens in a sample. The present sequence represents a HCv
CC clone.
XX
XX Sequence 281 BP; 50 A; 80 C; 91 G; 60 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 20; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGACCCCAACTACTC 20
DB 218 TTCCGACCCCAACTACTC 199
XX
XX RESULT 153
AD C02540/C
ID ADC02540 standard; DNA; 281 BP.
XX
XX AC ADC02540;
XX
XX 18-DEC-2003 (first entry)
XX
XX HCv clone 7.1.
XX
```

```
KW ds; nucleic acid treatment system; nucleic acid sequence detection;
KW nucleic acid sequence characterisation; microbial gene sequence change;
KW bacterial pathogen; viral pathogen.
XX
XX Hepatitis C virus.
OS
XX US2003108873-A1.
PN
XX 12-JUN-2003.
PD
XX 28-AUG-2001; 2001US-00941193.
PF
XX 07-DEC-1992; 92US-00986330.
PR 04-JUN-1993; 93US-00073384.
PR 06-JUN-1994; 94US-00254359.
PR 09-NOV-1994; 94US-00337164.
PR 09-MAR-1995; 95US-00402601.
PR 07-JUN-1995; 95US-00484956.
PR 30-AUG-1995; 95US-00520946.
PR 06-FEB-1997; 97US-00789079.
PR 19-FEB-1997; 97US-00802233.
PR 05-SEP-2000; 2000US-00655378.
XX
XX (DAHL/) DAHLBERG J E.
PA (BROW/) BROW M A D.
PA (LYAM/) LYAMICHEV V I.
XX
XX Dahlberg JE, Brow MAD, Lyamichev VI;
PI WPI; 2003-708773/67.
DR
XX Treatment system for detection and characterization of nucleic acid
PT sequences and sequence changes, comprises target nucleic acid, and three
PT oligonucleotides.
XX
XX Disclosure; SEQ ID NO 126; 165bp; English.
PS
XX The invention relates to a nucleic acid treatment system which consists
CC of a target nucleic acid having first and second regions; a first
CC oligonucleotide having a 3' portion complementary to the first region,
CC and a 5' portion; a second oligonucleotide having a portion complementary
CC to the second region; and a third oligonucleotide having a portion
CC complementary to 5' portion of first oligonucleotide. The system is
CC useful for detection and characterisation of nucleic acid sequences and
CC sequence changes in microbial gene sequences. The inventive system is
CC robust. The system allows detection of and identification of bacterial
CC and viral pathogens in a sample. The present sequence represents a HCv
CC clone.
XX
XX Sequence 281 BP; 51 A; 82 C; 91 G; 57 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 20; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCCGACCCCAACTACTC 20
DB 218 TTCCGACCCCAACTACTC 199
XX
XX RESULT 154
AAT29119/C
ID AAT29119 standard; DNA; 282 BP.
XX
XX AC AAT29119;
XX
XX 02-DEC-1996 (first entry)
XX
XX Hepatitis C virus genome fragment (Clone HCv4.2).
XX
XX p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
KW Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KW Staphylococcus; identification; detection; ds.
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XX OS Hepatitis C virus.
XX PN WO9615267-A1.
XX PD 23-MAY-1996.
XX PF 09-NOV-1995; 95WO-US014673.
XX PR 09-NOV-1994; 94US-00337164.
XX PR 09-MAR-1995; 95US-00402601.
XX PR 07-JUN-1995; 95US-00484956.
XX PR 30-AUG-1995; 95US-00520946.
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX PA Dahlberg JE, Lyamichiev VI, Brow MAD, Oldenburg MC, Heisler LM,
XX PI Fors L, Olive DM;
XX WPI; 1996-259862/26.
XX PT Cleavage of nucleic acids to detect mutation(s) - allows detection esp.
XX PT in human p53 gene, to identify strains of microorganisms and viruses.
XX PS Example 32; Page 301; 433pp; English.
XX CC Cleavage of nucleic acids using an enzyme, especially a nuclease selected
XX CC from the group consisting of cleavage (RTM) BN enzyme, Thermus aquaticus
XX CC DNA polymerase, Thermus thermophilus DNA polymerase, Escherichia coli
XX CC ExoIII and the Saccharomyces cerevisiae Rad1/Rad10 complex. The nucleic
XX CC acid substrate is preferably an oligonucleotide containing a human p53
XX CC gene sequence or alternatively, microbial gene sequences. Cleavage
XX CC products are compared to the cleavage products of reference gene
XX CC sequences. The method is used for detecting mutation in the human p53
XX CC gene, for identifying strains of microorganisms, especially bacteria
XX CC selected from the group of members of the genera Campylobacter,
XX CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The
XX CC method may also be used for the identification of viruses, especially
XX CC hepatitis C virus (HCV) and simian immunodeficiency virus (SIV). Four
XX CC primers (AAT29110-113) were used to generate six DNA HCV fragments by RT-
XX CC PCR. The sequence described in AAT29110 is an external antisense primer.
XX CC The sequence described in AAT29111 is a sense primer used after
XX CC termination of the reverse transcription reaction. The remaining two
XX CC primers (AAT29112, AAT29113) were used in a second round of amplification
XX CC reactions which produced a 281 bp product which corresponds to -4 of the
XX CC conserved 5' noncoding region of HCV between positions -284 and -4 of the
XX CC HCV genome. The amplified sequences are described in AAT29116-121
XX SQ Sequence 282 BP; 50 A; 79 C; 93 G; 60 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 282;
XX Best Local Similarity 100.0%; Pred. No. 0.053;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGCGAGCCCAACTACTC 20
DB 219 TTGCGAGCCCAACTACTC 200

RESULT 155
ADBI6265/c
ID ADBI6265 standard; DNA; 282 BP.
XX AC ADBI6265;
XX DT 20-NOV-2003 (first entry)
XX XX
XX DE Cleavage BN DNA substrate #42.
XX XX
XX ds; DNA polymerase; microorganism strain identification; bacteria;
XX KM Campylobacter; Escherichia; Mycobacterium; Salmonella; Shigella;
XX KM Staphylococcus; virus; hepatitis C virus; simian immunodeficiency virus;
XX KM Mycobacterium tuberculosis.

```

```

XX OS Hepatitis C virus.
XX PN US2003054338-A1.
XX PD 20-MAR-2003.
XX PF 28-AUG-2001; 2001US-00940925.
XX PR 07-DEC-1992; 92US-00986330.
XX PR 04-JUN-1993; 93US-00073384.
XX PR 06-JUN-1994; 94US-00254359.
XX PR 09-NOV-1994; 94US-00337164.
XX PR 09-MAR-1995; 95US-00402601.
XX PR 07-JUN-1995; 95US-00484956.
XX PR 30-AUG-1995; 95US-00520946.
XX PR 06-FEB-1997; 97US-00789079.
XX PR 19-FEB-1997; 97US-00802233.
XX PR 05-SEP-2000; 2000US-00655378.
XX PA (DAHL/) DAHLBERG J E.
XX PA (BROW/) BROW M A D.
XX PA (LYAM/) LYAMICHEV V I.
XX PT Dahlberg JE, Brow MAD, Lyamichiev VI;
XX WPI; 2003-615811/58.
XX PT Identification of strains of microorganisms, by treating nucleic acid
XX PT cleavage structure(s) derived from microorganisms with nuclease to form
XX PT cleavage products(s) and detecting the product(s).
XX XX
XX Example 34; Fig 82; 303pp; English.
XX
XX CC The invention relates to a method of detecting and identifying strains of
XX CC microorganisms by providing a nuclease and a nucleic acid substrate
XX CC containing sequences derived from microorganism(s), treating the nucleic
XX CC acid substrate to form cleavage structure(s) and reacting the nuclease
XX CC with the cleavage structures so that cleavage product(s) are produced.
XX CC The method is used for the identification of strains of microorganisms.
XX CC The microorganism comprises bacteria including Campylobacter,
XX CC Escherichia, Mycobacterium, Salmonella, Shigella or Staphylococcus.
XX CC Virus comprising hepatitis C virus or simian immunodeficiency virus. A
XX CC Mycobacterium comprises strains of multi-drug resistant Mycobacterium
XX CC tuberculosis. The method is less sensitive to size so that entire genes,
XX CC rather than gene fragments, may be analysed. It facilitates the use of
XX CC internal standards for subsequent analysis and data comparison, and
XX CC increases the productivity of personnel and equipment. The present
XX CC sequence represents a cleavage BN substrate DNA.
XX SQ Sequence 282 BP; 50 A; 79 C; 93 G; 60 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 9; Length 282;
XX Best Local Similarity 100.0%; Pred. No. 0.053;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGCGAGCCCAACTACTC 20
DB 219 TTGCGAGCCCAACTACTC 200

RESULT 156
ADBI6271
ID ADBI6271 standard; DNA; 282 BP.
XX AC ADBI6271;
XX DT 20-NOV-2003 (first entry)
XX XX
XX DE Cleavage BN DNA substrate #48.
XX XX
XX ds; DNA polymerase; microorganism strain identification; bacteria;
XX KM Campylobacter; Escherichia; Mycobacterium; Salmonella; Shigella;
XX KM

```

KW Staphylococcus; virus; hepatitis C virus; simian immunodeficiency virus;  
 KW Mycobacterium tuberculosis.  
 OS Hepatitis C virus.  
 XX US2003054338-A1.  
 XX  
 XX 20-MAR-2003.  
 PD  
 XX 28-AUG-2001; 2001US-00940925.  
 PF  
 XX 07-DEC-1992; 92US-00986330.  
 PR 04-JUN-1993; 93US-00073384.  
 PR 06-JUN-1994; 94US-00254359.  
 PR 09-NOV-1994; 94US-00337164.  
 PR 09-MAR-1995; 95US-00402601.  
 PR 07-JUN-1995; 95US-00484956.  
 PR 30-AUG-1995; 95US-00520946.  
 PR 06-FEB-1997; 97US-00789079.  
 PR 19-FEB-1997; 97US-00802233.  
 PR 05-SEP-2000; 2000US-00655378.  
 XX  
 XX (DAHL/) DAHLBERG J E.  
 PA (BROW/) BROW M A D.  
 PA (LYAM/) LYAMICHEV V I.  
 XX  
 PI Dahlberg JE, Brow MAD, Lyamichev VI;  
 DR WPI; 2003-615811/58.  
 XX  
 PT Identification of strains of microorganisms, by treating nucleic acid  
 PT cleavage structure(s) derived from microorganisms with nuclease to form  
 PT cleavage products(s) and detecting the product(s).  
 XX  
 PS Example 34; Page 164; 303pp; English.  
 XX  
 CC The invention relates to a method of detecting and identifying strains of  
 CC microorganisms by providing a nuclease and a nucleic acid substrate  
 CC containing sequences derived from microorganism(s), treating the nucleic  
 CC acid substrate to form cleavage structure(s) and reacting the nuclease  
 CC with the cleavage structures so that cleavage product(s) are produced.  
 CC The method is used for the identification of strains of microorganisms.  
 CC The microorganism comprises bacteria including Campylobacter,  
 CC Escherichia, Mycobacterium, Salmonella, Shigella or Staphylococcus or a  
 CC virus comprising hepatitis C virus or simian immunodeficiency virus. The  
 CC Mycobacterium comprises strains of multi-drug resistant Mycobacterium  
 CC tuberculosis. The method is less sensitive to size so that entire genes,  
 CC rather than gene fragments, may be analysed. It facilitates the use of  
 CC internal standards for subsequent analysis and data comparison, and  
 CC increases the productivity of personnel and equipment. The present  
 CC sequence represents a cleavage BN substrate DNA.  
 XX  
 SQ Sequence 282 BP; 60 A; 93 C; 79 G; 50 T; 0 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 20; DB 9; Length 282;  
 Best Local Similarity 100.0%; Pred. NO. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTCGCGACCCCAACTACTC 20  
 Db 64 TTCGCGACCCCAACTACTC 83  
 XX  
 RESULT 157  
 AAV70444/c  
 ID AAV70444 standard; DNA; 286 BP.  
 XX  
 AC AAV70444;  
 XX  
 DT 08-APR-1999 (first entry)  
 XX  
 DE HCV subtype 1b target sequence.  
 XX

KW Nucleic acid detection; nucleic acid characterisation; hybridisation;  
 KW infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.  
 OS Hepatitis C virus.  
 XX  
 XX WO9850403-A1.  
 XX  
 XX 12-NOV-1998.  
 PD  
 XX 05-MAY-1998; 98WO-US003194.  
 PF  
 XX 05-MAY-1997; 97US-00851588.  
 PR 19-SEP-1997; 97US-00934097.  
 PR 03-MAR-1998; 98US-00034205.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;  
 XX  
 DR WPI; 1998-610317/51.  
 XX  
 PT Detection and characterisation of nucleic acid sequences - by mixing a  
 PT folded target and one or more probes to form a probe/folded target  
 PT complex and detecting and characterising the complexes.  
 XX  
 PS Example 3; Fig 6; 279pp; English.  
 XX  
 CC The invention relates to methods and compositions of detection and  
 CC characterisation of nucleic acid sequences and sequence changes. One  
 CC method of detection and characterisation comprises: (a) providing: (i) a  
 CC folded target having a DNA sequence comprising at least 1 double stranded  
 CC region and at least 1 single stranded region; and (ii) at least 1 probe  
 CC complementary to at least a portion of the folded target; and (b) mixing  
 CC the target and probes so that the probe hybridises to form a probe  
 CC /folded target complex. Also provided are methods for determination of  
 CC structure formation in nucleic acid targets; for analysing folded nucleic  
 CC acids targets; and for analysis of nucleic acid structures. The methods  
 CC can be used for the detection and characterisation of nucleic acid  
 CC sequences to detect the presence of pathogenic nucleic acid sequences  
 CC indicative of an infection, the presence of variants or alleles of  
 CC mammalian genes associated with disease and cancers, and the  
 CC identification of the source of nucleic acids found in forensic samples,  
 CC as well as in paternity determinations. The methods allow simultaneous  
 CC analysis of both strands (e.g. the sense and antisense strands) and are  
 CC ideal for high-level multiplexing. The products produced are amenable to  
 CC qualitative, quantitative and positional analysis. The methods may be  
 CC performed in solution or in the solid phase (e.g. on a solid support).  
 CC The methods are powerful in that they allow for analysis of longer  
 CC fragments of nucleic acid than current methodologies. The present  
 CC sequence represents a hepatitis C virus (HCV) subtype 1b sequence that  
 CC can be used as a target in the hybridisation analysis using multiple  
 CC capture probes for HCV genotyping  
 XX  
 SQ Sequence 286 BP; 50 A; 80 C; 93 G; 63 T; 0 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 20; DB 2; Length 286;  
 Best Local Similarity 100.0%; Pred. NO. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTCGCGACCCCAACTACTC 20  
 Db 222 TTCGCGACCCCAACTACTC 203  
 XX  
 RESULT 158  
 ABL46054/c  
 ID ABL46054 standard; DNA; 286 BP.  
 XX  
 AC ABL46054;  
 XX  
 DT 26-APR-2002 (first entry)  
 XX

DE Hepatitis C virus subtype 1b target DNA sequence SEQ ID NO:21.  
 XX  
 KW Nucleic acid accessible hybridisation site; detection; hybridisation;  
 KW characterisation; identification; nucleic acid structure; diagnosis;  
 XX PCR primer; probe; ss.  
 OS Hepatitis C virus.  
 XX  
 PN WO200198537-A2.  
 XX  
 PD 27-DEC-2001.  
 XX  
 PF 15-JUN-2001; 2001WO-US019401.  
 XX  
 PR 17-JUN-2000; 2000US-0212308P.  
 XX  
 PR 15-JUN-2001; 2001US-00212308.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;  
 DR WPI; 2002-049698/06.  
 XX  
 PT Identifying oligonucleotides hybridizing to nucleic acids containing  
 PT secondary structure, useful in clinical diagnosis, comprises identifying  
 PT primers that interact with the target to form an extension product under  
 PT amplification conditions.  
 XX  
 PS Example 3; Fig 6; 409pp; English.  
 XX  
 CC The present invention describes a method for identifying oligonucleotides  
 CC with desired hybridisation properties to nucleic acid targets containing  
 CC secondary structure. The method comprises amplifying a target nucleic  
 CC acid having at least one accessible and one inaccessible site. Primers  
 CC that form an extension product are identified as the oligonucleotides  
 CC which can interact with the folded target nucleic acid. Oligonucleotides  
 CC from the present invention can be used in novel detection methods for  
 CC clinical diagnostic purposes, including the detection and identification  
 CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
 CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
 CC sequences used in the exemplification of the present invention  
 XX  
 SQ Sequence 286 BP; 50 A; 80 C; 93 G; 63 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 286;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 222 TTGCGACCCCAACTACTC 203  
 RESULT 159  
 ADK82244/c  
 ID ADK82244 standard; DNA; 286 BP.  
 XX  
 AC ADK82244;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Hepatitis C virus subtype 1b polynucleotide seqid 21.  
 XX  
 KW nucleic acid analysis; hepatitis C virus;  
 KW non-contiguous single-stranded region; NCSR; cleavage structure;  
 KW clinical; diagnostic; microorganism detection;  
 KW microorganism identification; hepatitis C virus; HCV; subtype 1b; ds.  
 OS Hepatitis C virus.  
 XX  
 PN US6709815-B1.  
 XX  
 PD 23-MAR-2004.

XX  
 PF 18-JUL-2000; 2000US-00402618.  
 XX  
 PR 05-MAY-1997; 97US-00851588.  
 PR 19-SEP-1997; 97US-00934097.  
 PR 03-MAR-1998; 98US-00034205.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;  
 DR WPI; 2004-256067/24.  
 XX  
 PT Analyzing nucleic acids, comprises mixing target nucleic acid such as  
 PT hepatitis C virus nucleic acid, bridging oligonucleotide, second  
 PT oligonucleotide and cleavage agent to form cleavage structure.  
 XX  
 PS Example 3; SEQ ID NO 21; 143pp; English.  
 XX  
 CC The invention describes a method of analysing nucleic acids comprising  
 CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
 CC having non-contiguous single-stranded regions (NCSR) separated by an  
 CC intervening region, a bridging oligonucleotide capable of binding to the  
 CC first and second NCSR, a second oligonucleotide binding to a portion of  
 CC the first NCSR and a cleavage agent, and mixing the contents to form a  
 CC cleavage structure. The method is useful for analysing nucleic acids,  
 CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
 CC purposes and detection and identification of pathogenic microorganisms  
 CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
 CC subtype 1b polynucleotide identified using the analysis methods of the  
 CC invention.  
 XX  
 SQ Sequence 286 BP; 50 A; 80 C; 93 G; 63 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 12; Length 286;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 222 TTGCGACCCCAACTACTC 203  
 RESULT 160  
 AAV70443/c  
 ID AAV70443 standard; DNA; 289 BP.  
 XX  
 AC AAV70443;  
 XX  
 DT 08-APR-1999 (first entry)  
 XX  
 DE HCV consensus sequence.  
 XX  
 KW Nucleic acid detection; nucleic acid characterisation; hybridisation;  
 KW infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.  
 OS Hepatitis C virus.  
 XX  
 PN WO9850403-A1.  
 XX  
 PD 12-NOV-1998.  
 XX  
 PF 05-MAY-1998; 98WO-US003194.  
 XX  
 PR 05-MAY-1997; 97US-00851588.  
 PR 19-SEP-1997; 97US-00934097.  
 PR 03-MAR-1998; 98US-00034205.  
 XX  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 XX  
 PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;  
 PI Anderson TA, Dahlberg JE;



XX DR WP; 1998-610317/51.  
XX PT Detection and characterisation of nucleic acid sequences - by mixing a  
PT folded target and one or more probes to form a probe/folded target  
PT complex and detecting and characterising the complexes.  
XX PS Example 3; Fig 6; 279pp; English.  
XX CC The invention relates to methods and compositions of detection and  
CC characterisation of nucleic acid sequences and sequence changes. One  
CC method of detection and characterisation comprises: (a) providing: (i) a  
CC folded target having a DNA sequence comprising at least 1 double stranded  
CC region and at least 1 single stranded region; and (ii) at least 1 probe  
CC complementary to at least a portion of the folded target; and (b) mixing  
CC the target and probes so that the probe hybridises to form a probe  
CC /folded target complex. Also provided are methods for determination of  
CC structure formation in nucleic acid targets; for analysing folded nucleic  
CC acids targets; and for analysis of nucleic acid structures. The methods  
CC can be used for the detection and characterisation of nucleic acid  
CC sequences to detect the presence of pathogenic nucleic acid sequences  
CC indicative of an infection, the presence of variants or alleles of  
CC mammalian genes associated with disease and cancers, and the  
CC identification of the source of nucleic acids found in forensic samples,  
CC as well as in paternity determinations. The methods allow simultaneous  
CC analysis of both strands (e.g. the sense and antisense strands) and are  
CC ideal for high-level multiplexing. The products produced are amenable to  
CC qualitative, quantitative and positional analysis. The methods may be  
CC performed in solution or in the solid phase (e.g. on a solid support).  
CC The methods are powerful in that they allow for analysis of longer  
CC fragments of nucleic acid than current methodologies. The present  
CC sequence represents a hepatitis C virus (HCV) consensus sequence. The HCV  
CC subtype 1a sequence is identical to this consensus sequence  
XX SO Sequence 289 BP; 53 A; 81 C; 92 G; 63 T; 0 U; 0 Other;  
XX Query Match 100.0%; Score 20; DB 2; Length 289;  
XX Best Local Similarity 100.0%; Pred. No. 0.053;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGGACCCCAACTACTC 20  
DB 222 TTGCGGACCCCAACTACTC 203  
XX  
XX RESULT 161  
XX AAV70446/c  
XX ID AAV70446 standard; DNA; 289 BP.  
XX AC AAV70446;  
XX DT 08-APR-1999 (first entry)  
XX DE HCV subtype 3a target sequence.  
XX KW Nucleic acid detection; nucleic acid characterisation; hybridisation;  
XX infection; disease; cancer; forensic; paternity; multiplexing; HCV; ds.  
XX OS Hepatitis C virus.  
XX PN MO9850403-A1.  
XX PD 12-NOV-1998.  
XX PF 05-MAY-1998; 98WO-US003194.  
XX PR 05-MAY-1997; 97US-00851588.  
XX PR 19-SEP-1997; 97US-00934097.  
XX PR 03-MAR-1998; 98US-00034205.  
XX PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XX PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neel BP, Brown MAD;

PI Anderson TA, Dahlberg JE;  
XX DR WP; 1998-610317/51.  
XX PT Detection and characterisation of nucleic acid sequences - by mixing a  
PT folded target and one or more probes to form a probe/folded target  
PT complex and detecting and characterising the complexes.  
XX PS Example 3; Fig 6; 279pp; English.  
XX CC The invention relates to methods and compositions of detection and  
CC characterisation of nucleic acid sequences and sequence changes. One  
CC method of detection and characterisation comprises: (a) providing: (i) a  
CC folded target having a DNA sequence comprising at least 1 double stranded  
CC region and at least 1 single stranded region; and (ii) at least 1 probe  
CC complementary to at least a portion of the folded target; and (b) mixing  
CC the target and probes so that the probe hybridises to form a probe  
CC /folded target complex. Also provided are methods for determination of  
CC structure formation in nucleic acid targets; for analysing folded nucleic  
CC acids targets; and for analysis of nucleic acid structures. The methods  
CC can be used for the detection and characterisation of nucleic acid  
CC sequences to detect the presence of pathogenic nucleic acid sequences  
CC indicative of an infection, the presence of variants or alleles of  
CC mammalian genes associated with disease and cancers, and the  
CC identification of the source of nucleic acids found in forensic samples,  
CC as well as in paternity determinations. The methods allow simultaneous  
CC analysis of both strands (e.g. the sense and antisense strands) and are  
CC ideal for high-level multiplexing. The products produced are amenable to  
CC qualitative, quantitative and positional analysis. The methods may be  
CC performed in solution or in the solid phase (e.g. on a solid support).  
CC The methods are powerful in that they allow for analysis of longer  
CC fragments of nucleic acid than current methodologies. The present  
CC sequence represents a hepatitis C virus (HCV) subtype 3a sequence that  
CC can be used as a target in the hybridisation analysis using multiple  
CC capture probes for HCV genotyping  
XX SO Sequence 289 BP; 55 A; 83 C; 91 G; 60 T; 0 U; 0 Other;  
XX Query Match 100.0%; Score 20; DB 2; Length 289;  
XX Best Local Similarity 100.0%; Pred. No. 0.053;  
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGGACCCCAACTACTC 20  
DB 222 TTGCGGACCCCAACTACTC 203  
XX  
XX RESULT 162  
XX ABL46053/c  
XX ID ABL46053 standard; DNA; 289 BP.  
XX AC ABL46053;  
XX DT 26-APR-2002 (first entry)  
XX DE Hepatitis C virus subtype 1a target DNA sequence SEQ ID NO:21.  
XX KW Nucleic acid accessible hybridisation site; detection; hybridisation;  
XX characterisation; identification; nucleic acid structure; diagnosis;  
XX PCR primer; probe; ss.  
XX OS Hepatitis C virus.  
XX PN WO200198537-A2.  
XX PD 27-DEC-2001.  
XX PF 15-JUN-2001; 2001WO-US019401.  
XX PR 17-JUN-2000; 2000US-0212308P.  
XX PR 15-JUN-2001; 2001US-00212308.  
XX PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XX PI

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XX
PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;
XX
DR WPI; 2002-049698/06.
XX
PT Identifying oligonucleotides hybridizing to nucleic acids containing
PT secondary structure, useful in clinical diagnosis, comprises identifying
PT primers that interact with the target to form an extension product under
PT amplification conditions.
XX
PS Example 3; Fig 6; 409pp; English.
XX
CC The present invention describes a method for identifying oligonucleotides
CC with desired hybridisation properties to nucleic acid targets containing
CC secondary structure. The method comprises amplifying a target nucleic
CC acid having at least one accessible and one inaccessible site. Primers
CC that form an extension product are identified as the oligonucleotides
CC which can interact with the folded target nucleic acid. Oligonucleotides
CC from the present invention can be used in novel detection methods for
CC clinical diagnostic purposes, including the detection and identification
CC of pathogenic organisms (e.g. HIV). The method allows the ability to
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 289 BP; 53 A; 81 C; 92 G; 63 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 6; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTGGGACCCACACTACTC 20
DB 222 TTGGGACCCACACTACTC 203
XX
RESULT 163
ABL46056/C
ID ABL46056 standard; DNA; 289 BP.
XX
AC ABL46056;
XX
DT 26-APR-2002 (first entry)
XX
DE Hepatitis C virus subtype 3a target DNA sequence SEQ ID NO:23.
XX
KM Nucleic acid accessible hybridisation site; detection; hybridisation;
KM characterisation; identification; nucleic acid structure; diagnosis;
KM PCR primer; probe; ss.
XX
OS Hepatitis C virus.
XX
PN WO200198537-A2.
XX
XX 27-DEC-2001.
XX
PF 15-JUN-2001; 2001WO-US019401.
XX
PR 17-JUN-2000; 2000US-0212308P.
PR 15-JUN-2001; 2001US-00212308.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;
XX
DR WPI; 2002-049698/06.
XX
PT Identifying oligonucleotides hybridizing to nucleic acids containing
PT secondary structure, useful in clinical diagnosis, comprises identifying
PT primers that interact with the target to form an extension product under
PT amplification conditions.
XX
PS Example 3; Fig 6; 409pp; English.
XX

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CC
CC The present invention describes a method for identifying oligonucleotides
CC with desired hybridisation properties to nucleic acid targets containing
CC secondary structure. The method comprises amplifying a target nucleic
CC acid having at least one accessible and one inaccessible site. Primers
CC that form an extension product are identified as the oligonucleotides
CC which can interact with the folded target nucleic acid. Oligonucleotides
CC from the present invention can be used in novel detection methods for
CC clinical diagnostic purposes, including the detection and identification
CC of pathogenic organisms (e.g. HIV). The method allows the ability to
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 289 BP; 55 A; 83 C; 91 G; 60 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 20; DB 6; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTGGGACCCACACTACTC 20
DB 222 TTGGGACCCACACTACTC 203
XX
RESULT 164
ADR82246/C
ID ADR82246 standard; DNA; 289 BP.
XX
AC ADR82246;
XX
DT 03-JUN-2004 (first entry)
XX
DE Hepatitis C virus subtype 3a polynucleotide seqid 23.
XX
KM nucleic acid analysis; hepatitis C virus;
KM non-contiguous single-stranded region; NCSR; cleavage structure;
KM clinical; diagnostic; microorganism detection;
KM microorganism identification; hepatitis C virus; HCV; subtype 3a; ds.
XX
OS Hepatitis C virus.
XX
PN US6709815-B1.
XX
PD 23-MAR-2004.
XX
PF 18-JUL-2000; 2000US-00402618.
XX
PR 05-MAY-1997; 97US-00851588.
PR 19-SEP-1997; 97US-00934097.
PR 03-MAR-1998; 98US-00034205.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MAD;
PI Anderson TA, Dahlberg JE;
XX
DR WPI; 2004-256067/24.
XX
XX Analyzing nucleic acids, comprises mixing target nucleic acid such as
XX hepatitis C virus nucleic acid, bridging oligonucleotide, second
XX oligonucleotide and cleavage agent to form cleavage structure.
XX
PS Example 3; SEQ ID NO 23; 143pp; English.
XX
CC The invention describes a method of analysing nucleic acids comprising
CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid
CC having non-contiguous single-stranded regions (NCSR) separated by an
CC intervening region, a bridging oligonucleotide capable of binding to the
CC first and second NCSR; a second oligonucleotide binding to a portion of
CC the first NCSR and a cleavage agent, and mixing the contents to form a
CC cleavage structure. The method is useful for analysing nucleic acids,
CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic
CC purposes and detection and identification of pathogenic microorganisms
CC such as hepatitis C virus. This sequence represents a hepatitis C virus

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CC subtype 3a polynucleotide identified using the analysis methods of the  
CC invention.  
XX  
SO Sequence 289 BP; 55 A; 83 C; 91 G; 60 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 289;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGACCCCACTACTC 20  
DB 222 TTCCGACCCCACTACTC 203  
RESULT 165  
ADK82243/c  
ID ADK82243 standard; DNA; 289 BP.  
XX  
AC ADK82243;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Hepatitis C virus subtype 1a polynucleotide seqid 20.  
XX  
KW nucleic acid analysis; hepatitis C virus;  
KW non-contiguous single-stranded region; NCSR; cleavage structure;  
KW clinical; diagnostic; microorganism detection;  
KW microorganism identification; hepatitis C virus; HCV; subtype 1a; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN US6709815-B1.  
XX  
PD 23-MAR-2004.  
XX  
PF 18-JUL-2000; 2000US-00402618.  
XX  
PR 05-MAY-1997; 97US-00851588.  
PR 19-SEP-1997; 97US-00934087.  
PR 03-MAR-1998; 98US-00034205.  
XX  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XX  
PI Dong F, Lyamichev VI, Prudent JR, Fors L, Neri BP, Brow MMD;  
PI Anderson TA, Dahlberg JE;  
XX  
DR WPI; 2004-256067/24.  
XX  
PT Analyzing nucleic acids, comprises mixing target nucleic acid such as  
PT hepatitis C virus nucleic acid, bridging oligonucleotide, second  
PT oligonucleotide and cleavage agent to form cleavage structure.  
XX  
PS Example 3; SEQ ID NO 20; 143bp; English.  
XX  
CC The invention describes a method of analysing nucleic acids comprising  
CC providing a target nucleic acid, e.g. hepatitis C virus nucleic acid  
CC having non-contiguous single-stranded regions (NCSR) separated by an  
CC intervening region, a bridging oligonucleotide capable of binding to the  
CC first and second NCSR; a second oligonucleotide binding to a portion of  
CC the first NCSR and a cleavage agent, and mixing the contents to form a  
CC cleavage structure. The method is useful for analysing nucleic acids,  
CC e.g. hepatitis C virus nucleic acid useful for clinical diagnostic  
CC purposes and detection and identification of pathogenic microorganisms  
CC such as hepatitis C virus. This sequence represents a hepatitis C virus  
CC subtype 1a polynucleotide identified using the analysis methods of the  
CC invention.  
XX  
SO Sequence 289 BP; 53 A; 81 C; 92 G; 63 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 289;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20  
DB 222 TTCCGACCCCACTACTC 203  
RESULT 166  
AAH75861/c  
ID AAH75861 standard; DNA; 297 BP.  
XX  
AC AAH75861;  
XX  
DT 26-OCT-2001 (first entry)  
XX  
DE Mycobacterium tuberculosis gene fragment #2.  
XX  
KW Mycobacterium tuberculosis detection; ds.  
XX  
OS Mycobacterium tuberculosis.  
XX  
PN RU2163638-C1.  
XX  
PD 27-FEB-2001.  
XX  
PF 06-DEC-1999; 99RU-00125164.  
XX  
PR 06-DEC-1999; 99RU-00125164.  
XX  
PA (ASIB=) AS SIBE BIOCHEM RES INST.  
XX  
PI Beklemishev AB, Khorocheva EM, Nomokonova N Yu;  
XX  
DR WPI; 2001-280317/29.  
XX  
PT Detection of DNA from tuberculosis mycobacterium complex comprising a  
PT polymerase chain reaction method.  
XX  
PS Claim 9; Col 19-20; 13pp; Russian.  
XX  
CC The present invention relates to a PCR-based method for the detection of  
CC Mycobacterium tuberculosis. The present sequence was used to illustrate  
CC the method of the present invention  
XX  
SO Sequence 297 BP; 50 A; 87 C; 97 G; 63 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 4; Length 297;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGACCCCACTACTC 20  
DB 233 TTCCGACCCCACTACTC 214  
RESULT 167  
AAD5556/c  
ID AAD5556 standard; DNA; 299 BP.  
XX  
AC AAD5556;  
XX  
DT 07-AUG-2003 (first entry)  
XX  
DE IG57272 Hepatitis C virus (HCV) isolate 5' non-coding region (NCR).  
XX  
KW Hepatitis C virus; HCV; HCV typing; infection; gene therapy; vaccine;  
KW virucide; hepatotropic; antiinflammatory; non-coding region; NCR; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003020970-A2.  
XX  
PD 13-MAR-2003.  
XX  
PF 30-AUG-2002; 2002WO-EP009731.

XX 31-AUG-2001; 2001EP-00120969.  
 PR 08-JAN-2002; 2002US-0345642P.  
 XX (INNO-) INNOGENETICS NV.  
 XX Sablon E, Van Doorn L, Quint W;  
 PI WPI; 2003-230206/28.  
 DR  
 XX Novel isolated hepatitis C virus polypeptide of a genotype different from  
 PT clade 6 genotypes 6-9 and 11, and polynucleotides encoding the  
 PT polypeptides, useful for preventing and treating HCV infection.  
 XX  
 PS Claim 1; Fig 1A; 78bp; English.  
 XX  
 CC The invention relates to genomic sequences and amino acid sequences  
 CC corresponding to the non-coding and coding region of a new type of  
 CC Hepatitis C virus (HCV). HCV protein is useful for detecting antibodies  
 CC to HCV and for HCV typing. HCV DNA is useful for detecting the presence  
 CC of HCV virus and for determining the genotype of a HCV virus. Antibody is  
 CC useful for detecting HCV antigens. The invention is useful for preventing  
 CC or treating a HCV infection and is also used in gene therapy. Vaccine is  
 CC useful for immunising a mammal against HCV infection. The present  
 CC sequence is 16572/2 HCV isolate 5' non-coding region (NCR).  
 SQ Sequence 299 BP; 53 A; 85 C; 95 G; 66 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 10; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 233 TTGCGACCCCAACTACTC 214  
 RESULT 168  
 ACD27586/C  
 ID ACD27586 standard; DNA; 301 BP.  
 AC ACD27586;  
 AC ACD27586;  
 DT 16-SEP-2003 (first entry)  
 DE Hepatitis B and C detection method associated cDNA #2.  
 DE Gene chip reagent kit; hepatitis B; hepatitis C; ss.  
 KM  
 XX Unidentified.  
 OS  
 XX CN1366067-A.  
 PN  
 XX 28-AUG-2002.  
 PD  
 XX 15-JAN-2001; 2001CN-00105214.  
 PF  
 XX 15-JAN-2001; 2001CN-00105214.  
 PR  
 XX (BOHU-) BOHUA GENE CHIP TECHNOLOGY CO LTD SHANGH.  
 PA  
 PI Mao Y, Xie Y, Wu H;  
 PI WPI; 2003-230559/23.  
 DR  
 XX Gene chip reagent kit for detecting hepatitis B and C and its preparing  
 PT process and application.  
 PT  
 XX Claim 6; Page 33 (Disclosure); 48bp; Chinese.  
 PS  
 XX The invention describes a gene chip reagent kit for detecting hepatitis B  
 CC and C, its components and preparing process. The method for detecting and  
 CC the result analysis, and the usage of the reagent kit are disclosed. This

CC sequence represents a cDNA associated with the method of detecting  
 CC hepatitis B and C  
 XX  
 SQ Sequence 301 BP; 66 A; 83 C; 91 G; 61 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 10; Length 301;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 114 TTGCGACCCCAACTACTC 95  
 RESULT 169  
 AAT87088/C  
 ID AAT87088 standard; DNA; 305 BP.  
 AC AAT87088;  
 AC AAT87088;  
 DT 25-MAR-2003 (revised)  
 DT 07-JAN-1998 (first entry)  
 DE HCV amplification product.  
 DE  
 XX RNA; plasma; HCV; polymerase chain reaction; PCR; ss.  
 XX Hepatitis C virus.  
 OS  
 XX US5654179-A.  
 PN  
 XX 05-ANG-1997.  
 PD  
 XX 03-OCT-1994; 94US-00317220.  
 PF  
 XX 14-NOV-1990; 90US-00614921.  
 PR 19-JUN-1992; 92US-00901545.  
 PR 08-APR-1993; 93US-00044649.  
 XX  
 PA (HYDS ) HRI RES INC.  
 PA  
 PI Lin L;  
 PI WPI; 1997-401849/37.  
 DR  
 XX Preparation of RNA samples from plasma - by alcohol precipitation after  
 PT lysis with guanidinium thiocyanate.  
 PT  
 XX Disclosure; Fig 22; 60pp; English.  
 PS  
 XX This DNA sequence comprises an RT-PCR amplification product of hepatitis  
 CC C virus RNA recovered from plasma. A claimed method for preparing RNA  
 CC samples comprises: (a) mixing plasma with an aqueous buffer solution  
 CC containing guanidinium thiocyanate and beta- mercaptoethanol; (b) heating  
 CC the mixture; (c) adding an equal volume of an alcohol to precipitate RNA;  
 CC and (d) recovering the RNA. The method can be used to prepare RNA samples  
 CC for subsequent amplification, especially for detecting pathogens, e.g.  
 CC HCV or HIV. Compared with the known "Isoquick" and "RNAzol" methods,  
 CC the method uses fewer tubes (just one), requires fewer steps, takes less  
 CC time and produces no toxic waste. (Updated on 25-MAR-2003 to correct PF  
 CC field.)  
 XX  
 SQ Sequence 305 BP; 59 A; 91 C; 92 G; 63 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 2; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 275 TTGCGACCCCAACTACTC 256

```

RESULT 170
ABN79969/C
ID   ABN79969 standard; DNA; 305 BP.
XX
XX   ABN79969;
AC
XX   15-JUL-2002 (first entry)
DT
XX   Hepatitis C virus 5' untranslated region genotype 1a.
DE
XX   Single nucleotide polymorphism; nucleic acid typing; hepatitis C virus;
KM   tissue typing; untranslated region; UTR; de; HCV.
XX
XX   Hepatitis C virus.
OS
XX   WO200220837-A2.
PN
XX   14-MAR-2002.
PD
XX   10-SEP-2001; 2001WO-GB004042.
PF
XX   08-SEP-2000; 2000GB-00022069.
PR
XX   (PYRO-) PYROSEQUENCING AB.
PA   (STRD ) UNIV LEIAND STANFORD JUNIOR.
PA   (GARD/) GARDNER R.
XX
XX   Ronaghi M, Ekstroem B, Pourmand N;
PI   WPI; 2002-393849/42.
XX
XX   Typing nucleic acid for obtaining information about several variable
PT   sites involves simultaneously or sequentially performing two or more
PT   primer extension reactions, and determining the pattern of nucleotide
PT   incorporation.
XX
XX   Example 1; Fig 2; 86pp; English.
XX
XX   The invention relates to a novel method for obtaining typing information
CC   about several variable sites within target nucleic acid, or typing one or
CC   more nucleic acid molecules. The methods of the invention are useful for
CC   typing one or more nucleic acid molecules containing two or more variable
CC   sites, preferably nucleic acid molecules containing three or more
CC   variable sites are typed, where three or more primer extension reactions
CC   are performed. The method is also useful for diagnosis of pathological
CC   conditions characterized by the presence of specific nucleic acid
CC   molecule(s). The methods are particularly suited for identifying
CC   microbial species or their subtypes, and in typing procedures e.g. typing
CC   of polymorphisms, tissue typing or in clinical applications. The sequence
CC   represents the 5' untranslated region (UTR) of a hepatitis C virus (HCV)
CC   genotype, amplified in the invention to type HCV-positive sera
XX
XX   Sequence 305 BP; 57 A; 88 C; 96 G; 64 T; 0 U; 0 Other;
SQ
Query Match          100.0%; Score 20; DB 6; Length 305;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY   1   TTCCGACCCCACTACTC 20
      |||||
DB   233 TTCCGACCCCACTACTC 214

RESULT 171
ABN79970/C
ID   ABN79970 standard; DNA; 305 BP.
XX
XX   ABN79970;
AC
XX   15-JUL-2002 (first entry)
DT
XX   Hepatitis C virus 5' untranslated region genotype 1b.
DE
XX

```

```

KM   Single nucleotide polymorphism; nucleic acid typing; hepatitis C virus;
KM   tissue typing; untranslated region; UTR; de; HCV.
XX
XX   Hepatitis C virus.
OS
XX   WO200220837-A2.
PN
XX   14-MAR-2002.
PD
XX   10-SEP-2001; 2001WO-GB004042.
PF
XX   08-SEP-2000; 2000GB-00022069.
PR
XX   (PYRO-) PYROSEQUENCING AB.
PA   (STRD ) UNIV LEIAND STANFORD JUNIOR.
PA   (GARD/) GARDNER R.
XX
XX   Ronaghi M, Ekstroem B, Pourmand N;
PI   WPI; 2002-393849/42.
XX
XX   Typing nucleic acid for obtaining information about several variable
PT   sites involves simultaneously or sequentially performing two or more
PT   primer extension reactions, and determining the pattern of nucleotide
PT   incorporation.
XX
XX   Example 1; Fig 2; 86pp; English.
XX
XX   The invention relates to a novel method for obtaining typing information
CC   about several variable sites within target nucleic acid, or typing one or
CC   more nucleic acid molecules. The methods of the invention are useful for
CC   typing one or more nucleic acid molecules containing two or more variable
CC   sites, preferably nucleic acid molecules containing three or more
CC   variable sites are typed, where three or more primer extension reactions
CC   are performed. The method is also useful for diagnosis of pathological
CC   conditions characterized by the presence of specific nucleic acid
CC   molecule(s). The methods are particularly suited for identifying
CC   microbial species or their subtypes, and in typing procedures e.g. typing
CC   of polymorphisms, tissue typing or in clinical applications. The sequence
CC   represents the 5' untranslated region (UTR) of a hepatitis C virus (HCV)
CC   genotype, amplified in the invention to type HCV-positive sera
XX
XX   Sequence 305 BP; 56 A; 87 C; 98 G; 64 T; 0 U; 0 Other;
SQ
Query Match          100.0%; Score 20; DB 6; Length 305;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY   1   TTCCGACCCCACTACTC 20
      |||||
DB   233 TTCCGACCCCACTACTC 214

RESULT 172
ABN79974/C
ID   ABN79974 standard; DNA; 305 BP.
XX
XX   ABN79974;
AC
XX   15-JUL-2002 (first entry)
DT
XX   Hepatitis C virus 5' untranslated region genotype 3b.
DE
XX   Single nucleotide polymorphism; nucleic acid typing; hepatitis C virus;
KM   tissue typing; untranslated region; UTR; de; HCV.
XX
XX   Hepatitis C virus.
OS
XX   WO200220837-A2.
PN
XX   14-MAR-2002.
PD
XX   10-SEP-2001; 2001WO-GB004042.
PF

```

XX 08-SEP-2000; 2000GB-00022069.  
 PR  
 XX

PA (PYRO-) PYROSEQUENCING AB.  
 PA (STRD) UNIV LELAND STANFORD JUNIOR.  
 PA (GARD/) GARDNER R.  
 XX

PI Ronaghi M, Ekstroem B, Pourmand N;  
 DR WPI; 2002-393849/42.  
 XX

PT Typing nucleic acid for obtaining information about several variable  
 PT sites involves simultaneously or sequentially performing two or more  
 PT primer extension reactions, and determining the pattern of nucleotide  
 PT incorporation.

PS Example 1; Fig 2; 86pp; English.

CC The invention relates to a novel method for obtaining typing information  
 CC about several variable sites within target nucleic acid, or typing one or  
 CC more nucleic acid molecules. The methods of the invention are useful for  
 CC typing one or more nucleic acid molecules containing two or more variable  
 CC sites, preferably nucleic acid molecules containing three or more variable  
 CC sites are performed. The method is also useful for diagnosis of pathological  
 CC conditions characterized by the presence of specific nucleic acid  
 CC molecular species or their subtypes, and in typing procedures e.g. typing  
 CC of polymorphisms, tissue typing or in clinical applications. The sequence  
 CC represents the 5' untranslated region (UTR) of a hepatitis C virus (HCV)  
 CC genotype, amplified in the invention to type HCV-positive sera  
 SO Sequence 305 BP; 56 A; 88 C; 98 G; 63 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 20; DB 6; Length 305;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 TTGGGACCCCAACTACTC 20  
 233 TTGGGACCCCAACTACTC 214

RESULT 173

AA067079/c  
 ID AA067079 standard; DNA; 306 BP.

XX AA067079;

DT 14-MAR-1995 (first entry)

DE Hepatitis C virus DNA fragment comprising KpnI restriction site.

KM Hepatitis C virus; restriction endonuclease; KpnI; marker; cleavage site;

KW HCV; ss.

OS Hepatitis C virus.

PN JP06181764-A.

PD 05-JUL-1994.

PF 20-JAN-1993; 93JP-00007721.

PR 22-SEP-1992; 92JP-00252793.

PA (SAKA) OTSUKA PHARM CO LTD.

DR WPI; 1994-251687/31.  
 XX DNA contg. KpnI recognition site as marker for hepatitis C virus - useful  
 PT in diagnosis of HC.  
 XX

PS Claim 1; Page 7; 9pp; Japanese.

CC This sequence, which is obtained from hepatitis C virus (HCV) comprises a  
 CC KpnI restriction endonuclease recognition site. The restriction site is  
 CC found in the wild type sequence and can therefore be used as a diagnostic  
 CC marker  
 XX

SO Sequence 306 BP; 55 A; 89 C; 96 G; 66 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 20; DB 2; Length 306;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 TTGGGACCCCAACTACTC 20  
 238 TTGGGACCCCAACTACTC 219

RESULT 174

ABS53053/c  
 ID ABS53053 standard; DNA; 306 BP.

XX ABS53053;

DT 15-NOV-2002 (first entry)

DE Hepatitis C virus target polynucleotide.

KM Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;

KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; varicella; cytostatic; antisense therapy;

KW gene therapy; ss.

OS Hepatitis C virus.

PN US2002081577-A1.

PD 27-JUN-2002.

PF 02-JUL-1997; 97US-00887505.

PR 06-JUN-1995; 95US-00471968.

PR 02-JUL-1996; 96US-0021104P.

PA (KILK/) KILKUSKIE R L.

PA (FRAN/) FRANK B L.

PA (GOOD/) GOODCHILD J.

PA (WOLF/) WOLFE J L.

PA (ROBE/) ROBERTS P C.

PA (HAML/) HAMLIN H A.

PA (ROBE/) ROBERTS N A.

PA (WALT/) WALTHER D M.

PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,

PI Hamlin HA, Roberts NA, Walther DM;

DR WPI; 2002-537132/57.

PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.

PS Disclosure; Fig 1; 74pp; English.

CC The invention describes synthetic oligonucleotides complementary to a  
 CC portion of the 5' untranslated region of hepatitis C virus. The  
 CC oligonucleotides may be used in methods for controlling, preventing, and  
 CC treating hepatitis C virus infection, in antisense technology and gene  
 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for

CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
CC acid and protein, and for treating HCV infections. This sequence  
CC represents a hepatitis C virus polynucleotide used as the target for  
CC inhibition of HCV replication and gene expression using the synthetic  
CC oligonucleotides of the invention  
XX  
SQ Sequence 306 BP; 63 A; 87 C; 95 G; 61 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 6; Length 306;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTCCGACCCCAACTACTC 20  
Db 212 TTCCGACCCCAACTACTC 193  
RESULT 175  
ID AAA75294 standard; cDNA; 308 BP.  
XX  
AC AAA75294;  
XX  
DT 15-JAN-2001 (first entry)  
XX  
DE Novel hepatitis C virus cDNA clone 189.  
XX  
KM Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;  
KM viral infectivity; viral replication; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN EPI034785-A2.  
XX  
PD 13-SEP-2000.  
XX  
PF 16-MAR-1990; 2000EP-00109602.  
XX  
PR 17-MAR-1989; 89US-00325338.  
PR 20-APR-1989; 89US-00341334.  
PR 18-MAY-1989; 89US-00355002.  
PR 16-MAR-1990; 90EP-00302866.  
XX  
PA (CHIR ) CHIRON CORP.  
XX  
PI Houghton M, Choo Q, Kuo G;  
XX  
DR WPI; 2000-566891/53.  
XX  
PT Novel composition comprising a hepatitis C virus antisense polynucleotide  
PT which is complementary to or corresponds to a sense strand of the virus  
PT genome, and selectively hybridizes to it.  
XX  
PS Example; Fig 14; 75pp; English.  
XX  
CC The specification describes a pharmaceutical composition which comprises  
CC a hepatitis C virus (HCV) antisense polynucleotide. The HCV is  
CC characterized by a positive stranded RNA genome which has 40% homology at  
CC the polypeptide level to a HCV polypeptide. The antisense polynucleotide  
CC binds to cellular polynucleotides which enhance and/or are required for  
CC viral infectivity, replicative ability or chronicity. The antisense  
CC polynucleotides may also be designed to bind with high specificity, to be  
CC of increased stability, to be stable and to have low toxicity. The  
CC composition also comprises an agent which causes viral RNA to be  
CC inactive. The composition is used for preventing HCV replication in a  
CC system. The present sequence represents a novel HCV cDNA sequence, which  
CC is used in the course of the invention  
XX  
SQ Sequence 308 BP; 59 A; 89 C; 94 G; 66 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 3; Length 308;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
Db 251 TTCCGACCCCAACTACTC 232  
RESULT 176  
ID ADN35973 standard; cDNA; 308 BP.  
XX  
AC ADN35973;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE HCV cDNA clone 189.  
XX  
KM Antiviral; Vaccine; hepatitis C virus infection; HCV infection; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN EPI394255-A2.  
XX  
PD 03-MAR-2004.  
XX  
PF 16-MAR-1990; 2003EP-00016585.  
XX  
PR 17-MAR-1989; 89US-00325338.  
PR 20-APR-1989; 89US-00341334.  
PR 18-MAY-1989; 89US-00355002.  
PR 16-MAR-1990; 90EP-00302866.  
XX  
PA (CHIR ) CHIRON CORP.  
XX  
PI Houghton M, Choo Q, Kuo G;  
XX  
DR WPI; 2004-193149/19.  
DR P-PSDB; ADN35972.  
XX  
PT Novel purified hepatitis C virus polypeptide comprising epitope encoded  
PT by hepatitis C virus cDNA, useful as vaccine for treating hepatitis C  
PT virus.  
XX  
PS Example 1; Fig 14; 79pp; English.  
XX  
CC The present invention relates to hepatitis C virus (HCV) proteins and  
CC cDNA sequences. The sequences are useful in immunoassays for detecting  
CC antibodies directed against HCV antigen; preparing host cells transformed  
CC with a recombinant polynucleotide; screening antiviral agents and  
CC determining the effect of antiviral agent in inhibiting viral replication  
CC in cell culture system; and developing vaccine for treating HCV  
CC infection.  
XX  
SQ Sequence 308 BP; 59 A; 89 C; 94 G; 66 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 308;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTCCGACCCCAACTACTC 20  
Db 251 TTCCGACCCCAACTACTC 232  
RESULT 177  
ID ABK70877 standard; DNA; 310 BP.  
XX  
AC ABK70877;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE HCV genome 5'UTR sequence #11 from HCV infected patient BU.  
XX

KW Hepatitis C virus infection; HCV; central nervous system; CNS;  
 KW microglial cell precursor; alpha-interferon; monocytic;  
 KW brain-specific envelope protein; antiviral therapy; virucide; ds.  
 OS Hepatitis C virus.  
 XX  
 XX MO200220054-A2.  
 XX  
 XX 14-MAR-2002.  
 XX  
 XX 31-AUG-2001; 2001MO-GB003901.  
 XX  
 XX 06-SEP-2000; 2000GB-00021859.  
 XX  
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 XX  
 XX Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;  
 DR WPI; 2002-383036/41.  
 XX  
 XX Treating patient with or at risk of hepatitis C virus (HCV) infection by  
 PT inhibiting infection by HCV of and/or replication of HCV in cells of  
 PT central nervous system.  
 XX  
 XX Example 1; Fig 14; 145pp; English.  
 PS  
 CC The present invention relates to a method of treating a patient with or  
 CC at risk of hepatitis C virus (HCV) infection. The method comprises  
 CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
 CC central nervous system (CNS) of the patient. The method is performed by  
 CC administering to the central nervous system (CNS) a compound capable of  
 CC inhibiting HCV infection and/or replication in the CNS of the patient  
 CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
 CC treating a patient with or at risk of HCV infection by inhibiting HCV  
 CC infection of and/or replication in cells and non-CNS cells. Preferably,  
 CC HCV infection of and/or replication in microglial cells or circulating  
 CC microglial cell precursors is inhibited. The method is carried out in a  
 CC patient who is, has been or will be administered alpha-interferon. Use of  
 CC a pharmacological agent that blocks binding of the brain-specific  
 CC envelope protein to the putative receptor prevents uptake of the virus to  
 CC the CNS, and improves long-term response rates. Reinfection of the liver  
 CC by the virus released by the CNS may be prevented by the above mentioned  
 CC method. The development of resistant strains is reduced or prevented. By  
 CC the therapeutic use of a vaccine against brain-specific envelope protein,  
 CC before, together with or after antiviral therapy. ABK70867-ABK70886  
 CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
 CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
 CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
 CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
 CC All sequences in Fig 14 have been typed in according to their correct  
 CC nucleotide positioning  
 XX  
 SQ Sequence 310 BP; 57 A; 91 C; 96 G; 66 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 310;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 247 TTGCGACCCCAACTACTC 228  
 RESULT 178  
 ID AA236198/c  
 XX AA236198 standard; DNA; 312 BP.  
 AC  
 XX AA236198;  
 AC  
 XX 11-FEB-2000 (first entry)  
 DT  
 XX Adapted HCV 5' non translated region from 5'HCV/R1.orig.  
 DE  
 XX

KW Pseudorevertant; RNA virus; chimera; BVDV; HCV; replication-competent;  
 KW 5' nontranslated region; 5'NTR; 3' NTR; pestivirus; antiviral;  
 KW bovine viral diarrhoea virus; NADL; vaccine; ss.  
 XX  
 XX Synthetic.  
 OS Hepatitis C virus.  
 XX  
 XX MO9955366-A1.  
 XX  
 XX 04-NOV-1999.  
 XX  
 XX 23-APR-1999; 99WO-US008850.  
 XX  
 XX 24-APR-1998; 98US-0082964P.  
 XX  
 XX (UNIV ) UNIV WASHINGTON.  
 XX  
 XX Rice CM, Frolow I, McBride MS, Loe Y, Agapov EV, Myers TM;  
 PI WPI; 2000-013359/01.  
 DR  
 XX Chimeric viral RNA, used in vaccine against BVDV.  
 PT  
 XX  
 XX Disclosure; Fig 14; 108pp; English.  
 PS  
 CC The present sequence represents an adapted Hepatitis C virus (HCV) 5' non  
 CC translated region (NTR) from a virus of the invention. Only the sequence  
 CC from the 5' base to the ATG initiating the polypeptide is shown. The  
 CC specification describes chimeric viral RNA comprising a 5' nontranslated  
 CC region (5'NTR); an open reading frame (ORF) region; and a 3' NTR; where  
 CC at least one of the regions is chimeric and comprises a nucleotide  
 CC sequence from a pestivirus in operable linkage with a heterologous  
 CC nucleotide sequence, preferably from HCV. The chimeric viral RNA is  
 CC replication-competent. The chimeric viral RNA can be used in a method for  
 CC identifying compounds having antiviral activity against HCV. When the  
 CC pestivirus viral nucleotide sequence is from bovine viral diarrhoea virus  
 CC (BVDV), the chimeric viral RNA can be used in a vaccine against BVDV  
 XX  
 SQ Sequence 312 BP; 60 A; 88 C; 97 G; 67 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 3; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 0.053;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCCAACTACTC 20  
 Db 243 TTGCGACCCCAACTACTC 224  
 RESULT 179  
 ID AA236197/c  
 XX AA236197 standard; DNA; 314 BP.  
 AC  
 XX AA236197;  
 AC  
 XX 11-FEB-2000 (first entry)  
 DT  
 XX Adapted HCV 5' non translated region from 5'HCV/R1.cons.  
 DE  
 XX  
 XX Pseudorevertant; RNA virus; chimera; BVDV; HCV; replication-competent;  
 KW 5' nontranslated region; 5'NTR; 3' NTR; pestivirus; antiviral;  
 KW bovine viral diarrhoea virus; NADL; vaccine; ss.  
 XX  
 XX Synthetic.  
 OS Hepatitis C virus.  
 XX  
 XX MO9955366-A1.  
 XX  
 XX 04-NOV-1999.  
 XX  
 XX 23-APR-1999; 99WO-US008850.  
 XX  
 XX 24-APR-1998; 98US-0082964P.  
 XX  
 XX



XX (UNIV) UNIV WASHINGTON.  
PA  
XX  
PI Rice CM, Frolov I, McBride MS, Lee Y, Agapov EV, Myers TM,  
XX  
DR WPI; 2000-013359/01.  
XX  
PT Chimeric viral RNA, used in vaccine against BVDV.  
PS  
PS Disclosure; Fig 13; 108pp; English.  
XX  
CC The present sequence represents an adapted Hepatitis C virus (HCV) 5' non  
CC translated region (NTR) from a virus of the invention. Only the sequence  
CC from the 5' base to the ATG initiating the polypeptide is shown. The  
CC specification describes chimeric viral RNA comprising a 5' nontranslated  
CC region (5'NTR); an open reading frame (ORF) region; and a 3' NTR; where  
CC at least one of the regions is chimeric and comprises a nucleotide  
CC sequence from a pestivirus in operable linkage with a heterologous  
CC nucleotide sequence, preferably from HCV. The chimeric viral RNA is  
CC a replication-competent. The chimeric viral RNA can be used in a method for  
CC identifying compounds having antiviral activity against HCV. When the  
CC pestivirus viral nucleotide sequence is from bovine viral diarrhoea virus  
CC (BVDV), the chimeric viral RNA can be used in a vaccine against BVDV  
CC  
SQ Sequence 314 BP; 61 A; 88 C; 97 G; 68 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 3; Length 314;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTGCGAGCCGACACTACTC 20  
DB 245 TTGCGAGCCGACACTACTC 226  
RESULT 180  
ABK70883/c  
ID ABK70883 standard; DNA; 323 BP.  
XX  
AC ABK70883;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE HCV genome 5'UTR sequence #17 from HCV infected patient BU.  
XX  
KW Hepatitis C virus infection; HCV; central nervous system; CNS;  
KW microglial cell precursor; alpha-interferon; monocyte;  
KW brain-specific envelope protein; antiviral therapy; virucide; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN WO200220054-A2.  
XX  
PD 14-MAR-2002.  
XX  
PF 31-AUG-2001; 2001MO-GB003901.  
XX  
PR 06-SEP-2000; 2000GB-00021859.  
XX  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX  
PI Thomas HC, Taylor-Robinson SD, Karayannis P, Forton DM;  
XX  
DR WPI; 2002-383036/41.  
XX  
PT Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.  
XX  
PS Example 1; Fig 14; 145pp; English.  
XX  
CC The present invention relates to a method of treating a patient with or  
CC at risk of hepatitis C virus (HCV) infection. The method comprises

CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC HCV infection of and/or replication in microglial cells or circulating  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of  
CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Reinflection of the liver  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70886  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
CC  
SQ Sequence 323 BP; 63 A; 95 C; 98 G; 67 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 6; Length 323;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTGCGAGCCGACACTACTC 20  
DB 260 TTGCGAGCCGACACTACTC 241  
RESULT 181  
ABK70882/c  
ID ABK70882 standard; DNA; 323 BP.  
XX  
AC ABK70882;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE HCV genome 5'UTR sequence #16 from HCV infected patient BU.  
XX  
KW Hepatitis C virus infection; HCV; central nervous system; CNS;  
KW microglial cell precursor; alpha-interferon; monocyte;  
KW brain-specific envelope protein; antiviral therapy; virucide; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN WO200220054-A2.  
XX  
PD 14-MAR-2002.  
XX  
PF 31-AUG-2001; 2001MO-GB003901.  
XX  
PR 06-SEP-2000; 2000GB-00021859.  
XX  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX  
PI Thomas HC, Taylor-Robinson SD, Karayannis P, Forton DM;  
XX  
DR WPI; 2002-383036/41.  
XX  
PT Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.  
XX  
PS Example 1; Fig 14; 145pp; English.  
XX  
CC The present invention relates to a method of treating a patient with or  
CC at risk of hepatitis C virus (HCV) infection. The method comprises

CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of  
CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Reinfection of the liver  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70886  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
CC XX

SO Sequence 323 BP; 63 A; 96 C; 97 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 323;

Best Local Similarity 100.0%; Pred. No. 0.053;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCGGACCCCAACTACTC 20  
Db 260 TTTCGGACCCCAACTACTC 241

RESULT 182  
ABK70880/c  
ID ABK70880 standard; DNA; 326 BP.

XX ABK70880;

DT 30-JUL-2002 (first entry)

DE HCV genome 5'UTR sequence #14 from HCV infected patient BU.

XX Hepatitis C virus infection; HCV; central nervous system; CNS;

KW microglial cell precursor; alpha-interferon; monocyte;

KW brain-specific envelope protein; antiviral therapy; virucide; ds.

OS Hepatitis C virus.

PN WO200220054-A2.

PD 14-MAR-2002.

PF 31-AUG-2001; 2001WO-GB003901.

PR 06-SEP-2000; 2000GB-00021859.

PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

PI Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;

DR WPI; 2002-383036/41.

PT Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.

PS Example 1; Fig 14; 145pp. English.

CC The present invention relates to a method of treating a patient with or  
at risk of hepatitis C virus (HCV) infection. The method comprises

CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of  
CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Reinfection of the liver  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70886  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
CC XX

SO Sequence 326 BP; 62 A; 94 C; 101 G; 69 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 326;

Best Local Similarity 100.0%; Pred. No. 0.053;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCGGACCCCAACTACTC 20  
Db 263 TTTCGGACCCCAACTACTC 244

RESULT 183  
ADP20410/c  
ID ADP20410 standard; DNA; 326 BP.

XX ADP20410;

DT 09-SEP-2004 (first entry)

DE Hepatitis C virus internal ribosome entry site, IRES, sequence, SEQ ID 1.

XX Virucide; Cytostatic; p110 subunit;

KW eukaryotic translation initiation factor eIF3; region II;

KW internal ribosome entry site; IRES; aminoglycoside;

KW hepatitis C infection; swine fever; bovine diarrhoea; viral infection;  
cancer; ds.

OS Hepatitis C virus.

PN FR2848572-A1.

PD 18-JUN-2004.

PF 12-DEC-2002; 2002FR-00015718.

PR 12-DEC-2002; 2002FR-00015718.

PA (UVEO-) UNIV FOURIER JOSEPH.

PI Balakireva L;

DR WPI; 2004-452919/43.

PT In vitro screening for antiviral agents, from ability to inhibit complex  
PT formation between the p110 subunit of translation initiation factor eIF3  
PT and region II of the viral internal ribosome binding site.

PS Example 1; SEQ ID NO 1; 45pp; French.

CC The present invention relates to an in vitro method of screening for  
CC compounds (A) that inhibit the formation of a complex between the p10  
CC subunit (ADP20412) of the eukaryotic translation initiation factor eIF3  
CC and region II of the internal ribosome entry site (IRES; ADP20411) of  
CC hepatitis C virus (HCV). Preferably the p10 recognition motif (ADP20414)  
CC and the region II consensus sequence (ADP20412), or fragment of it  
CC containing at least 8 consecutive nucleotides, are used. (A) is  
CC especially an aminoglycoside, specifically tobramycin or an  
CC oligonucleotide antisense to consensus sequence ADP20412, or parts of it.  
CC (A) are used for treating infection by hepatitis C, swine fever and  
CC bovine diarrhoea viruses, also for treating viral or non-viral diseases  
CC which involve proteins synthesis of which is initiated from an IRES, e.g.  
CC cancer. The present sequence is the full-length HCV IRES sequence.  
XX  
SQ Sequence 326 BP; 69 A; 90 C; 98 G; 69 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 326;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGAGCCCAACTACTC 20  
DB 236 TTGCGAGCCCAACTACTC 217  
RESULT 184  
AA236199/C  
ID AA236199 standard; DNA; 327 BP.  
XX  
AC AA236199;  
XX  
DT 11-FEB-2000 (first entry)  
XX  
DE Adapted HCV 5' non translated region from 5'HCV/R2.cons.  
XX  
KM Pseudorevertant; RNA virus; chimera; BVDV; HCV; replication-competent;  
KM 5' nontranslated region; 5'NTR; 3' NTR; pestivirus; antiviral;  
KM bovine viral diarrhoea virus; NADL; vaccine; ss.  
XX  
OS Synthetic.  
OS Hepatitis C virus.  
XX  
PN WO9955366-A1.  
XX  
PD 04-NOV-1999.  
XX  
PF 23-APR-1999; 99WO-US008850.  
XX  
PR 24-APR-1998; 98US-0082964P.  
XX  
PA (UNIW ) UNIV WASHINGTON.  
XX  
PI Rice CM, Frolov I, McBride MS, Lee Y, Agapov EV, Myers TM;  
XX WPI; 2000-013359/01.  
DR  
PT Chimeric viral RNA, used in vaccine against BVDV.  
XX  
PS Disclosure; Fig 15; 108pp; English.  
XX  
CC The present sequence represents an adapted Hepatitis C virus (HCV) 5' non  
CC translated region (NTR) from a virus of the invention. Only the sequence  
CC from the 5' base to the ATG initiating the polypeptide is shown. The  
CC specification describes chimeric viral RNA comprising a 5' nontranslated  
CC region (5'NTR); an open reading frame (ORF) region; and a 3' NTR; where  
CC at least one of the regions is chimeric and comprises a nucleotide  
CC sequence from a pestivirus in operable linkage with a heterologous  
CC nucleotide sequence, preferably from HCV. The chimeric viral RNA is  
CC replication-competent. The chimeric viral RNA can be used in a method for  
CC identifying compounds having antiviral activity against HCV. When the  
CC pestivirus viral nucleotide sequence is from bovine viral diarrhoea virus  
CC (BVDV), the chimeric viral RNA can be used in a vaccine against BVDV  
XX

SQ Sequence 327 BP; 65 A; 94 C; 98 G; 70 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 3; Length 327;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGAGCCCAACTACTC 20  
DB 258 TTGCGAGCCCAACTACTC 239  
RESULT 185  
ABK70884/C  
ID ABK70884 standard; DNA; 327 BP.  
XX  
AC ABK70884;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE HCV genome 5'UTR sequence #18 from HCV infected patient BU.  
XX  
KM Hepatitis C virus infection; HCV; central nervous system; CNS;  
KM microglial cell precursor; alpha-interferon; monocyte;  
KM brain-specific envelope protein; antiviral therapy; virucide; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN WO200220054-A2.  
XX  
PD 14-MAR-2002.  
XX  
PF 31-AUG-2001; 2001MO-GB003901.  
XX  
PR 06-SEP-2000; 2000GB-00021859.  
XX  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX  
PI Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;  
XX WPI; 2002-383036/41.  
DR  
PT Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.  
XX  
PS Example 1; Fig 14; 145pp; English.  
XX  
CC The present invention relates to a method of treating a patient with or  
CC at risk of hepatitis C virus (HCV) infection. The method comprises  
CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC HCV infection of and/or replication in microglial cells or circulating  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of  
CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Re-infection of the liver  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70886  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
XX



DE Hepatitis C virus subtype 3a mRNA sequence SEQ ID NO:245.  
XX  
XX Nucleic acid accessible hybridisation site; detection; hybridisation;  
KM characterisation; identification; nucleic acid structure; diagnosis;  
KM gene; ss.  
XX  
XX Hepatitis C virus.  
OS  
XX WO200198537-A2.  
PN  
XX  
XX 27-DEC-2001.  
PD  
XX  
XX 15-JUN-2001; 2001WO-US019401.  
PE  
XX  
XX 17-JUN-2000; 2000US-0212308P.  
PR  
XX  
XX 15-JUN-2001; 2001US-00212308.  
PR  
XX  
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.  
PA  
XX  
XX Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;  
PI  
XX WPI; 2002-049698/06.  
DR  
XX  
XX Identifying oligonucleotides hybridizing to nucleic acids containing  
PT secondary structure, useful in clinical diagnosis, comprises identifying  
PT primers that interact with the target to form an extension product under  
PT amplification conditions.  
XX  
XX Example 20; Fig 76; 409pp; English.  
PS  
XX  
XX The present invention describes a method for identifying oligonucleotides  
CC with desired hybridisation properties to nucleic acid targets containing  
CC secondary structure. The method comprises amplifying a target nucleic  
CC acid having at least one accessible and one inaccessible site. Primers  
CC that form an extension product are identified as the oligonucleotides  
CC which can interact with the folded target nucleic acid. Oligonucleotides  
CC from the present invention can be used in novel detection methods for  
CC clinical diagnostic purposes, including the detection and identification  
CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
CC sequences used in the exemplification of the present invention  
XX  
XX  
SQ Sequence 328 BP; 62 A; 98 C; 102 G; 0 T; 66 U; 0 Other;  
Query Match 100.0%; Score 20; DB 6; Length 328;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTGCGAGCCCAACTACTC 20  
DB 257 TTGCGAGCCCAACTACTC 238  
RESULT 189  
ABL46273/C  
ID ABL46273 standard; RNA; 328 BP.  
XX  
XX ABL46273;  
AC  
XX  
XX 26-APR-2002 (first entry)  
DT  
XX  
XX Hepatitis C virus subtype 1a mRNA sequence SEQ ID NO:240.  
DE  
XX  
XX Nucleic acid accessible hybridisation site; detection; hybridisation;  
KM characterisation; identification; nucleic acid structure; diagnosis;  
KM gene; ss.  
XX  
XX Hepatitis C virus.  
OS  
XX  
XX WO200198537-A2.  
PN  
XX  
XX 27-DEC-2001.  
PD  
XX

PE 15-JUN-2001; 2001WO-US019401.  
XX  
XX 17-JUN-2000; 2000US-0212308P.  
PR  
XX  
XX 15-JUN-2001; 2001US-00212308.  
PR  
XX  
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.  
PA  
XX  
XX Lyamichev V, Allawi H, Dong F, Neri BP, Vener IT;  
PI  
XX WPI; 2002-049698/06.  
DR  
XX  
XX Identifying oligonucleotides hybridizing to nucleic acids containing  
PT secondary structure, useful in clinical diagnosis, comprises identifying  
PT primers that interact with the target to form an extension product under  
PT amplification conditions.  
XX  
XX Example 20; Fig 73; 409pp; English.  
PS  
XX  
XX The present invention describes a method for identifying oligonucleotides  
CC with desired hybridisation properties to nucleic acid targets containing  
CC secondary structure. The method comprises amplifying a target nucleic  
CC acid having at least one accessible and one inaccessible site. Primers  
CC that form an extension product are identified as the oligonucleotides  
CC which can interact with the folded target nucleic acid. Oligonucleotides  
CC from the present invention can be used in novel detection methods for  
CC clinical diagnostic purposes, including the detection and identification  
CC of pathogenic organisms (e.g. HIV). The method allows the ability to  
CC rapidly analyse nucleic acid structures. ABL46034 to ABL46367 represent  
CC sequences used in the exemplification of the present invention  
XX  
XX  
SQ Sequence 328 BP; 65 A; 94 C; 101 G; 0 T; 68 U; 0 Other;  
Query Match 100.0%; Score 20; DB 6; Length 328;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTGCGAGCCCAACTACTC 20  
DB 257 TTGCGAGCCCAACTACTC 238  
RESULT 190  
AAL53724/C  
ID AAL53724 standard; RNA; 328 BP.  
XX  
XX AAL53724;  
AC  
XX  
XX 27-OCT-2003 (revised)  
DT  
XX 07-FEB-2003 (first entry)  
DT  
XX  
XX Hepatitis C virus target region SEQ ID NO 18.  
DE  
XX  
XX Target RNA; target RNA:support-attached test compound; flow cytometry;  
KM mass spectrometry; high-throughput screening; RNA motif; ss.  
XX  
XX Hepatitis C virus; Virus.  
OS  
XX  
XX WO200283837-A1.  
PN  
XX  
XX 24-OCT-2002.  
PD  
XX  
XX 11-APR-2002; 2002WO-US011758.  
PE  
XX  
XX 11-APR-2001; 2001US-0282966P.  
PR  
XX  
XX (PTCT-) PTC THERAPEUTICS INC.  
PA  
XX  
XX Altmstead NG;  
PI  
XX  
XX WPI; 2003-075534/07.  
DR  
XX  
XX Identifying a test compound that binds to a target RNA molecule by  
PT separating the detectably labeled target RNA:support-attached test

PT compound complex from uncomplexed target RNA molecules and test compounds  
XX by flow cytometry.  
PS Example; Page 60; 131pp; English.  
XX The invention relates to a novel method for identifying a test compound  
CC that binds to a target RNA molecule comprising separating the detectably  
CC labeled target RNA: support-attached test compound complex from  
CC uncomplexed target RNA molecules and test compounds. The separating  
CC process is carried out by flow cytometry and determining a structure of  
CC the type of test compound of the RNA: support-attached test compound  
CC complex by mass spectrometry. The method is useful for high-throughput  
CC screening of libraries of compounds to identify pharmaceutical leads.  
CC This polynucleotide sequence represents one of the target RNA motifs/  
CC regions of the invention. (Updated on 27-Oct-2003 to standardise OS  
CC field)  
SQ Sequence 328 BP; 61 A; 93 C; 103 G; 0 T; 71 U; 0 Other;  
Query Match 100.0%; Score 20; DB 8; Length 328;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGACCCCAACTACTC 20  
Db 263 TTGCGACCCCAACTACTC 244  
RESULT 191  
AAD9656/C  
ID AAD9656 standard; RNA; 328 BP.  
XX  
AC AAD9656;  
XX  
DT 24-MAR-2003 (first entry)  
XX  
DE Human internal ribosome entry site (IRES) RNA #2.  
XX  
KW Amyloidosis; haemophilia; Alzheimer's disease; atherosclerosis; cancer;  
KW gigantism; dwarfism; hypothyroidism; hyperthyroidism; cystic fibrosis;  
KW autoimmune disorder; aging; inflammation; diabetes; obesity; anorexia;  
KW neurodegenerative disorder; Parkinson's disease; gene therapy; virocid;  
KW haemostatic; antibacterial; noctropic; neuroprotective; cytosstatic;  
KW fungicide; human; internal ribosome entry site; IRES; ss.  
XX  
OS Homo sapiens.  
XX  
EN WO200283953-A1.  
XX  
PD 24-OCT-2002.  
XX  
PF 11-APR-2002; 2002WO-US011757.  
XX  
PR 11-APR-2001; 2001US-0282965P.  
XX  
PA (PTCT-) PTC THERAPEUTICS INC.  
XX  
PI Rando R, Welch E;  
XX  
PT WPI; 2003-075561/07.  
XX  
DR  
XX  
XX Identifying a test compound that binds to a target RNA molecule for  
PT treating or preventing amyloidosis, hemophilia, cancer, gigantism,  
PT diabetes, by contacting a detectably labeled target RNA molecule with a  
PT library of test compounds.  
XX  
XX Example; Page 68; 152pp; English.  
XX  
XX The invention relates to a method for identifying a test compound that  
CC binds to a target RNA molecule, which comprises contacting a detectably  
CC labeled target RNA molecule with a library of test compounds under  
CC conditions that permit direct binding of the labelled target RNA to a  
CC member of the library of test compounds so that a detectably labeled

CC target RNA: test compound complex is formed. The method is useful for  
CC screening libraries of compounds for those that are selectively bind to a  
CC pre-selected target RNA. The compounds are useful for inhibiting the  
CC formation of a specific bound RNA: host cell factor complexes in vivo.  
CC They are also useful for treating or preventing diseases associated with  
CC overproduction or decreased protein function, such as amyloidosis,  
CC haemophilia, Alzheimer's disease, atherosclerosis, cancer, gigantism,  
CC inflammation, hypothyroidism, hyperthyroidism, autoimmune disorders, aging,  
CC dwarfism, cystic fibrosis, diabetes, obesity, neurodegenerative  
CC disorders, Parkinson's disease or infections (bacterial, viral, fungal).  
CC The invention is also used in gene therapy. The present sequence is human  
CC internal ribosome entry site (IRES) RNA. This sequence is used to  
CC illustrate the method of the invention  
SQ Sequence 328 BP; 61 A; 93 C; 103 G; 0 T; 71 U; 0 Other;  
Query Match 100.0%; Score 20; DB 8; Length 328;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGACCCCAACTACTC 20  
Db 263 TTGCGACCCCAACTACTC 244  
RESULT 192  
ABK70871/C  
ID ABK70871 standard; DNA; 329 BP.  
XX  
AC ABK70871;  
XX  
DT 30-JUL-2002 (first entry)  
XX  
DE HCV genome 5'UTR sequence #5 from HCV infected patient BU.  
XX  
KW Hepatitis C virus infection; HCV; central nervous system; CNS;  
KW microglial cell precursor; alpha-interferon; monocyte;  
KW brain-specific envelope protein; antiviral therapy; virocid; ds.  
XX  
OS Hepatitis C virus.  
XX  
PN WO200220054-A2.  
XX  
PD 14-MAR-2002.  
XX  
PF 31-AUG-2001; 2001WO-GB003901.  
XX  
PR 06-SEP-2000; 2000GB-00021859.  
XX  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX  
PI Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;  
XX  
PT WPI; 2002-383036/41.  
XX  
DR  
XX  
XX Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.  
XX  
XX Example 1; Fig 14; 145pp; English.  
XX  
XX The present invention relates to a method of treating a patient with or  
CC at risk of hepatitis C virus (HCV) infection. The method comprises  
CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC HCV infection of and/or replication in microglial cells or circulating  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of

CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Re-infection of the liver  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70866  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
XX  
XX Sequence 329 BP; 60 A; 98 C; 100 G; 71 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 20; DB 6; Length 329;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTCCGACCCCAACTACTC 20  
DB 266 TTCCGACCCCAACTACTC 247  
RESULT 193  
ABK70861/C  
ID ABK70861 standard; DNA; 333 BP.  
XX  
XX ABK70861;  
AC  
XX 30-JUL-2002 (first entry)  
DT  
XX HCV genome 5'UTR sequence #15 from HCV infected patient BU.  
DE  
XX Hepatitis C virus infection; HCV; central nervous system; CNS;  
KW microglial cell precursor; alpha-interferon; monocyte;  
KW brain-specific envelope protein; antiviral therapy; virucide; ds.  
XX  
XX Hepatitis C virus.  
OS  
XX WO200220054-A2.  
PN  
XX 14-MAR-2002.  
PD  
XX 31-AUG-2001; 2001WO-GB003901.  
PF  
XX 06-SEP-2000; 2000GB-00021859.  
PR  
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
PA  
XX Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;  
PI  
XX WPI; 2002-383036/41.  
DR  
XX  
XX Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.  
XX  
XX Example 1; Fig 14; 145pp; English.  
PS  
XX The present invention relates to a method of treating a patient with or  
CC at risk of hepatitis C virus (HCV) infection. The method comprises  
CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC HCV infection of and/or replication in microglial cells or circulating  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of

CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Re-infection of the liver  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70866  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
XX  
XX Sequence 333 BP; 60 A; 100 C; 101 G; 72 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 20; DB 6; Length 333;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 TTCCGACCCCAACTACTC 20  
DB 270 TTCCGACCCCAACTACTC 251  
RESULT 194  
ABK70867/C  
ID ABK70867 standard; DNA; 333 BP.  
XX  
XX ABK70867;  
AC  
XX 30-JUL-2002 (first entry)  
DT  
XX HCV genome 5'UTR sequence #1 from HCV infected patient BU.  
DE  
XX Hepatitis C virus infection; HCV; central nervous system; CNS;  
KW microglial cell precursor; alpha-interferon; monocyte;  
KW brain-specific envelope protein; antiviral therapy; virucide; ds.  
XX  
XX Hepatitis C virus.  
OS  
XX WO200220054-A2.  
PN  
XX 14-MAR-2002.  
PD  
XX 31-AUG-2001; 2001WO-GB003901.  
PF  
XX 06-SEP-2000; 2000GB-00021859.  
PR  
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PA  
XX Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;  
PI  
XX WPI; 2002-383036/41.  
DR  
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XX Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.  
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CC administering to the central nervous system (CNS) a compound capable of  
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CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
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CC infection of and/or replication in cells and non-CNS cells. Preferably,  
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CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of

CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Reinflection of the liver  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70886  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
XX

SQ Sequence 333 BP; 60 A; 100 C; 101 G; 72 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 333;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 270 TTGCGACCCCAACTACTC 251

RESULT 195  
ABK70879/C  
ID ABK70879 standard; DNA; 333 BP.

AC ABK70879;

DT 30-JUL-2002 (first entry)

DE HCV genome 5'UTR sequence #13 from HCV infected patient BU.

KM Hepatitis C virus infection; HCV; central nervous system; CNS;

KW microglial cell precursor; alpha-interferon; monocyte;

KX brain-specific envelope protein; antiviral therapy; virucide; ds.

OS Hepatitis C virus.

PN WO200220054-A2.

PD 14-MAR-2002.

PF 31-AUG-2001; 2001WO-GB003901.

PR 06-SEP-2000; 2000GB-00021859.

PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

PI Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;

DR WPI; 2002-383036/41.

PT Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.

PS Example 1; Fig 14; 145bp; English.

XX The present invention relates to a method of treating a patient with or  
CC at risk of hepatitis C virus (HCV) infection. The method comprises  
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CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC HCV infection of and/or replication in microglial cells or circulating  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of

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CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Reinflection of the liver  
CC by the virus released by the CNS may be prevented by the above mentioned  
CC method. The development of resistant strains is reduced or prevented, by  
CC the therapeutic use of a vaccine against brain-specific envelope protein,  
CC before, together with or after antiviral therapy. ABK70867-ABK70886  
CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
XX

SQ Sequence 333 BP; 63 A; 97 C; 102 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 333;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 270 TTGCGACCCCAACTACTC 251

RESULT 196  
ABK70876/C  
ID ABK70876 standard; DNA; 333 BP.

AC ABK70876;

DT 30-JUL-2002 (first entry)

DE HCV genome 5'UTR sequence #10 from HCV infected patient BU.

KM Hepatitis C virus infection; HCV; central nervous system; CNS;

KW microglial cell precursor; alpha-interferon; monocyte;

KX brain-specific envelope protein; antiviral therapy; virucide; ds.

OS Hepatitis C virus.

PN WO200220054-A2.

PD 14-MAR-2002.

PF 31-AUG-2001; 2001WO-GB003901.

PR 06-SEP-2000; 2000GB-00021859.

PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

PI Thomas HC, Taylor-Robinson SD, Karayiannis P, Forton DM;

DR WPI; 2002-383036/41.

PT Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.

PS Example 1; Fig 14; 145bp; English.

XX The present invention relates to a method of treating a patient with or  
CC at risk of hepatitis C virus (HCV) infection. The method comprises  
CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
CC treating a patient with or at risk of HCV infection by inhibiting HCV  
CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC HCV infection of and/or replication in microglial cells or circulating  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of



a pharmacological agent that blocks binding of the brain-specific envelope protein to the putative receptor prevents uptake of the virus to the CNS, and improves long-term response rates. Reinfection of the liver by the virus released by the CNS may be prevented by the above mentioned method. The development of resistant strains is reduced or prevented, by the therapeutic use of a vaccine against brain-specific envelope protein, before, together with or after antiviral therapy. ABK70867-ABK70886 represent HCV genome 5'UTR sequences derived from HCV infected patient BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in the Fig, and should be page 4 of 6 as the nucleotide numbering of the sequences on this page follow correctly from page 3 of 6 (page 16/19). All sequences in Fig 14 have been typed in according to their correct nucleotide positioning

Sequence 333 BP; 60 A; 100 C; 101 G; 72 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 333;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTCCGACCCCAACTACTC 20

Db 270 TTCCGACCCCAACTACTC 251

RESULT 197  
AAQ98272/c  
ID AAQ98272 standard; DNA; 334 BP.  
XX  
XX AAQ98272;  
AC  
XX  
XX 19-MAR-1996 (first entry)  
DT  
XX  
XX Hepatitis C virus 5' non-translated region for detection primer design.  
DE  
XX  
XX Primer; hepatitis C virus; PCR; amplification; reverse transcription;  
KM detection; non-translated region; ss.  
KW  
XX  
XX Synthetic.  
OS  
XX  
XX JP07184695-A.  
PN  
XX  
XX 25-JUL-1995.  
PD  
XX  
XX 27-DEC-1993; 93JP-00332682.  
PF  
XX  
XX 27-DEC-1993; 93JP-00332682.  
PR  
XX  
XX (SANW ) SANWA KAGAKU KENKYUSHO CO LTD.  
PA  
XX  
XX WPI; 1995-287992/38.  
DR  
XX  
XX  
PT Simple detection of Hepatitis C virus in a single reaction tube - useful  
PT for high sensitivity and ease of reproduction.  
XX  
XX  
XX Example 3; Page 11; 14pp; Japanese.  
PS  
XX  
XX The primers AAQ98270-94 are used in a novel simple method for the  
CC detection of hepatitis C virus. The novel method involves the steps of  
CC extracting the virus from a sample, synthesising cDNA from the viral RNA  
CC by reverse transcription, amplifying the cDNA by a first PCR and  
CC reamplifying the amplified product in a second PCR, all of which occur in  
CC a single reaction tube. The primers are designed based on a 334 bp  
CC sequence (AAQ98272) derived from a 5' non-translated region of the viral  
CC genome  
XX  
XX  
XX Sequence 334 BP; 68 A; 98 C; 101 G; 67 T; 0 U; 0 Other;

Db 258 TTCCGACCCCAACTACTC 239

RESULT 198  
ABK70869/c  
ID ABK70869 standard; DNA; 334 BP.  
XX  
XX ABK70869;  
AC  
XX  
XX 30-JUN-2002 (first entry)  
DT  
XX  
XX HCV genome 5'UTR sequence #3 from HCV infected patient BU.  
DE  
XX  
XX Hepatitis C virus infection; HCV; central nervous system; CNS;  
KM microglial cell precursor; alpha-interferon; monocyte;  
KW brain-specific envelope protein; antiviral therapy; virucide; ds.  
XX  
XX Hepatitis C virus.  
OS  
XX  
XX WO200220054-A2.  
FN  
XX  
XX 14-MAR-2002.  
PD  
XX  
XX 31-AUG-2001; 2001WO-GB003901.  
PE  
XX  
XX 06-SEP-2000; 2000GB-00021859.  
PR  
XX  
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
PA  
XX  
XX Thomas HC, Taylor-Robinson SD, Karayannis P, Forton DM;  
PI  
XX  
XX WPI; 2002-383036/41.  
DR  
XX  
XX  
PT Treating patient with or at risk of hepatitis C virus (HCV) infection by  
PT inhibiting infection by HCV of and/or replication of HCV in cells of  
PT central nervous system.  
XX  
XX  
XX Example 1; Fig 14; 145pp; English.  
PS  
XX  
XX The present invention relates to a method of treating a patient with or  
CC at risk of hepatitis C virus (HCV) infection. The method comprises  
CC inhibiting infection by HCV of, and/or replication of HCV in cells of the  
CC central nervous system (CNS) of the patient. The method is performed by  
CC administering to the central nervous system (CNS) a compound capable of  
CC inhibiting HCV infection and/or replication in the CNS of the patient  
CC e.g. in monocytes or cells of monocytic lineage. The method is useful for  
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CC infection of and/or replication in cells and non-CNS cells. Preferably,  
CC HCV infection of and/or replication in microglial cells or circulating  
CC microglial cell precursors is inhibited. The method is carried out in a  
CC patient who is, has been or will be administered alpha-interferon. Use of  
CC a pharmacological agent that blocks binding of the brain-specific  
CC envelope protein to the putative receptor prevents uptake of the virus to  
CC the CNS, and improves long-term response rates. Reinfection of the liver  
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CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
CC the Fig, and should be page 4 of 6 as the nucleotide numbering of the  
CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
XX  
XX  
XX Sequence 334 BP; 60 A; 101 C; 101 G; 72 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 334;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TTCCGACCCCAACTACTC 20

Db 271 TTGGGACCCACACTACTC 252

|||||  
RESULT 199  
ABK70868/c  
ID ABK70868 standard; DNA; 335 BP.  
XX  
XX ABK70868;  
AC  
XX  
XX  
DT 30-JUL-2002 (first entry)  
XX  
XX HCV genome 5'UTR sequence #2 from HCV infected patient BU.  
DE  
XX Hepatitis C virus infection; HCV; central nervous system; CNS;  
XX microglial cell precursor; alpha-interferon; monocyte;  
KM brain-specific envelope protein; antiviral therapy; virucide; ds.  
XX  
XX Hepatitis C virus.  
OS  
XX WO200220054-A2.  
PN  
XX  
XX 14-MAR-2002.  
PD  
XX  
XX 31-AUG-2001; 2001WO-GB003901.  
PF  
XX  
XX 06-SEP-2000; 2000GB-00021859.  
PR  
XX  
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
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CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
XX  
SO Sequence 335 BP; 61 A; 101 C; 101 G; 72 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCACACTACTC 20

Db 271 TTGGGACCCACACTACTC 252

|||||  
RESULT 200  
ABK70885/c  
ID ABK70885 standard; DNA; 335 BP.  
XX  
XX ABK70885;  
AC  
XX  
XX  
DT 30-JUL-2002 (first entry)  
XX  
XX HCV genome 5'UTR sequence #19 from HCV infected patient BU.  
DE  
XX Hepatitis C virus infection; HCV; central nervous system; CNS;  
XX microglial cell precursor; alpha-interferon; monocyte;  
KM brain-specific envelope protein; antiviral therapy; virucide; ds.  
XX  
XX Hepatitis C virus.  
OS  
XX WO200220054-A2.  
PN  
XX  
XX 14-MAR-2002.  
PD  
XX  
XX 31-AUG-2001; 2001WO-GB003901.  
PF  
XX  
XX 06-SEP-2000; 2000GB-00021859.  
PR  
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XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
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PI WPI; 2002-383036/41.  
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CC represent HCV genome 5'UTR sequences derived from HCV infected patient  
CC BU. Note: Fig 14 page 6 of 6 (page 19/19) is in the incorrect position in  
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CC sequences on this page follow correctly from page 3 of 6 (page 16/19).  
CC All sequences in Fig 14 have been typed in according to their correct  
CC nucleotide positioning  
XX  
SO Sequence 335 BP; 64 A; 100 C; 99 G; 72 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 335;  
Best Local Similarity 100.0%; Pred. No. 0.053;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCACACTACTC 20

Tue Apr 26 09:53:17 2005

us-08-887-505b-28.011.rng

Page 101

Db 272 TTGGGACCAACTACTC 253

Search completed: April 25, 2005, 13:45:10  
Job time : 259.947 secs

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OM nucleic - nucleic search, using sw model

Run on: April 25, 2005, 13:09:42 ; Search time 865.789 Seconds

(without alignments)  
1119.330 Million cell updates/sec

Title: US-08-887-505B-28

Perfect score: 20

Sequence: 1 TTCCGACCACTACTCTC 20

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sbs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	20	100.0	20 6 AX803565	AX803565 Sequence
2	20	100.0	24 6 AX803712	AX803712 Sequence
3	20	100.0	25 6 AR411549	AR411549 Sequence
4	20	100.0	25 6 BD000275	BD000275 Oligonuc
5	20	100.0	27 6 AR106359	AR106359 Sequence
6	20	100.0	27 6 AR400923	AR400923 Sequence
7	20	100.0	27 6 AR411548	AR411548 Sequence
8	20	100.0	27 6 AX286630	AX286630 Sequence
9	20	100.0	27 6 BD000257	BD000257 Oligonuc
10	20	100.0	27 6 BD000274	BD000274 Oligonuc
11	20	100.0	28 6 AX803705	AX803705 Sequence
12	20	100.0	28 6 AX803711	AX803711 Sequence
13	20	100.0	29 6 BD183048	BD183048 Nucleic a
14	20	100.0	33 6 AR004396	AR004396 Sequence
15	20	100.0	33 6 AR064935	AR064935 Sequence
16	20	100.0	33 6 AR097188	AR097188 Sequence
17	20	100.0	33 6 AR130686	AR130686 Sequence
18	20	100.0	33 6 AR172035	AR172035 Sequence
19	20	100.0	33 6 BD189152	BD189152 HCV Genom

20	20	100.0	33 6 BD189299	BD189299 HCV Genom
21	20	100.0	33 6 BD189446	BD189446 HCV Genom
22	20	100.0	33 6 I82871	I82871 Sequence 50
23	20	100.0	40 6 AR153179	AR153179 Sequence
24	20	100.0	40 6 AR163348	AR163348 Sequence
25	20	100.0	40 6 BD242950	BD242950 Method fo
26	20	100.0	46 6 AR53156	AR53156 Sequence
27	20	100.0	46 6 I4581	I4581 Sequence 10
28	20	100.0	46 6 I70986	I70986 Sequence 10
29	20	100.0	50 6 AX397948	AX397948 Sequence
30	20	100.0	50 6 AX397960	AX397960 Sequence
31	20	100.0	57 6 BD183034	BD183034 Nucleic a
32	20	100.0	60 6 AX616614	AX616614 Sequence
33	20	100.0	108 6 AR338416	AR338416 Sequence
34	20	100.0	108 6 AR33611	AR33611 Sequence
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37	20	100.0	126 6 BD183033	BD183033 Nucleic a
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44	20	100.0	139 14 AF282638	AF282638 Hepatitis
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C 93	20	100.0	139	14	AY004007	AY004007	Hepatitis	C 166	20	100.0	178	14	AF463463	AF463463	Hepatitis
C 94	20	100.0	139	14	AY004008	AY004008	Hepatitis	C 167	20	100.0	178	14	AF463464	AF463464	Hepatitis
C 95	20	100.0	139	14	AY004009	AY004009	Hepatitis	C 168	20	100.0	178	14	AF463465	AF463465	Hepatitis
C 96	20	100.0	139	14	AY004010	AY004010	Hepatitis	C 169	20	100.0	178	14	AF463467	AF463467	Hepatitis
C 97	20	100.0	139	14	AY004011	AY004011	Hepatitis	C 170	20	100.0	178	14	AF463468	AF463468	Hepatitis
C 98	20	100.0	139	14	AY004012	AY004012	Hepatitis	C 171	20	100.0	178	14	AF463469	AF463469	Hepatitis
C 99	20	100.0	139	14	AY004013	AY004013	Hepatitis	C 172	20	100.0	178	14	AF463470	AF463470	Hepatitis
C 100	20	100.0	157	14	AF506651	AF506651	Hepatitis	C 173	20	100.0	178	14	AF463471	AF463471	Hepatitis
C 101	20	100.0	163	6	AX172758	AX172758	Sequence	C 174	20	100.0	178	14	AF463472	AF463472	Hepatitis
C 102	20	100.0	164	14	AY147807	AY147807	Hepatitis	C 175	20	100.0	178	14	AF463474	AF463474	Hepatitis
C 103	20	100.0	164	14	AY344037	AY344037	Hepatitis	C 176	20	100.0	178	14	AF463475	AF463475	Hepatitis
C 104	20	100.0	165	14	AF506628	AF506628	Hepatitis	C 177	20	100.0	178	14	AF463476	AF463476	Hepatitis
C 105	20	100.0	165	14	AY147800	AY147800	Hepatitis	C 178	20	100.0	178	14	AF463477	AF463477	Hepatitis
C 106	20	100.0	165	14	AY147801	AY147801	Hepatitis	C 179	20	100.0	178	14	AF463478	AF463478	Hepatitis
C 107	20	100.0	165	14	AY147802	AY147802	Hepatitis	C 180	20	100.0	178	14	AF463479	AF463479	Hepatitis
C 108	20	100.0	165	14	AY147803	AY147803	Hepatitis	C 181	20	100.0	178	14	AF463480	AF463480	Hepatitis
C 109	20	100.0	165	14	AY147804	AY147804	Hepatitis	C 182	20	100.0	178	14	AF463486	AF463486	Hepatitis
C 110	20	100.0	165	14	AY147805	AY147805	Hepatitis	C 183	20	100.0	178	14	AF463487	AF463487	Hepatitis
C 111	20	100.0	165	14	AY147806	AY147806	Hepatitis	C 184	20	100.0	178	14	AF463488	AF463488	Hepatitis
C 112	20	100.0	165	14	AY147808	AY147808	Hepatitis	C 185	20	100.0	178	14	AF463489	AF463489	Hepatitis
C 113	20	100.0	165	14	AY147809	AY147809	Hepatitis	C 186	20	100.0	178	14	AF463491	AF463491	Hepatitis
C 114	20	100.0	165	14	AY147810	AY147810	Hepatitis	C 187	20	100.0	179	14	AY145950	AY145950	Hepatitis
C 115	20	100.0	165	14	AY147811	AY147811	Hepatitis	C 188	20	100.0	180	14	AY145973	AY145973	Hepatitis
C 116	20	100.0	165	14	AY147812	AY147812	Hepatitis	C 189	20	100.0	180	14	AF134750	AF134750	Hepatitis
C 117	20	100.0	165	14	AY147813	AY147813	Hepatitis	C 190	20	100.0	181	14	AF134751	AF134751	Hepatitis
C 118	20	100.0	165	14	AY147814	AY147814	Hepatitis	C 191	20	100.0	181	14	AF134754	AF134754	Hepatitis
C 119	20	100.0	165	14	AY147815	AY147815	Hepatitis	C 192	20	100.0	181	14	AF134755	AF134755	Hepatitis
C 120	20	100.0	165	14	AY147816	AY147816	Hepatitis	C 193	20	100.0	181	14	AF134756	AF134756	Hepatitis
C 121	20	100.0	165	14	AY344028	AY344028	Hepatitis	C 194	20	100.0	181	14	AF134757	AF134757	Hepatitis
C 122	20	100.0	165	14	AY344029	AY344029	Hepatitis	C 195	20	100.0	181	14	AF134758	AF134758	Hepatitis
C 123	20	100.0	165	14	AY344030	AY344030	Hepatitis	C 196	20	100.0	181	14	AF134759	AF134759	Hepatitis
C 124	20	100.0	165	14	AY344031	AY344031	Hepatitis	C 197	20	100.0	181	14	AF134760	AF134760	Hepatitis
C 125	20	100.0	165	14	AY344032	AY344032	Hepatitis	C 198	20	100.0	181	14	AF158605	AF158605	Hepatitis
C 126	20	100.0	165	14	AY344033	AY344033	Hepatitis	C 199	20	100.0	181	14	AF158607	AF158607	Hepatitis
C 127	20	100.0	165	14	AY344034	AY344034	Hepatitis	C 200	20	100.0	181	14	AF158608	AF158608	Hepatitis
C 128	20	100.0	165	14	AY344035	AY344035	Hepatitis	C 201	20	100.0	181	14	AF158609	AF158609	Hepatitis
C 129	20	100.0	166	14	AF506648	AF506648	Hepatitis	C 202	20	100.0	181	14	AF158611	AF158611	Hepatitis
C 130	20	100.0	166	14	AF506649	AF506649	Hepatitis	C 203	20	100.0	181	14	AF158612	AF158612	Hepatitis
C 131	20	100.0	167	14	AF506642	AF506642	Hepatitis	C 204	20	100.0	181	14	AF158617	AF158617	Hepatitis
C 132	20	100.0	167	14	AF506684	AF506684	Hepatitis	C 205	20	100.0	181	14	AY190378	AY190378	Hepatitis
C 133	20	100.0	169	14	AF506682	AF506682	Hepatitis	C 206	20	100.0	181	14	AY190381	AY190381	Hepatitis
C 134	20	100.0	169	14	AF506695	AF506695	Hepatitis	C 207	20	100.0	181	14	AY190382	AY190382	Hepatitis
C 135	20	100.0	170	14	AY146006	AY146006	Hepatitis	C 208	20	100.0	181	14	AY190383	AY190383	Hepatitis
C 136	20	100.0	171	14	AF506691	AF506691	Hepatitis	C 209	20	100.0	181	14	AY190385	AY190385	Hepatitis
C 137	20	100.0	172	14	AY545676	AY545676	Hepatitis	C 210	20	100.0	181	14	AY190386	AY190386	Hepatitis
C 138	20	100.0	173	14	AY545677	AY545677	Hepatitis	C 211	20	100.0	181	14	AY190388	AY190388	Hepatitis
C 139	20	100.0	173	14	AY545678	AY545678	Hepatitis	C 212	20	100.0	181	14	AY190389	AY190389	Hepatitis
C 140	20	100.0	174	14	AF506673	AF506673	Hepatitis	C 213	20	100.0	181	14	AY190390	AY190390	Hepatitis
C 141	20	100.0	174	14	AF506685	AF506685	Hepatitis	C 214	20	100.0	181	14	AY190391	AY190391	Hepatitis
C 142	20	100.0	174	14	AF506692	AF506692	Hepatitis	C 215	20	100.0	181	14	AY190392	AY190392	Hepatitis
C 143	20	100.0	174	14	AF506693	AF506693	Hepatitis	C 216	20	100.0	181	14	AY190393	AY190393	Hepatitis
C 144	20	100.0	174	14	AF523463	AF523463	Hepatitis	C 217	20	100.0	181	14	AY190394	AY190394	Hepatitis
C 145	20	100.0	174	14	AF523464	AF523464	Hepatitis	C 218	20	100.0	181	14	AY190395	AY190395	Hepatitis
C 146	20	100.0	174	14	AF523465	AF523465	Hepatitis	C 219	20	100.0	181	14	AY190396	AY190396	Hepatitis
C 147	20	100.0	174	14	AF523466	AF523466	Hepatitis	C 220	20	100.0	181	14	AY190397	AY190397	Hepatitis
C 148	20	100.0	174	14	AF545671	AF545671	Hepatitis	C 221	20	100.0	181	14	AY190398	AY190398	Hepatitis
C 149	20	100.0	174	14	AF545672	AF545672	Hepatitis	C 222	20	100.0	181	14	AY190400	AY190400	Hepatitis
C 150	20	100.0	174	14	AF545674	AF545674	Hepatitis	C 223	20	100.0	181	14	AY190401	AY190401	Hepatitis
C 151	20	100.0	174	14	AF545675	AF545675	Hepatitis	C 224	20	100.0	181	14	AY190404	AY190404	Hepatitis
C 152	20	100.0	175	14	AF545677	AF545677	Hepatitis	C 225	20	100.0	181	14	AY190405	AY190405	Hepatitis
C 153	20	100.0	175	14	AF506661	AF506661	Hepatitis	C 226	20	100.0	181	14	AY190406	AY190406	Hepatitis
C 154	20	100.0	176	14	AF506645	AF506645	Hepatitis	C 227	20	100.0	181	14	AY190408	AY190408	Hepatitis
C 155	20	100.0	176	14	AF506658	AF506658	Hepatitis	C 228	20	100.0	181	14	AY190409	AY190409	Hepatitis
C 156	20	100.0	176	14	AF506694	AF506694	Hepatitis	C 229	20	100.0	181	14	AY190410	AY190410	Hepatitis
C 157	20	100.0	176	14	AF506694	AF506694	Hepatitis	C 230	20	100.0	181	14	AY190411	AY190411	Hepatitis
C 158	20	100.0	176	14	AF506694	AF506694	Hepatitis	C 231	20	100.0	181	14	AY190413	AY190413	Hepatitis
C 159	20	100.0	176	14	AF506694	AF506694	Hepatitis	C 232	20	100.0	181	14	AY190414	AY190414	Hepatitis
C 160	20	100.0	176	14	AF506694	AF506694	Hepatitis	C 233	20	100.0	181	14	AY190415	AY190415	Hepatitis
C 161	20	100.0	177	14	AF506677	AF506677	Hepatitis	C 234	20	100.0	181	14	AY190416	AY190416	Hepatitis
C 162	20	100.0	177	14	AF506680	AF506680	Hepatitis	C 235	20	100.0	181	14	AY190417	AY190417	Hepatitis
C 163	20	100.0	177	14	AF506686	AF506686	Hepatitis	C 236	20	100.0	181	14	AY190418	AY190418	Hepatitis
C 164	20	100.0	178	14	AF463460	AF463460	Hepatitis	C 237	20	100.0	181	14	AY190420	AY190420	Hepatitis
C 165	20	100.0	178	14	AF463462	AF463462	Hepatitis	C 238	20	100.0	181	14	AY190421	AY190421	Hepatitis

C 239	20	100.0	181	14	AY190423	Hepatitis	C 312	20	100.0	182	14	AY190384	AY190384	Hepatitis
C 240	20	100.0	181	14	AY190424	Hepatitis	C 313	20	100.0	182	14	AY190387	AY190387	Hepatitis
C 241	20	100.0	181	14	AY190425	Hepatitis	C 314	20	100.0	182	14	AY190399	AY190399	Hepatitis
C 242	20	100.0	181	14	AY190426	Hepatitis	C 315	20	100.0	182	14	AY190403	AY190403	Hepatitis
C 243	20	100.0	181	14	AY190427	Hepatitis	C 316	20	100.0	182	14	AY190407	AY190407	Hepatitis
C 244	20	100.0	181	14	AY190429	Hepatitis	C 317	20	100.0	182	14	AY190419	AY190419	Hepatitis
C 245	20	100.0	181	14	AY190430	Hepatitis	C 318	20	100.0	182	14	AY190428	AY190428	Hepatitis
C 246	20	100.0	181	14	AY190434	Hepatitis	C 319	20	100.0	182	14	AY190431	AY190431	Hepatitis
C 247	20	100.0	181	14	AY190436	Hepatitis	C 320	20	100.0	182	14	AY190432	AY190432	Hepatitis
C 248	20	100.0	181	14	AY190437	Hepatitis	C 321	20	100.0	182	14	AY190433	AY190433	Hepatitis
C 249	20	100.0	181	14	AY190438	Hepatitis	C 322	20	100.0	182	14	AY190435	AY190435	Hepatitis
C 250	20	100.0	181	14	AY190439	Hepatitis	C 323	20	100.0	182	14	AY190442	AY190442	Hepatitis
C 251	20	100.0	181	14	AY190440	Hepatitis	C 324	20	100.0	182	14	AY190450	AY190450	Hepatitis
C 252	20	100.0	181	14	AY190441	Hepatitis	C 325	20	100.0	182	14	AY190467	AY190467	Hepatitis
C 253	20	100.0	181	14	AY190443	Hepatitis	C 326	20	100.0	182	14	AY190473	AY190473	Hepatitis
C 254	20	100.0	181	14	AY190444	Hepatitis	C 327	20	100.0	182	14	AY190481	AY190481	Hepatitis
C 255	20	100.0	181	14	AY190445	Hepatitis	C 328	20	100.0	182	14	AY190493	AY190493	Hepatitis
C 256	20	100.0	181	14	AY190446	Hepatitis	C 329	20	100.0	182	14	AY190494	AY190494	Hepatitis
C 257	20	100.0	181	14	AY190447	Hepatitis	C 330	20	100.0	182	14	AY190496	AY190496	Hepatitis
C 258	20	100.0	181	14	AY190449	Hepatitis	C 331	20	100.0	183	14	AF245282	AF245282	Hepatitis
C 259	20	100.0	181	14	AY190451	Hepatitis	C 332	20	100.0	183	14	AF245283	AF245283	Hepatitis
C 260	20	100.0	181	14	AY190452	Hepatitis	C 333	20	100.0	183	14	AF245284	AF245284	Hepatitis
C 261	20	100.0	181	14	AY190453	Hepatitis	C 334	20	100.0	183	14	AF245285	AF245285	Hepatitis
C 262	20	100.0	181	14	AY190454	Hepatitis	C 335	20	100.0	183	14	AF245286	AF245286	Hepatitis
C 263	20	100.0	181	14	AY190455	Hepatitis	C 336	20	100.0	183	14	AF245287	AF245287	Hepatitis
C 264	20	100.0	181	14	AY190456	Hepatitis	C 337	20	100.0	183	14	AF245290	AF245290	Hepatitis
C 265	20	100.0	181	14	AY190457	Hepatitis	C 338	20	100.0	184	14	AF146054	AF146054	Hepatitis
C 266	20	100.0	181	14	AY190458	Hepatitis	C 339	20	100.0	184	14	HPCB079C	HPCB079C	Hepatitis
C 267	20	100.0	181	14	AY190459	Hepatitis	C 340	20	100.0	185	14	HPCB074B	HPCB074B	Hepatitis
C 268	20	100.0	181	14	AY190460	Hepatitis	C 341	20	100.0	185	14	HPCB80D	HPCB80D	Hepatitis
C 269	20	100.0	181	14	AY190461	Hepatitis	C 342	20	100.0	186	6	E10302	E10302	Anti-gene
C 270	20	100.0	181	14	AY190462	Hepatitis	C 343	20	100.0	187	6	AX172757	AX172757	Sequence
C 271	20	100.0	181	14	AY190463	Hepatitis	C 344	20	100.0	187	6	AY306296	AY306296	Hepatitis
C 272	20	100.0	181	14	AY190464	Hepatitis	C 345	20	100.0	187	14	AY306297	AY306297	Hepatitis
C 273	20	100.0	181	14	AY190465	Hepatitis	C 346	20	100.0	187	14	AY311048	AY311048	Hepatitis
C 274	20	100.0	181	14	AY190466	Hepatitis	C 347	20	100.0	188	14	AY306229	AY306229	Hepatitis
C 275	20	100.0	181	14	AY190468	Hepatitis	C 348	20	100.0	188	14	AY306230	AY306230	Hepatitis
C 276	20	100.0	181	14	AY190469	Hepatitis	C 349	20	100.0	188	14	AY306231	AY306231	Hepatitis
C 277	20	100.0	181	14	AY190470	Hepatitis	C 350	20	100.0	188	14	AY306232	AY306232	Hepatitis
C 278	20	100.0	181	14	AY190471	Hepatitis	C 351	20	100.0	188	14	AY306233	AY306233	Hepatitis
C 279	20	100.0	181	14	AY190472	Hepatitis	C 352	20	100.0	188	14	AY306234	AY306234	Hepatitis
C 280	20	100.0	181	14	AY190474	Hepatitis	C 353	20	100.0	188	14	AY306235	AY306235	Hepatitis
C 281	20	100.0	181	14	AY190475	Hepatitis	C 354	20	100.0	188	14	AY306236	AY306236	Hepatitis
C 282	20	100.0	181	14	AY190476	Hepatitis	C 355	20	100.0	188	14	AY306237	AY306237	Hepatitis
C 283	20	100.0	181	14	AY190477	Hepatitis	C 356	20	100.0	188	14	AY306238	AY306238	Hepatitis
C 284	20	100.0	181	14	AY190478	Hepatitis	C 357	20	100.0	188	14	AY306239	AY306239	Hepatitis
C 285	20	100.0	181	14	AY190479	Hepatitis	C 358	20	100.0	188	14	AY306240	AY306240	Hepatitis
C 286	20	100.0	181	14	AY190480	Hepatitis	C 359	20	100.0	188	14	AY306241	AY306241	Hepatitis
C 287	20	100.0	181	14	AY190482	Hepatitis	C 360	20	100.0	188	14	AY306242	AY306242	Hepatitis
C 288	20	100.0	181	14	AY190483	Hepatitis	C 361	20	100.0	188	14	AY306243	AY306243	Hepatitis
C 289	20	100.0	181	14	AY190484	Hepatitis	C 362	20	100.0	188	14	AY306244	AY306244	Hepatitis
C 290	20	100.0	181	14	AY190485	Hepatitis	C 363	20	100.0	188	14	AY306245	AY306245	Hepatitis
C 291	20	100.0	181	14	AY190486	Hepatitis	C 364	20	100.0	188	14	AY306246	AY306246	Hepatitis
C 292	20	100.0	181	14	AY190487	Hepatitis	C 365	20	100.0	188	14	AY306247	AY306247	Hepatitis
C 293	20	100.0	181	14	AY190488	Hepatitis	C 366	20	100.0	188	14	AY306248	AY306248	Hepatitis
C 294	20	100.0	181	14	AY190489	Hepatitis	C 367	20	100.0	188	14	AY306249	AY306249	Hepatitis
C 295	20	100.0	181	14	AY190490	Hepatitis	C 368	20	100.0	188	14	AY306250	AY306250	Hepatitis
C 296	20	100.0	181	14	AY190491	Hepatitis	C 369	20	100.0	188	14	AY306251	AY306251	Hepatitis
C 297	20	100.0	181	14	AY190492	Hepatitis	C 370	20	100.0	188	14	AY306252	AY306252	Hepatitis
C 298	20	100.0	181	14	AY190495	Hepatitis	C 371	20	100.0	188	14	AY306253	AY306253	Hepatitis
C 299	20	100.0	181	14	AY190497	Hepatitis	C 372	20	100.0	188	14	AY306254	AY306254	Hepatitis
C 300	20	100.0	181	14	AY190498	Hepatitis	C 373	20	100.0	188	14	AY306256	AY306256	Hepatitis
C 301	20	100.0	181	14	AY190499	Hepatitis	C 374	20	100.0	188	14	AY306257	AY306257	Hepatitis
C 302	20	100.0	181	14	AY190500	Hepatitis	C 375	20	100.0	188	14	AY306258	AY306258	Hepatitis
C 303	20	100.0	181	14	AY190501	Hepatitis	C 376	20	100.0	188	14	AY306259	AY306259	Hepatitis
C 304	20	100.0	181	14	AY190503	Hepatitis	C 377	20	100.0	188	14	AY306260	AY306260	Hepatitis
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C 829	20	100.0	188	14	AV310058	HepatitIs	C 902	20	100.0	188	14	AV310933	AV310933	HepatitIs
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C 850	20	100.0	188	14	AV310079	HepatitIs	C 923	20	100.0	188	14	AV310954	AV310954	HepatitIs
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## ALIGNMENTS

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AX803665 20 bp DNA linear PAT 24-NOV-2003
LOCUS AX803665
DEFINITION Sequence 28 from Patent EP1331267.
ACCESSION AX803665
VERSION AX803665.1 GI:38502207
KEYWORDS
SOURCE
ORGANISM
unidentified
unidentified
unclassified.
REFERENCE
1 Frank,B.L., Goodchild,J., Hamlin,H.A., Kulikskie,R.E.,
AUTHORS Roberts,P.C., Roberts,N.A., Walther,D.M. and Wolfe,J.L.
TITLE Oligonucleotides specific for Hepatitis C Virus
JOURNAL Patent: EP 1331267-A 28 30-JUL-2003;
HYBRIDON, INC. (US)
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AX803712 24 bp DNA linear PAT 24-NOV-2003
LOCUS AX803712
DEFINITION Sequence 75 from Patent EP1331267.

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ACCESSION AX803712
VERSION AX803712.1 GI:38502254
KEYWORDS
SOURCE
ORGANISM
unidentified
unidentified
unclassified.
REFERENCE
1 Frank,B.L., Goodchild,J., Hamlin,H.A., Kulikskie,R.E.,
AUTHORS Roberts,P.C., Roberts,N.A., Walther,D.M. and Wolfe,J.L.
TITLE Oligonucleotides specific for Hepatitis C Virus
JOURNAL Patent: EP 1331267-A 75 30-JUL-2003;
HYBRIDON, INC. (US)
FEATURES
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location/Qualifiers
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LOCUS AR411549
DEFINITION Sequence 13 from patent US 6638714.
ACCESSION AR411549
VERSION AR411549.1 GI:40163893
KEYWORDS
SOURCE
ORGANISM
Unknown.
unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS Linmen,J.M. and Gorman,K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C
JOURNAL Patent: US 6638714-A 13 28-OCT-2003;
LOCATION/Qualifiers
1..25
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BD000275 25 bp DNA linear PAT 31-JAN-2002
LOCUS BD000275
DEFINITION Oligonucleotide primers for efficient detection of hepatitis C
virus (HCV) and methods of use thereof.
ACCESSION BD000275
VERSION BD000275.1 GI:18623354
KEYWORDS JP 2000279200-A/13.
SOURCE synthetic construct
ORGANISM
other sequences: artificial sequences.
1 (bases 1 to 25)
REFERENCE
1 Lyneen,J.M. and Gorman,K.M.
AUTHORS Oligonucleotide primers for efficient detection of hepatitis C
virus (HCV) and methods of use thereof
TITLE

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JOURNAL Patent: JP 2000279200-A 13 10-OCT-2000;  
ORTHIO CLINICAL DIAGNOSTICS INC  
COMMENT OS Artificial Sequence  
PN JP 2000279200-A/13  
PD 10-OCT-2000  
PF 03-FEB-2000 JP 2000032656  
PR 03-FEB-1999 US 60/118497  
PI JEFFREY M LYNNEN KEVIN M GORMAN  
PC C12Q1/68, C12N15/09// (C12N15/09, C12R1:92), C12N15/00, (C12N15/00, C12R1:92)  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION AR106359  
VERSION AR106359.1 GI:12820889  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Kay, M. A. and Lieber, A.  
TITLE Ribozymes for treating hepatitis C  
JOURNAL Patent: US 6107028-A 21 22-AUG-2000;  
FEATURES Location/Qualifiers  
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Db 1 TTGGGACCCACACTACTC 20  
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DEFINITION Sequence 12 from patent US 6623919.  
ACCESSION AR400923  
VERSION AR400923.1 GI:40148215  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Gorman, K. M., Patterson, D. R., Linnen, J. M. and Song, K.  
TITLE Oligonucleotide primers for efficient multiplex detection of hepatitis C virus (HCV) and human immunodeficiency virus (HIV) and

JOURNAL method of use thereof  
Patent: US 6623919-A 12 23-SEP-2003;  
FEATURES Location/Qualifiers  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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4 TTGGGACCCACACTACTC 23

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DEFINITION Sequence 12 from patent US 6638714.  
ACCESSION AR411548  
VERSION AR411548.1 GI:40163892  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Linnen, J. M. and Gorman, K. M.  
TITLE Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof  
JOURNAL Patent: US 6638714-A 12 28-OCT-2003;  
FEATURES Location/Qualifiers  
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DEFINITION Sequence 1 from Patent WO0181627.  
ACCESSION AX286630  
VERSION AX286630.1 GI:17048706  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1  
AUTHORS Klinck, R., Walker, S., Afshar, M., Collier, A., Aboul-Ela, F. and Westhof, E.  
TITLE In-silico-screening for docking on sub-domain IId of hcv-ires  
JOURNAL Patent: WO 0181627-A 1 01-NOV-2001;  
FEATURES Ribotargets limited (GB)  
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Db 23 TTGGCGACCCCAACTACTC 4

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DEFINITION Oligonucleotide primers for efficient multiplex detection of hepatitis C virus (HCV) and human immunodeficiency virus (HIV) and methods of use thereof.  
ACCESSION BD000257.1 GI:18623336  
VERSION JP 2000279198-A/12.  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Gorman,K.M., Paterson,D.R., Lynen,J.M. and Son,K.  
TITLE Oligonucleotide primers for efficient multiplex detection of hepatitis C virus (HCV) and human immunodeficiency virus (HIV), and methods of use thereof  
PATENT: JP 2000279198-A 12 10-OCT-2000;  
ORWHO CLINICAL DIAGNOSTICS INC

COMMENT  
JOURNAL  
OS Artificial Sequence  
PN JP 2000279198-A/12  
PD 10-OCT-2000  
PE 02-FEB-2000 JP 2000030237  
PR 03-FEB-1999 US 60/118498  
PT KEVIN M GORMAN, DAVID R PATERSON, JEFFREY M LYNNEN, KEVIN SON PC  
C1201/68, C12N15/09/(C12N15/09, C12R1.92), C12N15/00, (C12N15/00, PC  
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Db 4 TTGGCGACCCCAACTACTC 23

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DEFINITION Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof.  
ACCESSION BD000274.1 GI:18623353  
VERSION JP 2000279200-A/12  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Lynen,J.M. and Gorman,K.M.  
TITLE Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof  
PATENT: JP 2000279200-A 12 10-OCT-2000;  
ORWHO CLINICAL DIAGNOSTICS INC

COMMENT  
JOURNAL  
OS Artificial Sequence  
PN JP 2000279200-A/12  
PD 10-OCT-2000  
PE 02-FEB-2000 JP 2000030237  
PR 03-FEB-1999 US 60/118498  
PT KEVIN M GORMAN, DAVID R PATERSON, JEFFREY M LYNNEN, KEVIN SON PC  
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PD 10-OCT-2000  
PF 03-FEB-2000 JP 2000032656  
PR 03-FEB-1999 US 60/118497  
PI JEFFREY M LYNNEN, KEVIN M GORMAN  
PC C1201/68, C12N15/09/(C12N15/09, C12R1.92), C12N15/00, (C12N15/00, C12R1.92)  
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Db 4 TTGGCGACCCCAACTACTC 23

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DEFINITION Sequence 68 from Patent EP1331267.  
ACCESSION AX803705  
VERSION AX803705.1 GI:38502247  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Frank,B.L., Goodchild,J., Hamlin,H.A., Kulkuskie,R.E.,  
Roberts,P.C., Roberts,N.A., Walther,D.M. and Wolfe,J.L.  
TITLE Oligonucleotides specific for Hepatitis C Virus  
JOURNAL Patent: EP 1331267-A 68 30-JUL-2003;  
HYBRIDON, INC. (US)  
FEATURES  
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DEFINITION Sequence 74 from Patent EP1331267.  
ACCESSION AX803711  
VERSION AX803711.1 GI:38502253  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Frank,B.L., Goodchild,J., Hamlin,H.A., Kulkuskie,R.E.,  
Roberts,P.C., Roberts,N.A., Walther,D.M. and Wolfe,J.L.  
TITLE Oligonucleotides specific for Hepatitis C Virus  
JOURNAL Patent: EP 1331267-A 74 30-JUL-2003;

FEATURES HYBRIDON, INC. (US)  
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LOCUS Nucleic acids for grouping hepatitis C virus and method for group  
DEFINITION ing hepatitis C virus using the same.  
ACCESSION BD183048  
VERSION BD183048.1 GI:31875248  
KEYWORDS JP 2002345467-A/20.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 29)  
AUTHORS Mukai, M., Teunoda, K. and Hikiji, K.  
TITLE Nucleic acids for grouping hepatitis C virus and method for group  
JOURNAL ing hepatitis C virus using the same  
PATENT: JP 2002345467-A 20 03-DEC-2002;  
SRL INC  
COMMENT OS Artificial Sequence  
PN JP 2002345467-A/20  
PD 03-DEC-2002  
PF 17-APR-2001 JP 2001118810  
PI MASAKAZU MUKAI, KOICHI TSUNODA, KAZUMASA HIKIJI PC  
C12N15/09, C12Q1/68, G01N33/53, G01N33/566, C12N15/00 CC Nucleic Acid  
Used as signal-amplifying probe which hybridizes CC  
with a  
CC region in HCV 5'-UTR region  
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ORIGIN  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14  
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LOCUS Sequence 50 from patent US 5747244.  
DEFINITION AR004396  
ACCESSION AR004396  
VERSION AR004396.1 GI:3965275  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 33)

AUTHORS Sheridan, P., Chang, C.-A., Running, J. and Urdea, M.S.  
TITLE Nucleic acid probes immobilized on polystyrene surfaces  
JOURNAL Patent: US 5747244-A 50 05-MAY-1998;  
FEATURES Location/Qualifiers  
source 1..33 /organism="unknown"  
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ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
|||||  
10 TTCCGACCCCAACTACTC 29

RESULT 15  
AR064935 33 bp DNA linear PAT 29-SEP-1999  
LOCUS Sequence 60 from patent US 5849481.  
DEFINITION AR064935  
ACCESSION AR064935  
VERSION AR064935.1 GI:5995151  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Urdea, M.S., Horn, T., Chang, C.-A., Warner, B. and Fultz, T.J.  
TITLE Nucleic acid hybridization assays employing large comb-type  
JOURNAL branched polynucleotides  
PATENT: US 5849481-A 60 15-DEC-1998;  
FEATURES Location/Qualifiers  
source 1..33 /organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
|||||  
10 TTCCGACCCCAACTACTC 29

RESULT 16  
AR097188 33 bp DNA linear PAT 14-FEB-2001  
LOCUS Sequence 126 from patent US 6071693.  
DEFINITION AR097188  
ACCESSION AR097188  
VERSION AR097188.1 GI:12805918  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Cha, T.-A., Beall, E., Irvine, B., Kolberg, J. and Urdea, M.S.  
TITLE HCV genomic sequences for diagnostics and therapeutics  
JOURNAL Patent: US 6071693-A 126 06-JUN-2000;  
FEATURES Location/Qualifiers  
source 1..33 /organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20

Db 10 TTCCGACCCCAACTACTC 29

RESULT 17  
LOCUS ARI130686 33 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 126 from patent US 6190864.  
ACCESSION ARI130686  
VERSION ARI130686.1 GI:14119011  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS Cha,T.-A., Beall,E., Irvine,B., Kolberg,J. and Urdea,M.S.  
TITLE HCV genomic sequences for diagnostics and therapeutics  
JOURNAL Patent: US 6190864-A 126 20-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..33  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
Db 10 TTCCGACCCCAACTACTC 29

RESULT 18  
LOCUS ARI172035 33 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 126 from patent US 6297370.  
ACCESSION ARI172035  
VERSION ARI172035.1 GI:17910985  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS Cha,T.-A., Beall,E., Irvine,B., Kolberg,J. and Urdea,M.S.  
TITLE HCV genomic sequences for diagnostics and therapeutics  
JOURNAL Patent: US 6297370-A 126 02-OCT-2001;  
FEATURES Location/Qualifiers  
source 1..33  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
Db 10 TTCCGACCCCAACTACTC 29

RESULT 19  
LOCUS BDI89152 33 bp DNA linear PAT 17-JUL-2003  
DEFINITION HCV Genomic Sequences For Diagnostics And Therapeutics.  
ACCESSION BDI89152  
VERSION BDI89152.1 GI:32998891  
KEYWORDS JP 2003009891-A/126.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 33)

Db 10 TTCCGACCCCAACTACTC 29

Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
Db 10 TTCCGACCCCAACTACTC 29

RESULT 20  
LOCUS BDI89299 33 bp DNA linear PAT 17-JUL-2003  
DEFINITION HCV Genomic Sequences For Diagnostics And Therapeutics.  
ACCESSION BDI89299  
VERSION BDI89299.1 GI:32999038  
KEYWORDS JP 2003009892-A/126.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Adair,M.S., Cha,T., Irvine,B., Kolberg,J. and Beal,E.  
TITLE HCV Genomic Sequences For Diagnostics And Therapeutics  
JOURNAL Patent: JP 2003009892-A 126 14-JAN-2003;  
COMMENT Chiron Corporation  
OS Artificial Sequence  
PN JP 2003009892-A/126  
PD 14-JAN-2003  
PF 10-MAY-2002 JP 2002134999  
PR 08-MAY-1991 US 697326  
PI Michael S Adair, tai-ann cha, bruce irvine, janice kolberg, eileen beal  
PI beal  
CC synthetic construct  
FH Key Location/Qualifiers.  
FEATURES Location/Qualifiers  
source 1..33  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
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Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
Db 10 TTCCGACCCCAACTACTC 29

RESULT 21  
LOCUS BDI89446 33 bp DNA linear PAT 17-JUL-2003



DEFINITION HCV Genomic Sequences For Diagnostics And Therapeutics.  
ACCESSION BD189446  
VERSION BD189446.1 GI:32899185  
KEYWORDS JP 2003009893-A/126.  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Adair,M.S., Cha,T., Beal,E., Irvine,B. and Kolberg,J.  
TITLE HCV Genomic Sequences For Diagnostics And Therapeutics  
JOURNAL Patent: JP 2003009893-A 126 14-JAN-2003;  
COMMENT Chiron Corporation  
OS Artificial Sequence  
PN JP 2003009893-A/126  
PD 14-JAN-2003  
PF 10-MAY-2002 JP 2002135000  
PR 08-MAY-1991 US 697326  
PI Michael S Adair, tai-ann cha, eleven beal, bruce irvine, janice  
PI kolberg  
CC synthetic construct  
FH Key Location/Qualifiers.  
FEATURES  
source Location/Qualifiers  
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/mol\_type="genomic DNA"  
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ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGGACCCCAACTACTC 20  
Db 10 TTCCGGACCCCAACTACTC 29  
RESULT 22  
LOCUS 182871 33 bp DNA linear PAT 10-JUN-1998  
DEFINITION Sequence 50 from patent US 5712383.  
ACCESSION 182871  
VERSION 182871.1 GI:3211168  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Sheridan,P., Chang,C.-A., Running,J. and Urdea,M.S.  
TITLE Process for immobilizing nucleic acid probes on polystyrene  
surfaces  
JOURNAL Patent: US 5712383-A 50 27-JAN-1998;  
FEATURES  
source Location/Qualifiers  
1..33  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGGACCCCAACTACTC 20  
Db 10 TTCCGGACCCCAACTACTC 29  
RESULT 23  
LOCUS AR153179 40 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 181 from patent US 6235480.  
ACCESSION AR153179  
VERSION AR153179.1 GI:15120711

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 40)  
AUTHORS Shultz,J.William., Lewis,M.K., Leippe,D., Mandrekar,M., Kephart,D.,  
Rhodes,R.Byron., Andrews,C.Ann., Hartnett,J.Robert., Gu,T.,  
Olson,R.J., Wood,K.V. and Welch,R.  
TITLE Detection of nucleic acid hybrids  
JOURNAL Patent: US 6235480-A 181 22-MAY-2001;  
FEATURES  
source Location/Qualifiers  
1..40  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGGACCCCAACTACTC 20  
Db 29 TTCCGGACCCCAACTACTC 10  
RESULT 24  
LOCUS AR163348 40 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 43 from patent US 6270974.  
ACCESSION AR163348  
VERSION AR163348.1 GI:16233929  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 40)  
AUTHORS Shultz,J.William., Lewis,M.K., Leippe,D., Mandrekar,M., Kephart,D.,  
Rhodes,R.Byron., Andrews,C.Ann., Hartnett,J.Robert., Gu,T.,  
Olson,R.J., Wood,K.V. and Welch,R.  
TITLE Exogenous nucleic acid detection  
JOURNAL Patent: US 6270974-A 43 07-AUG-2001;  
FEATURES  
source Location/Qualifiers  
1..40  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 20; DB 6; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.16;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGGACCCCAACTACTC 20  
Db 29 TTCCGGACCCCAACTACTC 10  
RESULT 25  
LOCUS BD242950 40 bp DNA linear PAT 17-JUL-2003  
DEFINITION Method for assaying the presence of target nucleic acid sequence  
and its application.  
ACCESSION BD242950  
VERSION BD242950.1 GI:33052720  
KEYWORDS JP 2002536981-A/43.  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 40)  
AUTHORS Shultz,J.W., Lewis,M.K., Leippe,D., Mandrekar,M., Kephart,D.,  
Rhodes,R.B., Andrews,C.A., Hartnett,J.R., Gu,T., Olson,R.J.,  
Wood,K.V. and Welch,R.  
TITLE Method for assaying the presence of target nucleic acid sequence  
and its application

JOURNAL Patent: JP 2002536981-A 43 05-NOV-2002;  
 PROMEGA CORP  
 COMMENT Hepatitis virus (hepatitis C virus)  
 OS JP 2002536981-A/43  
 PN 05-NOV-2002  
 PD 18-FEB-2000 JP 2000599902  
 PR 18-FEB-1999 US 09/252436,21-JUL-1999 US 09/358972 PR  
 27-SEP-1999 US 09/406147  
 P1 JOHN W SHULTZ,MARTIN K LEWIS,DONNA LEIPPE,MICHELLE MANDREKAR,  
 DANIEL KEPHART,RICHARD B RHODES,CHRISTINE ANN ANDREWS,JAMES R  
 HARTNETT,  
 P1 TRENT GU,RYAN J OLSON,KEITH V WOOD ROY WELCH  
 PC C1201/68,C12N15/09,C12Q1/48,G01N21/78,G01N33/02,G01N33/483, PC  
 G01N33/53  
 CC Method for assaying the presence of target nucleic acid CC  
 CC sequence and its  
 CC application  
 CC Key Location/Qualifiers  
 FT source 1..40 /organism='Hepatitis virus (hepatitis C FT  
 FT virus)'  
 FEATURES Location/Qualifiers  
 1..40 /organism='unidentified'  
 /mol\_type='genomic DNA'  
 /db\_xref='taxon:32644'  
 ORIGIN  
 Query Match 100.0%; Score 20; DB 6; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 0.16;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGGGACCCCAACTACTC 20  
 Db 29 TTGGGACCCCAACTACTC 10  
 RESULT 26 40 bp DNA linear PAT 08-OCT-2004  
 AR533156  
 LOCUS Sequence 181 from patent US 6730479.  
 DEFINITION AR533156  
 ACCESSION AR533156  
 VERSION AR533156.1 GI:53922709  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 1 (bases 1 to 40)  
 SHULTZ,J.W., LEWIS,M.K., LEIPPE,D., MANDREKAR,M., KEPHART,D.,  
 RHODES,R.B., ANDREWS,C.A., HARTNETT,J.R., GU,T., OLSON,R.J.,  
 WOOD,K.V. and WELCH,R.  
 TITLE Detection of nucleic acid hybrids  
 JOURNAL Patent: US 6730479-A 181 04-MAY-2004;  
 FEATURES Location/Qualifiers  
 1..40 /organism='unknown'  
 /mol\_type='genomic DNA'  
 ORIGIN  
 Query Match 100.0%; Score 20; DB 6; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 0.16;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGGGACCCCAACTACTC 20  
 Db 29 TTGGGACCCCAACTACTC 10  
 RESULT 27 46 bp DNA linear PAT 07-OCT-1997  
 I44581  
 LOCUS Sequence 10 from patent US 5635352.  
 DEFINITION

ACCESSION I44581  
 VERSION I44581.1 GI:2469294  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 1 (bases 1 to 46)  
 URDEA,M.S., FULTZ,T., WARNER,B.D. and COLLINS,M.  
 TITLE Solution phase nucleic acid sandwich assays having reduced  
 background noise  
 JOURNAL Patent: US 5635352-A 10 03-JUN-1997;  
 FEATURES Location/Qualifiers  
 1..46 /organism='unknown'  
 /mol\_type='unassigned DNA'  
 ORIGIN  
 Query Match 100.0%; Score 20; DB 6; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 0.16;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGGGACCCCAACTACTC 20  
 Db 10 TTGGGACCCCAACTACTC 29  
 RESULT 28 46 bp DNA linear PAT 03-APR-1998  
 I70986  
 LOCUS Sequence 10 from patent US 5681697.  
 DEFINITION I70986  
 ACCESSION I70986  
 VERSION I70986.1 GI:3007121  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 1 (bases 1 to 46)  
 URDEA,M.S., FULTZ,T., WARNER,B.D. and COLLINS,M.  
 TITLE Solution phase nucleic acid sandwich assays having reduced  
 background noise and kits therefor  
 JOURNAL Patent: US 5681697-A 10 28-OCT-1997;  
 FEATURES Location/Qualifiers  
 1..46 /organism='unknown'  
 /mol\_type='unassigned DNA'  
 ORIGIN  
 Query Match 100.0%; Score 20; DB 6; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 0.16;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGGGACCCCAACTACTC 20  
 Db 10 TTGGGACCCCAACTACTC 29  
 RESULT 29 50 bp DNA linear PAT 27-MAY-2002  
 AX397948  
 LOCUS Sequence 26 from Patent WO0220054.  
 DEFINITION AX397948  
 ACCESSION AX397948  
 VERSION AX397948.1 GI:21260805  
 KEYWORDS  
 SOURCE Hepatitis C virus  
 ORGANISM Hepatitis C virus  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 Hepacivirus.  
 1  
 THOMAS,H.C., TAYLOR-ROBINSON,S.D., KARAYIANNIS,P. and FORTON,D.M.  
 TITLE Methods of treatment and diagnosis of HCV infection in CNS based on  
 magnetic resonance spectroscopy  
 JOURNAL Patent: WO 0220054-A 26 14-MAR-2002;  
 IMPERIAL COLLEGE OF SCIENCE, TECHNOLOGY AND MEDICINE (GB)

FEATURES	source	grouping
CC	hepatitis C virus using the same	
PH	key	Location/Qualifiers
FT	source	1..57
		/organism='Hepatitis virus (hepatitis C FT virus)'
	location/Qualifiers	
	1..57	
	/organism="unidentified"	
	/mol_type="genomic DNA"	
	/db_xref="taxon:32644"	
ORIGIN		
Query Match	100.0%; Score 20; DB 6; Length 57;	
Best Local Similarity	100.0%; Pred. No. 0.16;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 TTGCGACCCGACACTACTC 20	
Db	46 TTGCGACCCGACACTACTC 27	
RESULT 32		
AX616614/c	60 bp	Linear PAT 20-FEB-2003
LOCUS	AX616614	
DEFINITION	Sequence 1 from Patent EP1262566.	
ACCESSION	AX616614	
VERSION	AX616614.1 GI:28447591	
KEYWORDS		
SOURCE	Hepatitis C virus	
ORGANISM	Hepatitis C virus	
REFERENCE	1 Amorese,D.A., Shannon,K.W., Collins,P.J. and Wolber,P.K.	
AUTHORS	Composite polynucleotide arrays	
TITLE	Patent: EP 1262566-A 1 04-DEC-2002;	
JOURNAL	Agilent Technologies, Inc. (US)	
FEATURES	Location/Qualifiers	
source	1..60	
	/organism="Hepatitis C virus"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:11103"	
ORIGIN		
Query Match	100.0%; Score 20; DB 6; Length 60;	
Best Local Similarity	100.0%; Pred. No. 0.16;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 TTGCGACCCGACACTACTC 20	
Db	24 TTGCGACCCGACACTACTC 5	
RESULT 33		
AR338416	108 bp	DNA linear PAT 17-AUG-2003
LOCUS	AR338416	
DEFINITION	Sequence 31 from patent US 6569647.	
ACCESSION	AR338416	
VERSION	AR338416.1 GI:33725188	
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	1 (bases 1 to 108)	
AUTHORS	Zhang,D.Y., Brandwein,M. and Heufl,T.C.H.	
TITLE	Nucleic acid amplification method: ramification-extension	
JOURNAL	amplification method (RAM)	
FEATURES	Patent: US 6569647-A 31 27-MAY-2003;	
	Location/Qualifiers	
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	/organism="unknown"	
	/mol_type="genomic DNA"	

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ORIGIN		
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Best Local Similarity	100.0%; Pred. No. 0.15;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	1 TTGCGACCCACACTACTC 20       4 TTGCGACCCACACTACTC 23	
Db		
RESULT 37		
BD183033/c		
LOCUS	126 bp	DNA linear PAT 17-JUN-2003
DEFINITION	Nucleic acids for grouping hepatitis C virus and method for group	
ACCESSION	BD183033	
VERSION	BD183033.1 GI:31875233	
KEYWORDS	JF 2002345467-A/5.	
SOURCE	unidentified	
ORGANISM	unidentified	
FEATURES		
source	Location/Qualifiers 1..108 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"	
ORIGIN		
Query Match	100.0%; Score 20; DB 6; Length 108;	
Best Local Similarity	100.0%; Pred. No. 0.15;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	1 TTGCGACCCACACTACTC 20       4 TTGCGACCCACACTACTC 23	
Db		
RESULT 36		
BD083967		
LOCUS	108 bp	DNA linear PAT 27-AUG-2002
DEFINITION	Nucleic acid amplification method: Hybridization signal	
ACCESION	BD083967	
VERSION	BD083967.1 GI:22629577	
KEYWORDS	JP 2001521373-A/31.	
SOURCE	unidentified	
ORGANISM	unclassified.	
REFERENCE	1 (bases 1 to 108) Zhang,D.Y. and Brandwein,M. Nucleic acid amplification method: Hybridization signal	
AUTHORS	Patent: JP 2001521373-A 31 06-NOV-2001; DAVID Y ZHANG,MARGARET BRANDWEIN	
TITLE	OS Unidentified	
JOURNAL	PN JP 2001521373-A/31	
COMMENT	PD 06-NOV-2001 PF 30-JUL-1997 JP 1998509121 PR 31-JUL-1996 US 08/690495 PI DAVID Y ZHANG,MARGARET BRANDWEIN PC C12Q1/68,C12Q1/70,C12P19/34,C07H21/02,C07H21/04 CC Strandedness: Single; CC Topology: Linear; CC Nucleic acid amplification method: Hybridization signal CC amplification CC method (HSAM)	
FT	key Location/Qualifiers 1..108 /organism='Unidentified'. source	



AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1.139

/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H071"  
/db\_xref="taxon:11103"  
/clone="I1"  
1.139  
misc\_feature  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
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Db 116 TTGGGACCCCAACTACTC 97

RESULT 41  
AF282634/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H071 clone II 5' non-coding region  
DEFINITION  
ACCESSION AF282634  
VERSION AF282634.1 GI:10764497  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1.139

/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H071"  
/db\_xref="taxon:11103"  
/clone="I1"  
1.139  
misc\_feature  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 116 TTGGGACCCCAACTACTC 97

RESULT 42  
AF282635/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS

DEFINITION Hepatitis C virus isolate H075 clone I 5' non-coding region  
sequence.  
ACCESSION AF282635  
VERSION AF282635.1 GI:10764498  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1.139

/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H075"  
/db\_xref="taxon:11103"  
/clone="I1"  
1.139  
misc\_feature  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 116 TTGGGACCCCAACTACTC 97

RESULT 43  
AF282637/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H075 clone III 5' non-coding region  
DEFINITION  
ACCESSION AF282637  
VERSION AF282637.1 GI:10764500  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1.139

/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H075"  
/db\_xref="taxon:11103"

misc\_feature 1..139  
/note="5' non-coding region"  
ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
|||||  
116 TTCCGACCCCAACTACTC 97

RESULT 44  
AF282638/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H075 clone IV 5' non-coding region  
DEFINITION  
AF282638  
AF282638.1 GI:10764501  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)

MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory, Central Public Health Laboratory, 61 Colindale Avenue, London NW9 5HT, UK

FEATURES  
source 1..139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H858"  
/db\_xref="taxon:11103"  
/clone="I1"  
1..139  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
|||||  
116 TTCCGACCCCAACTACTC 97

RESULT 45  
AF282639/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H058 clone I 5' non-coding region  
DEFINITION  
AF282639  
AF282639.1 GI:10764502  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.

TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory, Central Public Health Laboratory, 61 Colindale Avenue, London NW9 5HT, UK

FEATURES  
source 1..139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H858"  
/db\_xref="taxon:11103"  
/clone="I1"  
1..139  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
|||||  
116 TTCCGACCCCAACTACTC 97

RESULT 46  
AF282640/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H858 clone II 5' non-coding region  
DEFINITION  
AF282640  
AF282640.1 GI:10764503  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)

MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory, Central Public Health Laboratory, 61 Colindale Avenue, London NW9 5HT, UK

FEATURES  
source 1..139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H858"  
/db\_xref="taxon:11103"  
/clone="I1"  
1..139  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
|||||  
116 TTCCGACCCCAACTACTC 97

Db 116 TTGGGACCCCAACTACTC 97

RESULT 47  
AF282641/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H858 clone III 5' non-coding region  
DEFINITION  
AF282641  
ACCESSION AF282641.1 GI:10764504  
VERSION  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE  
AUTHORS 1 (bases 1 to 139)  
TITLE Harris, K.A. and Teo, C.G.  
JOURNAL Diversity of hepatitis C virus quasispecies evaluated by denaturing  
MEDLINE gradient gel electrophoresis  
20579439 Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
PUBMED 11139197

REFERENCE  
AUTHORS 2 (bases 1 to 139)  
TITLE Harris, K.A. and Teo, C.G.  
JOURNAL Direct Submission  
Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source 1. .139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
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/db\_xref="taxon:11103"  
/clone="I11"  
1. .139  
/note="5' non-coding region"

ORIGIN  
misc\_feature  
1. .139  
/note="5' non-coding region"

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15; 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||  
116 TTGGGACCCCAACTACTC 97

Db 116 TTGGGACCCCAACTACTC 97

RESULT 48  
AF282642/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H865 clone I 5' non-coding region  
DEFINITION  
AF282642  
ACCESSION AF282642  
VERSION AF282642.1 GI:10764505  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE  
AUTHORS 1 (bases 1 to 139)  
TITLE Harris, K.A. and Teo, C.G.  
JOURNAL Diversity of hepatitis C virus quasispecies evaluated by denaturing  
MEDLINE gradient gel electrophoresis  
20579439 Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
PUBMED 11139197

REFERENCE  
AUTHORS 2 (bases 1 to 139)  
TITLE Harris, K.A. and Teo, C.G.  
JOURNAL Direct Submission  
Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source 1. .139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H865"  
/db\_xref="taxon:11103"  
/clone="I1"  
1. .139  
/note="5' non-coding region"

ORIGIN  
misc\_feature  
1. .139  
/note="5' non-coding region"

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15; 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||  
116 TTGGGACCCCAACTACTC 97

Db 116 TTGGGACCCCAACTACTC 97

RESULT 49  
AF282643/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H865 clone II 5' non-coding region  
DEFINITION  
AF282643  
ACCESSION AF282643  
VERSION AF282643.1 GI:10764506  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE  
AUTHORS 1 (bases 1 to 139)  
TITLE Harris, K.A. and Teo, C.G.  
JOURNAL Diversity of hepatitis C virus quasispecies evaluated by denaturing  
MEDLINE gradient gel electrophoresis  
20579439 Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
PUBMED 11139197

REFERENCE  
AUTHORS 2 (bases 1 to 139)  
TITLE Harris, K.A. and Teo, C.G.  
JOURNAL Direct Submission  
Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source 1. .139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H865"  
/db\_xref="taxon:11103"  
/clone="I1"  
1. .139  
/note="5' non-coding region"

ORIGIN  
misc\_feature  
1. .139  
/note="5' non-coding region"

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15; 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||  
116 TTGGGACCCCAACTACTC 97

Db 116 TTGGGACCCCAACTACTC 97

RESULT 50  
AF282644/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H865 clone IV 5' non-coding region  
DEFINITION  
AF282644  
ACCESSION AF282644  
VERSION AF282644.1 GI:10764507  
KEYWORDS



SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1..139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H865"  
/db\_xref="taxon:11103"  
/clone="IV"  
1..139  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGGACCCCAACTACTC 20  
|||||  
Db 116 TTCGGACCCCAACTACTC 97

RESULT 51  
AF282645/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H865 clone V 5' non-coding region  
DEFINITION  
sequence.  
AF282645  
ACCESSION AF282645.1 GI:10764508  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1..139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H865"  
/db\_xref="taxon:11103"  
/clone="V"  
1..139  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGGACCCCAACTACTC 20  
|||||  
Db 116 TTCGGACCCCAACTACTC 97

RESULT 52  
AF282646/c 139 bp RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate H865 clone VI 5' non-coding region  
DEFINITION  
sequence.  
AF282646  
ACCESSION AF282646.1 GI:10764509  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1..139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="H865"  
/db\_xref="taxon:11103"  
/clone="VI"  
1..139  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGGACCCCAACTACTC 20  
|||||  
Db 116 TTCGGACCCCAACTACTC 97

RESULT 53  
AY003921/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD244 clone I 5' non-coding region,  
partial sequence.  
AY003921  
ACCESSION AY003921.1 GI:9858202  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

misc\_feature  
1..139  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGGACCCCAACTACTC 20  
|||||  
Db 116 TTCGGACCCCAACTACTC 97

RESULT 53  
AY003921/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD244 clone I 5' non-coding region,  
partial sequence.  
AY003921  
ACCESSION AY003921.1 GI:9858202  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1.139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="BD244"  
/db\_xref="taxon:11103"  
/clone="I"  
/note="genotype: 1a"  
/note="5' non-coding region"

ORIGIN  
misc\_feature  
100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred.No.0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred.No.0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 116 TTGGGACCCACACTACTC 20  
116 TTGGGACCCACACTACTC 97

RESULT 54  
LOCUS AY003922/c 139 bp ss-RNA linear VRL 01-MAR-2001  
DEFINITION Hepatitis C virus isolate BD244 clone III 5' non-coding region,  
partial sequence.  
ACCESSION AY003922  
VERSION AY003922.1 GI:9858203  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1.139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="BD244"  
/db\_xref="taxon:11103"  
/clone="II"  
/note="genotype: 1a"  
/note="5' non-coding region"

ORIGIN  
misc\_feature  
100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred.No.0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred.No.0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 116 TTGGGACCCACACTACTC 20  
116 TTGGGACCCACACTACTC 97

RESULT 55  
LOCUS AY003923/c 139 bp ss-RNA linear VRL 01-MAR-2001  
DEFINITION Hepatitis C virus isolate BD244 clone III 5' non-coding region,  
partial sequence.  
ACCESSION AY003923  
VERSION AY003923.1 GI:9858204  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1.139  
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/mol\_type="genomic RNA"  
/isolate="BD244"  
/db\_xref="taxon:11103"  
/clone="III"  
/note="genotype: 1a"  
/note="5' non-coding region"

ORIGIN  
misc\_feature  
100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred.No.0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred.No.0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 116 TTGGGACCCACACTACTC 20  
116 TTGGGACCCACACTACTC 97

RESULT 56  
LOCUS AY003924/c 139 bp ss-RNA linear VRL 01-MAR-2001  
DEFINITION Hepatitis C virus isolate BD244 clone IV 5' non-coding region,  
partial sequence.  
ACCESSION AY003924  
VERSION AY003924.1 GI:9858205  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1.139

misc\_feature  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="BD244"  
/db\_xref="taxon:11103"  
/clone="IV"  
/note="genotype: 1a"  
<1..>139  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCACACTACTC 20  
|||||  
116 TTGGGACCCACACTACTC 97

Db

RESULT 57  
AY003925/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS  
DEFINITION Hepatitis C virus isolate BD244 clone V 5' non-coding region,  
partial sequence.  
ACCESSION AY003925  
VERSION AY003925.1 GI:9858206  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
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/note="genotype: 1a"  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCACACTACTC 20  
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116 TTGGGACCCACACTACTC 97

Db

RESULT 58  
AY003928/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS  
DEFINITION Hepatitis C virus isolate BD244 clone VIII 5' non-coding region,  
partial sequence.  
ACCESSION AY003928  
VERSION AY003928.1 GI:9858209  
KEYWORDS

SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source  
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/db\_xref="taxon:11103"  
/clone="VIII"  
/note="genotype: 1a"  
/note="5' non-coding region"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCACACTACTC 20  
|||||  
116 TTGGGACCCACACTACTC 97

Db

RESULT 59  
AY003929/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS  
DEFINITION Hepatitis C virus isolate BD259 clone I 5' non-coding region,  
partial sequence.  
ACCESSION AY003929  
VERSION AY003929.1 GI:9858210  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source  
1..139  
Location/Qualifiers  
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/mol\_type="genomic RNA"  
/isolate="BD259"  
/db\_xref="taxon:11103"  
/clone="I"  
/note="genotype: 1b"  
/note="5' non-coding region"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCACACTACTC 20  
|||||  
116 TTGGGACCCACACTACTC 97

Db

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGCGACCCACACTACTC 20  
116 TTGGCGACCCACACTACTC 97

Db

RESULT 60  
AY003930/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS  
DEFINITION Hepatitis C virus isolate BD259 clone II 5' non-coding region,  
partial sequence.  
ACCESSION AY003930  
VERSION AY003930.1 GI:9858211  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source 1.139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="BD259"  
/db\_xref="taxon:11103"  
/clone="I1"  
/note="genotype: 1b"  
<1..>139  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGCGACCCACACTACTC 20  
116 TTGGCGACCCACACTACTC 97

Db

RESULT 61  
AY003932 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS  
DEFINITION Hepatitis C virus isolate BD268 clone I 5' non-coding region,  
partial sequence.  
ACCESSION AY003932  
VERSION AY003932.1 GI:9858213  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis

JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source 1.139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="BD268"  
/db\_xref="taxon:11103"  
/clone="I1"  
/note="genotype: 1b"  
<1..>139  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGCGACCCACACTACTC 20  
116 TTGGCGACCCACACTACTC 97

Db

RESULT 62  
AY003933/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS  
DEFINITION Hepatitis C virus isolate BD268 clone II 5' non-coding region,  
partial sequence.  
ACCESSION AY003933  
VERSION AY003933.1 GI:9858214  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source 1.139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="BD268"  
/db\_xref="taxon:11103"  
/clone="I1"  
/note="genotype: 1b"  
<1..>139  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGCGACCCACACTACTC 20  
116 TTGGCGACCCACACTACTC 97

Db

Db 116 TTGGGACCCCAACTACTC 97

RESULT 63  
AY003934/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD268 clone III 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003934  
VERSION AY003934.1 GI:9858215  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source 1..139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="BD268"  
/db\_xref="taxon:11103"  
/clone="I11"  
/note="genotype: 1b"  
misc\_feature <1..>139  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
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Db 116 TTGGGACCCCAACTACTC 97

RESULT 64  
AY003935/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD268 clone IV 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003935  
VERSION AY003935.1 GI:9858216  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

5HT, UK

FEATURES  
source 1..139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
/isolate="BD268"  
/db\_xref="taxon:11103"  
/clone="I11"  
/note="genotype: 1b"  
misc\_feature <1..>139  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 116 TTGGGACCCCAACTACTC 97

RESULT 65  
AY003936/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD268 clone V 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003936  
VERSION AY003936.1 GI:9858217  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
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/isolate="BD268"  
/db\_xref="taxon:11103"  
/clone="V"  
/note="genotype: 1b"  
misc\_feature <1..>139  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 116 TTGGGACCCCAACTACTC 97

RESULT 66  
AY003937/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD268 clone VI 5' non-coding region,  
DEFINITION partial sequence.

ACCESSION AY003937  
VERSION AY003937.1 GI:9858218  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory, Central Public Health Laboratory, 61 Colindale Avenue, London NW9 5HT, UK

FEATURES  
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<1..>139  
/note="5' non-coding region"

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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 116 TTGGGACCCCACTACTC 97

RESULT 67  
AY003938 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD268 clone VII 5' non-coding region,  
DEFINITION Partial sequence.  
ACCESSION AY003938  
VERSION AY003938.1 GI:9858219  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory, Central Public Health Laboratory, 61 Colindale Avenue, London NW9 5HT, UK

FEATURES  
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<1..>139  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 116 TTGGGACCCCACTACTC 97

RESULT 68  
AY003939 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD424 clone I 5' non-coding region,  
DEFINITION Partial sequence.  
ACCESSION AY003939  
VERSION AY003939.1 GI:9858220  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory, Central Public Health Laboratory, 61 Colindale Avenue, London NW9 5HT, UK

FEATURES  
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/db\_xref="taxon:11103"  
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/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 116 TTGGGACCCCACTACTC 97

RESULT 69  
AY003940 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD424 clone II 5' non-coding region,  
DEFINITION Partial sequence.  
ACCESSION AY003940  
VERSION AY003940.1 GI:9858221  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1 (bases 1 to 139)



TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source  
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ORIGIN  
misc\_feature

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 116 TTGGGACCCCAACTACTC 97

RESULT 73  
AY003944/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate BD426 clone I 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003944  
VERSION AY003944.1 GI:9858225  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source  
1. .139  
/organism="Hepatitis C virus"  
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ORIGIN  
misc\_feature

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 116 TTGGGACCCCAACTACTC 97

LOCUS AY003945 139 bp ss-RNA linear VRL 01-MAR-2001  
DEFINITION Hepatitis C virus isolate BD426 clone II 5' non-coding region,  
partial sequence.  
ACCESSION AY003945  
VERSION AY003945.1 GI:9858226  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source  
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/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"

ORIGIN  
misc\_feature

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 116 TTGGGACCCCAACTACTC 97

RESULT 75  
AY003980/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU189 clone I 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003980  
VERSION AY003980.1 GI:9858294  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source  
1. .139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"



/isolate="IDU189"  
/db\_xref="taxon:11103"  
/clone="I"  
/note="genotype: 1a"  
<1..>139  
/note="5' non-coding region"

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
|||||  
116 TTGCGACCCCAACTACTC 97

Db 116 TTGCGACCCCAACTACTC 97

RESULT 76  
AY003981/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU189 clone II 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003981  
VERSION AY003981.1 GI:9858295  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepatitis C virus  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
1..139  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
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/clone="I"  
/note="genotype: 1a"  
<1..>139  
/note="5' non-coding region"

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Query Match 100.0%; Score 20; DB 14; Length 139;  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
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116 TTGCGACCCCAACTACTC 97

Db 116 TTGCGACCCCAACTACTC 97

RESULT 77  
AY003982 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU189 clone III 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003982  
VERSION AY003982.1 GI:9858296  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepatitis C virus  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
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REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
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/note="5' non-coding region"

ORIGIN

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepatitis C virus  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
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/isolate="IDU189"  
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/clone="I"  
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/note="5' non-coding region"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
|||||  
116 TTGCGACCCCAACTACTC 97

Db 116 TTGCGACCCCAACTACTC 97

RESULT 78  
AY003983/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU189 clone IV 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003983  
VERSION AY003983.1 GI:9858297  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepatitis C virus  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source Location/Qualifiers  
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/db\_xref="taxon:11103"  
/clone="I"  
/note="genotype: 1a"  
<1..>139  
/note="5' non-coding region"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCAGCCCAACACTACTC 20  
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116 TTGGCAGCCCAACACTACTC 97

Db

RESULT 79  
AY003984/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU189 clone V 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003984  
VERSION AY003984.1 GI:9858298  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

RESULT 81  
AY003986/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU189 clone V 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003986  
VERSION AY003986.1 GI:9858300  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

FEATURES  
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/note="5' non-coding region"

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCAGCCCAACACTACTC 20  
|||||  
116 TTGGCAGCCCAACACTACTC 97

Db

RESULT 80  
AY003985/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU189 clone VI 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003985  
VERSION AY003985.1 GI:9858299  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439

PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
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/mol\_type="genomic RNA"  
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misc\_feature <1..>139  
/note="5' non-coding region"

ORIGIN  
Query Match 100.0%; Score 20; DB 14; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCAGCCCAACACTACTC 20  
|||||  
116 TTGGCAGCCCAACACTACTC 97

Db

RESULT 81  
AY003986/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU189 clone VII 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003986  
VERSION AY003986.1 GI:9858300  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris,K.A. and Teo,C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 11139197

FEATURES  
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QY 1 TTGGCAGCCCAACACTACTC 20  
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116 TTGGCAGCCCAACACTACTC 97

Db

RESULT 82  
AY003987/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU191 clone VII 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003987  
VERSION AY003987.1 GI:9858301  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
20579439  
PUBMED 11139197  
2 (bases 1 to 139)  
REFERENCE Harris, K.A. and Teo, C.G.  
AUTHORS Direct Submission  
TITLE Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
JOURNAL Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK  
FEATURES  
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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGACCCCAACTACTC 20  
Db 116 TTCCGACCCCAACTACTC 97  
RESULT 83  
AY003989/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU191 clone I 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003989  
VERSION AY003989.1 GI:9858303  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
20579439  
PUBMED 11139197  
2 (bases 1 to 139)  
REFERENCE Harris, K.A. and Teo, C.G.  
AUTHORS Direct Submission  
TITLE Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
JOURNAL Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK  
FEATURES  
Location/Qualifiers  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGACCCCAACTACTC 20  
Db 116 TTCCGACCCCAACTACTC 97  
RESULT 84  
AY003990/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU191 clone II 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003990  
VERSION AY003990.1 GI:9858304  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
20579439  
PUBMED 11139197  
2 (bases 1 to 139)  
REFERENCE Harris, K.A. and Teo, C.G.  
AUTHORS Direct Submission  
TITLE Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
JOURNAL Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 116 TTCCGACCCCAACTACTC 97  
RESULT 85  
AY003992/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU191 clone IV 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003992  
VERSION AY003992.1 GI:9858306  
FEATURES  
Location/Qualifiers

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/db\_xref="taxon:11103"  
/clone="I"  
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/note="5' non-coding region"  
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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGACCCCAACTACTC 20  
Db 116 TTCCGACCCCAACTACTC 97  
RESULT 86  
AY003992/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU191 clone IV 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003992  
VERSION AY003992.1 GI:9858306  
FEATURES  
Location/Qualifiers

**KEYWORDS**  
Hepatitis C virus

**SOURCE**  
Hepatitis C virus

**ORGANISM**  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

**REFERENCE**  
1 (bases 1 to 139)  
Hepatitis C virus

**AUTHORS**  
Harris, K.A. and Teo, C.G.

**TITLE**  
Diversity of hepatitis C virus quasispecies evaluated by denaturing gradient gel electrophoresis

**JOURNAL**  
Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)

**MEDLINE**  
20579439

**PUBMED**  
11139197

**REFERENCE**  
2 (bases 1 to 139)  
Harris, K.A. and Teo, C.G.

**AUTHORS**  
Harris, K.A. and Teo, C.G.

**TITLE**  
Direct Submission

**JOURNAL**  
Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory, Central Public Health Laboratory, 61 Colindale Avenue, London NW9 5HT, UK

**FEATURES**  
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**Db**  
116 TTGCGAGCCCAACTACTC 97

**RESULT 86**  
AY003993/c 139 bp ss-RNA linear VRL 01-MAR-2001

**LOCUS**  
Hepatitis C virus isolate IDU191 clone V 5' non-coding region, partial sequence.

**DEFINITION**  
AY003993

**ACCESSION**  
AY003993.1 GI:9858307

**VERSION**  
AY003993.1

**KEYWORDS**  
Hepatitis C virus

**SOURCE**  
Hepatitis C virus

**ORGANISM**  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepatitis C virus

**REFERENCE**  
1 (bases 1 to 139)  
Harris, K.A. and Teo, C.G.

**AUTHORS**  
Harris, K.A. and Teo, C.G.

**TITLE**  
Diversity of hepatitis C virus quasispecies evaluated by denaturing gradient gel electrophoresis

**JOURNAL**  
Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)

**MEDLINE**  
20579439

**PUBMED**  
11139197

**REFERENCE**  
2 (bases 1 to 139)  
Harris, K.A. and Teo, C.G.

**AUTHORS**  
Harris, K.A. and Teo, C.G.

**TITLE**  
Direct Submission

**JOURNAL**  
Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory, Central Public Health Laboratory, 61 Colindale Avenue, London NW9 5HT, UK

**FEATURES**  
Location/Qualifiers  
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**Qy**  
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116 TTGCGAGCCCAACTACTC 97

**Db**  
116 TTGCGAGCCCAACTACTC 97

**RESULT 87**  
AY003995/c 139 bp ss-RNA linear VRL 01-MAR-2001

**LOCUS**  
Hepatitis C virus isolate IDU230 clone I 5' non-coding region, partial sequence.

**DEFINITION**  
AY003995

**ACCESSION**  
AY003995.1 GI:9858309

**VERSION**  
AY003995.1

**KEYWORDS**  
Hepatitis C virus

**SOURCE**  
Hepatitis C virus

**ORGANISM**  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepatitis C virus

**REFERENCE**  
1 (bases 1 to 139)  
Harris, K.A. and Teo, C.G.

**AUTHORS**  
Harris, K.A. and Teo, C.G.

**TITLE**  
Diversity of hepatitis C virus quasispecies evaluated by denaturing gradient gel electrophoresis

**JOURNAL**  
Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)

**MEDLINE**  
20579439

**PUBMED**  
11139197

**REFERENCE**  
2 (bases 1 to 139)  
Harris, K.A. and Teo, C.G.

**AUTHORS**  
Harris, K.A. and Teo, C.G.

**TITLE**  
Direct Submission

**JOURNAL**  
Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory, Central Public Health Laboratory, 61 Colindale Avenue, London NW9 5HT, UK

**FEATURES**  
Location/Qualifiers  
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/note="5' non-coding region"

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116 TTGCGAGCCCAACTACTC 97

**Db**  
116 TTGCGAGCCCAACTACTC 97

**RESULT 88**  
AY003996/c 139 bp ss-RNA linear VRL 01-MAR-2001

**LOCUS**  
Hepatitis C virus isolate IDU230 clone II 5' non-coding region, partial sequence.

**DEFINITION**  
AY003996

**ACCESSION**  
AY003996.1 GI:9858310

**VERSION**  
AY003996.1

**KEYWORDS**  
Hepatitis C virus

**SOURCE**  
Hepatitis C virus

**ORGANISM**  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepatitis C virus

**REFERENCE**  
1 (bases 1 to 139)  
Harris, K.A. and Teo, C.G.

**AUTHORS**  
Harris, K.A. and Teo, C.G.

**TITLE**  
Diversity of hepatitis C virus quasispecies evaluated by denaturing

**ORIGIN**  
/note="5' non-coding region"

**Query Match** 100.0%; Score 20; DB 14; Length 139;  
**Best Local Similarity** 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;  
**Matches** 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy**  
1 TTGCGAGCCCAACTACTC 20  
|||||  
116 TTGCGAGCCCAACTACTC 97

**Db**  
116 TTGCGAGCCCAACTACTC 97

**RESULT 87**  
AY003995/c 139 bp ss-RNA linear VRL 01-MAR-2001

**LOCUS**  
Hepatitis C virus isolate IDU230 clone I 5' non-coding region, partial sequence.

**DEFINITION**  
AY003995

**ACCESSION**  
AY003995.1 GI:9858309

**VERSION**  
AY003995.1

**KEYWORDS**  
Hepatitis C virus

**SOURCE**  
Hepatitis C virus

**ORGANISM**  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepatitis C virus

**REFERENCE**  
1 (bases 1 to 139)  
Harris, K.A. and Teo, C.G.

**AUTHORS**  
Harris, K.A. and Teo, C.G.

**TITLE**  
Diversity of hepatitis C virus quasispecies evaluated by denaturing gradient gel electrophoresis

**JOURNAL**  
Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)

**MEDLINE**  
20579439

**PUBMED**  
11139197

**REFERENCE**  
2 (bases 1 to 139)  
Harris, K.A. and Teo, C.G.

**AUTHORS**  
Harris, K.A. and Teo, C.G.

**TITLE**  
Direct Submission

**JOURNAL**  
Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory, Central Public Health Laboratory, 61 Colindale Avenue, London NW9 5HT, UK

**FEATURES**  
Location/Qualifiers  
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**ORIGIN**  
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Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;  
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**Qy**  
1 TTGCGAGCCCAACTACTC 20  
|||||  
116 TTGCGAGCCCAACTACTC 97

**Db**  
116 TTGCGAGCCCAACTACTC 97

**RESULT 88**  
AY003996/c 139 bp ss-RNA linear VRL 01-MAR-2001

**LOCUS**  
Hepatitis C virus isolate IDU230 clone II 5' non-coding region, partial sequence.

**DEFINITION**  
AY003996

**ACCESSION**  
AY003996.1 GI:9858310

**VERSION**  
AY003996.1

**KEYWORDS**  
Hepatitis C virus

**SOURCE**  
Hepatitis C virus

**ORGANISM**  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepatitis C virus

**REFERENCE**  
1 (bases 1 to 139)  
Harris, K.A. and Teo, C.G.

**AUTHORS**  
Harris, K.A. and Teo, C.G.

**TITLE**  
Diversity of hepatitis C virus quasispecies evaluated by denaturing

JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
JOURNAL Direct Submission  
Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
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Db 116 TTGCGACCCCAACTACTC 97

RESULT 89  
AY003997/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU230 clone III 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003997  
VERSION AY003997.1 GI:9858311  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepciviruses.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
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/db\_xref="taxon:11103"  
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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
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Db 116 TTGCGACCCCAACTACTC 97

RESULT 91  
AY004000/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU230 clone VI 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY004000  
VERSION AY004000.1 GI:9858314  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepciviruses.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,

Db 116 TTGCGACCCCAACTACTC 97  
|||||  
RESULT 90  
AY003998/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU230 clone IV 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY003998  
VERSION AY003998.1 GI:9858312  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepciviruses.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,

Db 116 TTGCGACCCCAACTACTC 97  
|||||  
RESULT 91  
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LOCUS Hepatitis C virus isolate IDU230 clone VI 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY004000  
VERSION AY004000.1 GI:9858314  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepciviruses.  
REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasispecies evaluated by denaturing  
JOURNAL gradient gel electrophoresis  
MEDLINE Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
20579439  
PUBMED 11139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,

Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
source

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCAACTACTC 20  
116 TTGGGACCCCAACTACTC 97

RESULT 92  
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139 bp ss-RNA linear VRL 01-MAR-2001  
Hepatitis C virus isolate IDU230 clone VII 5' non-coding region.  
partial sequence.

ACCESSION  
AY004001.1 GI:9858315

VERSION  
KEYWORDS  
SOURCE

Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

REFERENCE  
AUTHORS

1 (bases 1 to 139)  
Harris,K.A. and Teo,C.G.  
Diversity of hepatitis C virus quasiespecies evaluated by denaturing

gradient gel electrophoresis  
Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001).

JOURNAL  
MEDLINE  
PUBMED

2 (bases 1 to 139)  
Harris,K.A. and Teo,C.G.  
Direct Submission

Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9

5HT, UK

FEATURES  
source

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCAACTACTC 20  
116 TTGGGACCCCAACTACTC 97

RESULT 93  
AY004007/c

139 bp ss-RNA linear VRL 01-MAR-2001  
Hepatitis C virus isolate IDU23 clone I 5' non-coding region.

partial sequence.

ACCESSION  
AY004007  
AY004007.1 GI:9858321

VERSION  
KEYWORDS  
SOURCE

Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepatitis C virus  
1 (bases 1 to 139)  
Harris,K.A. and Teo,C.G.  
Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)

JOURNAL  
MEDLINE  
PUBMED

2 (bases 1 to 139)  
Harris,K.A. and Teo,C.G.  
Direct Submission

Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9

5HT, UK

FEATURES  
source

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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCAACTACTC 20  
116 TTGGGACCCCAACTACTC 97

RESULT 94  
AY004008/c

139 bp ss-RNA linear VRL 01-MAR-2001  
Hepatitis C virus isolate IDU23 clone II 5' non-coding region.  
partial sequence.

ACCESSION  
AY004008  
AY004008.1 GI:9858322

VERSION  
KEYWORDS  
SOURCE

Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepatitis C virus  
1 (bases 1 to 139)  
Harris,K.A. and Teo,C.G.  
Diversity of hepatitis C virus quasiespecies evaluated by denaturing  
gradient gel electrophoresis  
Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)

JOURNAL  
MEDLINE  
PUBMED

2 (bases 1 to 139)  
Harris,K.A. and Teo,C.G.  
Direct Submission

Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9

5HT, UK

FEATURES  
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Best Local Similarity 100.0%; Pred. No. 0.15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGGACCCCACTACTC 20  
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Db 116 TTCGGACCCCACTACTC 97

RESULT 95  
AY004009/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU323 clone III 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY004009  
VERSION AY004009.1 GI:9858323  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasisppecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 1139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
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Qy 1 TTCGGACCCCACTACTC 20  
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Db 116 TTCGGACCCCACTACTC 97

RESULT 96  
AY004010/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU323 clone IV 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY004010  
VERSION AY004010.1 GI:9858324  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepatitis C virus.

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasisppecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 1139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

FEATURES  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCGGACCCCACTACTC 20  
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Db 116 TTCGGACCCCACTACTC 97

RESULT 97  
AY004011/c 139 bp ss-RNA linear VRL 01-MAR-2001  
LOCUS Hepatitis C virus isolate IDU323 clone V 5' non-coding region,  
DEFINITION partial sequence.  
ACCESSION AY004011  
VERSION AY004011.1 GI:9858325  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

REFERENCE 1 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Diversity of hepatitis C virus quasisppecies evaluated by denaturing gradient gel electrophoresis  
JOURNAL Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)  
MEDLINE 20579439  
PUBMED 1139197  
REFERENCE 2 (bases 1 to 139)  
AUTHORS Harris, K.A. and Teo, C.G.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory,  
Central Public Health Laboratory, 61 Colindale Avenue, London NW9  
5HT, UK

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Db	116	TTGCGACCCAACTACTC	97						
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LOCUS	AY004012/c								
DEFINITION	AY004012	139 bp ss-RNA	linear	VRL 01-MAR-2001					
ACCESSION	AY004012	Hepatitis C virus isolate IDU323 clone VI 5'	non-coding region,						
VERSION	AY004012.1	GI:9858326							
KEYWORDS									
SOURCE									
ORGANISM									
REFERENCE									
AUTHORS	1 (bases 1 to 139)								
TITLE	Harris, K.A. and Teo, C.G.								
JOURNAL	Diversity of hepatitis C virus quasiproteins evaluated by denaturing								
MEDLINE	gradient gel electrophoresis								
PUBMED	Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)								
REFERENCE	11139197								
AUTHORS	2 (bases 1 to 139)								
TITLE	Harris, K.A. and Teo, C.G.								
JOURNAL	Direct Submission								
FEATURES	Submitted (28-JUN-2000) Hepatitis and Rotavirus Laboratory,								
source	Central Public Health Laboratory, 61 Colindale Avenue, London NW9								
	5HT, UK								
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	Best local Similarity 100.0%; Pred. No. 0.15;								
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
QY	1	TTGCGACCCAACTACTC	20						
Db	116	TTGCGACCCAACTACTC	97						
RESULT 99									
LOCUS	AY004013/c								
DEFINITION	AY004013	139 bp ss-RNA	linear	VRL 01-MAR-2001					
ACCESSION	AY004013	Hepatitis C virus isolate IDU323 clone VII 5'	non-coding region,						
VERSION	AY004013.1	GI:9858327							
KEYWORDS									
SOURCE									
ORGANISM									
REFERENCE									
AUTHORS	1 (bases 1 to 139)								
TITLE	Harris, K.A. and Teo, C.G.								
JOURNAL	Diversity of hepatitis C virus quasiproteins evaluated by denaturing								
MEDLINE	gradient gel electrophoresis								
PUBMED	Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)								
REFERENCE	11139197								
	2 (bases 1 to 139)								
	Harris, K.A. and Teo, C.G.								

FEATURES	source	Location/Qualifiers
AUTHORS	Harits, K.A. and Teo, C.G.	
TITLE	Direct Submission	
JOURNAL	Submitted (28-JUN-2000) Hepatitis and Retrovirus Laboratory, Central Public Health Laboratory, 61 Colindale Avenue, London NW9 5HT, UK	
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Best Local Similarity	100.0%; Pred. No. 0.15;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 TTCCGACCCACACTACTC 20	
Db	116 TTCCGACCCACACTACTC 97	
RESULT 100		
AF506651/C	157 bp RNA linear VRL 20-MAY-2000	
LOCUS	Hepatitis C virus isolate KGV130 5' untranslated region, partial sequence.	
DEFINITION	AF506651.1 GI:20977995	
ACCESSION		
VERSION		
KEYWORDS	Hepatitis C virus	
SOURCE	Hepatitis C virus	
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.	
REFERENCE	1 (bases 1 to 157)	
AUTHORS	Shustov, A.V., Gavrilova, I.V. and Netesov, S.V.	
TITLE	Genetic variability of hepatitis C virus in Western Siberia	
JOURNAL	Unpublished.	
REFERENCE	2 (bases 1 to 157)	
AUTHORS	Shustov, A.V., Gavrilova, I.V. and Netesov, S.V.	
TITLE	Direct Submission	
JOURNAL	Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia	
FEATURES		
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ORIGIN		
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Query Match	100.0%; Score 20; DB 14; Length 157;	
Best Local Similarity	100.0%; Pred. No. 0.15;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 TTCCGACCCACACTACTC 20	
Db	150 TTCCGACCCACACTACTC 131	
RESULT 101		
AX172758/C	163 bp RNA linear PAT 03-JUL-2001	
LOCUS	Sequence 6 from Patent WO0144266.	
DEFINITION		
ACCESSION		
VERSION	AX172758.1 GI:14597854	



KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE  
1 Karn,J.C. and Walker,S.C.  
TITLE Nucleic acid compounds and screening assays using the same  
AUTHORS Patient: MO 0144266-A 6 21-JUN-2001;  
JOURNAL Ribotargets Limited (GB)  
FEATURES  
source Location/Qualifiers  
1.163  
/organism="synthetic construct"  
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/db\_xref="taxon:32630"  
/note="Probe"

ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
Db 145 TTGGGACCCCAACTACTC 126

RESULT 102  
AY147807 164 bp RNA linear VRL 12-NOV-2002  
LOCUS Hepatitis C virus isolate 3-1C 5' untranslated region, partial  
DEFINITION  
sequence.  
ACCESSION AY147807 GI:24935230  
VERSION  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE  
1 (bases 1 to 164)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 164)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey  
FEATURES  
source Location/Qualifiers  
1.164  
/organism="Hepatitis C virus"  
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ORIGIN  
5'UTR  
Query Match 100.0%; Score 20; DB 14; Length 164;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
Db 161 TTGGGACCCCAACTACTC 142

RESULT 103  
AY344037/c 164 bp RNA linear VRL 23-APR-2004  
LOCUS

DEFINITION Hepatitis C virus isolate SL3-S33 5' UTR.  
ACCESSION AY344037 GI:37790676  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE  
1 (bases 1 to 164)  
AUTHORS Bhattacharya,S., Mapa,K., Prabhavathi,S., Sudhamani,S.R.,  
Menon,P.K., John,K.P., Shivaram,C., Amarnath,S. and Das,S.  
TITLE Phylogenetic conservation of the stem-loop III structure of the  
5' untranslated region of Hepatitis C virus RNA among natural  
variants in samples collected from Southern India  
JOURNAL Arch. Virol. 149 (5), 1015-1026 (2004)  
PUBMED 15098115

REFERENCE  
2 (bases 1 to 164)  
AUTHORS Bhattacharya,S., Prabhavathi,S., Mapa,K. and Das,S.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUN-2003) Microbiology & Cell Biology, Indian  
Institute of Science, C.V. Raman Street, Bangalore, Karnataka  
560012, India  
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DEFINITION  
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VERSION AF506628 GI:20977972  
KEYWORDS  
SOURCE  
ORGANISM Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE  
1 (bases 1 to 165)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research  
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.  
630559, Russia  
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RESULT 105  
AY147800/c 165 bp RNA linear VRL 12-NOV-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate 3-13 5' untranslated region, partial  
sequence.  
ACCESSION AY147800 GI:24935223  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdaiy,A.M., Aslan,N., Bozdaiy,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdaiy,A.M., Aslan,N., Bozdaiy,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey  
FEATURES  
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Db

RESULT 106  
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DEFINITION Hepatitis C virus isolate 3-14 5' untranslated region, partial  
sequence.  
ACCESSION AY147801  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdaiy,A.M., Aslan,N., Bozdaiy,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdaiy,A.M., Aslan,N., Bozdaiy,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey  
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RESULT 108  
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DEFINITION Hepatitis C virus isolate 3-02 5' untranslated region, partial  
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ACCESSION AY147803

Wend,U., Erkan,O. and Aydemir,F.  
Direct Submission  
Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
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162 TTGGCGACCCCAACTACTC 143

Db

RESULT 107  
AY147802/c 165 bp RNA linear VRL 12-NOV-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate 3-01 5' untranslated region, partial  
sequence.  
ACCESSION AY147802  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdaiy,A.M., Aslan,N., Bozdaiy,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdaiy,A.M., Aslan,N., Bozdaiy,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey  
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162 TTGGCGACCCCAACTACTC 143

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RESULT 108  
AY147803 165 bp RNA linear VRL 12-NOV-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate 3-02 5' untranslated region, partial  
sequence.  
ACCESSION AY147803

VERSION AY147803.1 GI:24935226  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
TITLE Wend,U., Erkan,O. and Aydemir,F.  
Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
Hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
TITLE Wend,U., Erkan,O. and Aydemir,F.  
Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey  
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Db 162 TTGGGACCCCAACTACTC 143

RESULT 109  
AY147804 165 bp RNA linear VRL 12-NOV-2002  
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DEFINITION Hepatitis C virus isolate 3-05 5' untranslated region, partial  
sequence.  
ACCESSION AY147804.1 GI:24935227  
VERSION  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
TITLE Wend,U., Erkan,O. and Aydemir,F.  
Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
Hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
TITLE Wend,U., Erkan,O. and Aydemir,F.  
Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey  
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Db 162 TTGGGACCCCAACTACTC 143

RESULT 110  
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LOCUS AY147805  
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sequence.  
ACCESSION AY147805.1 GI:24935228  
VERSION  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
TITLE Wend,U., Erkan,O. and Aydemir,F.  
Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
Hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
TITLE Wend,U., Erkan,O. and Aydemir,F.  
Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey  
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Db 162 TTGGGACCCCAACTACTC 143

RESULT 111  
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LOCUS AY147806  
DEFINITION Hepatitis C virus isolate 3-09 5' untranslated region, partial  
sequence.  
ACCESSION AY147806  
VERSION AY147806.1 GI:24935229  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
TITLE Wend,U., Erkan,O. and Aydemir,F.  
Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
Hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
TITLE Wend,U., Erkan,O. and Aydemir,F.  
Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey  
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AUTHORS Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T.,  
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TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebeçi, Ankara 06100, Turkey  
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DB 162 TTCCGACCCCAACTACTC 143

RESULT 112  
AY147808 165 bp RNA linear VRL 12-NOV-2002  
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DEFINITION  
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ACCESSION AY147808 GI:24935231  
VERSION AY147808  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
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1 (bases 1 to 165)  
Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
hepatitis virus infections  
Unpublished  
2 (bases 1 to 165)  
Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
Direct Submission  
Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebeçi, Ankara 06100, Turkey  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 162 TTCCGACCCCAACTACTC 143

RESULT 113  
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LOCUS Hepatitis C virus isolate 1-11 5' untranslated region, partial  
DEFINITION  
sequence.

ACCESSION AY147809  
VERSION AY147809.1 GI:24935232  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.  
1 (bases 1 to 165)  
Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
hepatitis virus infections  
Unpublished  
2 (bases 1 to 165)  
Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
Direct Submission  
Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebeçi, Ankara 06100, Turkey  
Location/Qualifiers  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
DB 162 TTCCGACCCCAACTACTC 143

RESULT 114  
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LOCUS Hepatitis C virus isolate 1-14 5' untranslated region, partial  
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ACCESSION AY147810 GI:24935233  
VERSION AY147810  
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ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
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1 (bases 1 to 165)  
Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
hepatitis virus infections  
Unpublished  
2 (bases 1 to 165)  
Bozdagi,A.M., Aslan,N., Bozdagi,G., Turkylmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
Direct Submission  
Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebeçi, Ankara 06100, Turkey  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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162 TTCCGACCCCAACTACTC 143

RESULT 115  
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LOCUS Hepatitis C virus isolate 1-15 5' untranslated region, partial  
DEFINITION  
ACCESSION AY147811 GI:24935234  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.

REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
Hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebecl, Ankara 06100, Turkey

FEATURES  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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162 TTCCGACCCCAACTACTC 143

RESULT 116  
AY147812/c 165 bp RNA linear VRL 12-NOV-2002  
LOCUS Hepatitis C virus isolate 1-16 5' untranslated region, partial  
DEFINITION  
ACCESSION AY147812  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.

REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
Hepatitis virus infections  
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebecl, Ankara 06100, Turkey

FEATURES  
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RESULT 117  
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LOCUS Hepatitis C virus isolate 1-04 5' untranslated region, partial  
DEFINITION  
ACCESSION AY147813 GI:24935236  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM  
Virus; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.

REFERENCE 1 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus  
genotypes and Hepatitis Delta virus types in Turkish patients with  
Hepatitis virus infections  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,  
Wend,U., Erkan,O. and Aydemir,F.  
TITLE Direct Submission  
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute  
of Hepatology, Ankara University, Cebecl, Ankara 06100, Turkey

FEATURES  
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/note="genotype: 1b"  
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162 TTCCGACCCCAACTACTC 143

RESULT 118  
AY147814/c 165 bp RNA linear VRL 12-NOV-2002  
LOCUS Hepatitis C virus isolate 1-05 5' untranslated region, partial  
DEFINITION

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ACCESSION AY147814 GI:24935237
VERSION AY147814.1
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnavirus.
REFERENCE 1 (bases 1 to 165)
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,
Wend,U., Erkan,O. and Aydemir,F.
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus
genotypes and Hepatitis Delta virus types in Turkish patients with
hepatitis virus infections
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 165)
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,
Wend,U., Erkan,O. and Aydemir,F.
TITLE Direct Submission
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute
of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey
FEATURES
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/note="genotype: 1b"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 162 TTGCGACCCCAACTACTC 143

RESULT 119
AY147815 165 bp RNA linear VRL 12-NOV-2002
LOCUS Hepatitis C virus isolate 1-07 5' untranslated region, partial
sequence.
ACCESSION AY147815
VERSION AY147815.1 GI:24935238
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnavirus.
REFERENCE 1 (bases 1 to 165)
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,
Wend,U., Erkan,O. and Aydemir,F.
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus
genotypes and Hepatitis Delta virus types in Turkish patients with
hepatitis virus infections
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 165)
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,
Wend,U., Erkan,O. and Aydemir,F.
TITLE Direct Submission
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute
of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey
FEATURES
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/note="genotype: 1b"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20
DB 162 TTGCGACCCCAACTACTC 143

RESULT 120
AY147816 165 bp RNA linear VRL 12-NOV-2002
LOCUS Hepatitis C virus isolate 1-09 5' untranslated region, partial
sequence.
ACCESSION AY147816
VERSION AY147816.1 GI:24935239
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnavirus.
REFERENCE 1 (bases 1 to 165)
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,
Wend,U., Erkan,O. and Aydemir,F.
TITLE Hepatitis B virus genotypes and subtypes, Hepatitis C virus
genotypes and Hepatitis Delta virus types in Turkish patients with
hepatitis virus infections
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 165)
AUTHORS Bozdayi,A.M., Aslan,N., Bozdayi,G., Turkyilmaz,A.R., Sengezer,T.,
Wend,U., Erkan,O. and Aydemir,F.
TITLE Direct Submission
JOURNAL Submitted (04-SEP-2002) Department of Gastroenterology, Institute
of Hepatology, Ankara University, Cebeci, Ankara 06100, Turkey
FEATURES
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/mol_type="genomic RNA"
/isolate="1-09"
/db_xref="taxon:11103"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20
DB 162 TTGCGACCCCAACTACTC 143

RESULT 121
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LOCUS Hepatitis C virus isolate SL3-57 5' UTR.
ACCESSION AY344028
VERSION AY344028.1 GI:37790667
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnavirus.
REFERENCE 1 (bases 1 to 165)
AUTHORS Bhatnacharya,S., Mapa,K., Prabhavathi,S., Sudhantani,S.R.,
Menon,P.K., John,K.P., Shivaram,C., Amarnath,S. and Das,S.
TITLE Phylogenetic conservation of the stem-loop III structure of the
5 untranslated region of Hepatitis C virus RNA among natural
variants in samples collected from Southern India
JOURNAL Arch. Virol. 149 (5), 1015-1026 (2004)

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PUBMED 15098115  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bhattacharya,S., Prabhavathi,S., Mapa,K. and Das,S.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUL-2003) Microbiology & Cell Biology, Indian  
Institute of Science, C.V. Raman Street, Bangalore, Karnataka  
560012, India  
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148 TTGGGACCCCAACTACTC 129  
Db 148 TTGGGACCCCAACTACTC 129  
RESULT 122  
LOCUS AY344029 165 bp RNA linear VRL 23-APR-2004  
DEFINITION Hepatitis C virus isolate SL3-S10 5' UTR.  
ACCESSION AY344029  
VERSION AY344029.1 GI:37790668  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
1 (bases 1 to 165)  
REFERENCE 1 Bhattacharya,S., Mapa,K., Prabhavathi,S., Sudhamani,S.R.,  
Menon,P.K., John,K.P., Shivaram,C., Amarnath,S. and Das,S.  
TITLE Phylogenetic conservation of the stem-loop III structure of the  
5' untranslated region of Hepatitis C virus RNA among natural  
variants in samples collected from Southern India  
JOURNAL Arch. Virol. 149 (5), 1015-1026 (2004)  
PUBMED 15098115  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bhattacharya,S., Prabhavathi,S., Mapa,K. and Das,S.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUL-2003) Microbiology & Cell Biology, Indian  
Institute of Science, C.V. Raman Street, Bangalore, Karnataka  
560012, India  
FEATURES  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
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148 TTGGGACCCCAACTACTC 129  
Db 148 TTGGGACCCCAACTACTC 129  
RESULT 123  
LOCUS AY344030 165 bp RNA linear VRL 23-APR-2004  
DEFINITION Hepatitis C virus isolate SL3-S16 5' UTR.  
ACCESSION AY344030

VERSION AY344030.1 GI:37790669  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
1 (bases 1 to 165)  
REFERENCE 1 Bhattacharya,S., Mapa,K., Prabhavathi,S., Sudhamani,S.R.,  
Menon,P.K., John,K.P., Shivaram,C., Amarnath,S. and Das,S.  
TITLE Phylogenetic conservation of the stem-loop III structure of the  
5' untranslated region of Hepatitis C virus RNA among natural  
variants in samples collected from Southern India  
JOURNAL Arch. Virol. 149 (5), 1015-1026 (2004)  
PUBMED 15098115  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bhattacharya,S., Prabhavathi,S., Mapa,K. and Das,S.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUL-2003) Microbiology & Cell Biology, Indian  
Institute of Science, C.V. Raman Street, Bangalore, Karnataka  
560012, India  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
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148 TTGGGACCCCAACTACTC 129  
Db 148 TTGGGACCCCAACTACTC 129  
RESULT 124  
LOCUS AY344031 165 bp RNA linear VRL 23-APR-2004  
DEFINITION Hepatitis C virus isolate SL3-S17 5' UTR.  
ACCESSION AY344031  
VERSION AY344031.1 GI:37790670  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
1 (bases 1 to 165)  
REFERENCE 1 Bhattacharya,S., Mapa,K., Prabhavathi,S., Sudhamani,S.R.,  
Menon,P.K., John,K.P., Shivaram,C., Amarnath,S. and Das,S.  
TITLE Phylogenetic conservation of the stem-loop III structure of the  
5' untranslated region of Hepatitis C virus RNA among natural  
variants in samples collected from Southern India  
JOURNAL Arch. Virol. 149 (5), 1015-1026 (2004)  
PUBMED 15098115  
REFERENCE 2 (bases 1 to 165)  
AUTHORS Bhattacharya,S., Prabhavathi,S., Mapa,K. and Das,S.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUL-2003) Microbiology & Cell Biology, Indian  
Institute of Science, C.V. Raman Street, Bangalore, Karnataka  
560012, India  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
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148 TTGGCGACCCCAACTACTC 129

Db

RESULT 125  
LOCUS AY344032 165 bp RNA linear VRL 23-APR-2004  
DEFINITION Hepatitis C virus isolate SL3-S24 5' UTR.  
ACCESSION AY344032  
VERSION AY344032.1 GI:37790671  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
1 (bases 1 to 165)  
Bhattacharya,S., Mapa,K., Prabhavathi,S., Sudhamani,S.R.,  
Menon,P.K., John,K.P., Shivaram,C., Amarnath,S. and Das,S.,  
Phylogenetic conservation of the stem-loop III structure of the  
5' untranslated region of Hepatitis C virus RNA among natural  
variants in samples collected from Southern India  
Arch. Virol. 149 (5), 1015-1026 (2004)  
15098115  
2 (bases 1 to 165)  
Bhattacharya,S., Srinivasan,P., Mapa,K. and Das,S.,  
Direct Submission  
Submitted (15-JUL-2003) Microbiology & Cell Biology, Indian  
Institute of Science, C.V. Raman Street, Bangalore, Karnataka  
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5'UTR

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148 TTGGCGACCCCAACTACTC 129

Db

RESULT 126  
LOCUS AY344033 165 bp RNA linear VRL 23-APR-2004  
DEFINITION Hepatitis C virus isolate SL3-S24 5' UTR.  
ACCESSION AY344033  
VERSION AY344033.1 GI:37790672  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
1 (bases 1 to 165)  
Bhattacharya,S., Mapa,K., Prabhavathi,S., Sudhamani,S.R.,  
Menon,P.K., John,K.P., Shivaram,C., Amarnath,S. and Das,S.,  
Phylogenetic conservation of the stem-loop III structure of the  
5' untranslated region of Hepatitis C virus RNA among natural  
variants in samples collected from Southern India  
Arch. Virol. 149 (5), 1015-1026 (2004)  
15098115  
2 (bases 1 to 165)  
Bhattacharya,S., Srinivasan,P., Mapa,K. and Das,S.,  
Direct Submission  
Submitted (15-JUL-2003) Microbiology & Cell Biology, Indian  
Institute of Science, C.V. Raman Street, Bangalore, Karnataka  
560012, India  
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148 TTGGCGACCCCAACTACTC 129

Db

RESULT 127  
LOCUS AY344034 165 bp RNA linear VRL 23-APR-2004  
DEFINITION Hepatitis C virus isolate SL3-S25 5' UTR.  
ACCESSION AY344034  
VERSION AY344034.1 GI:37790673  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
1 (bases 1 to 165)  
Bhattacharya,S., Mapa,K., Prabhavathi,S., Sudhamani,S.R.,  
Menon,P.K., John,K.P., Shivaram,C., Amarnath,S. and Das,S.,  
Phylogenetic conservation of the stem-loop III structure of the  
5' untranslated region of Hepatitis C virus RNA among natural  
variants in samples collected from Southern India  
Arch. Virol. 149 (5), 1015-1026 (2004)  
15098115  
2 (bases 1 to 165)  
Bhattacharya,S., Srinivasan,P., Mapa,K. and Das,S.,  
Direct Submission  
Submitted (15-JUL-2003) Microbiology & Cell Biology, Indian  
Institute of Science, C.V. Raman Street, Bangalore, Karnataka  
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148 TTGGCGACCCCAACTACTC 129

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RESULT 128  
LOCUS AY344035 165 bp RNA linear VRL 23-APR-2004  
DEFINITION Hepatitis C virus isolate SL3-S26 5' UTR.  
ACCESSION AY344035  
VERSION AY344035.1 GI:37790674  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus

JOURNAL Submitted (15-JUL-2003) Microbiology & Cell Biology, Indian  
Institute of Science, C.V. Raman Street, Bangalore, Karnataka  
560012, India  
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ORIGIN  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCGACCCCAACTACTC 20  
148 TTGGCGACCCCAACTACTC 129

Db

RESULT 127  
LOCUS AY344034 165 bp RNA linear VRL 23-APR-2004  
DEFINITION Hepatitis C virus isolate SL3-S25 5' UTR.  
ACCESSION AY344034  
VERSION AY344034.1 GI:37790673  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
1 (bases 1 to 165)  
Bhattacharya,S., Mapa,K., Prabhavathi,S., Sudhamani,S.R.,  
Menon,P.K., John,K.P., Shivaram,C., Amarnath,S. and Das,S.,  
Phylogenetic conservation of the stem-loop III structure of the  
5' untranslated region of Hepatitis C virus RNA among natural  
variants in samples collected from Southern India  
Arch. Virol. 149 (5), 1015-1026 (2004)  
15098115  
2 (bases 1 to 165)  
Bhattacharya,S., Srinivasan,P., Mapa,K. and Das,S.,  
Direct Submission  
Submitted (15-JUL-2003) Microbiology & Cell Biology, Indian  
Institute of Science, C.V. Raman Street, Bangalore, Karnataka  
560012, India  
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ORIGIN  
5'UTR

Query Match 100.0%; Score 20; DB 14; Length 165;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGCGACCCCAACTACTC 20  
148 TTGGCGACCCCAACTACTC 129

Db

RESULT 128  
LOCUS AY344035 165 bp RNA linear VRL 23-APR-2004  
DEFINITION Hepatitis C virus isolate SL3-S26 5' UTR.  
ACCESSION AY344035  
VERSION AY344035.1 GI:37790674  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus



Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

REFERENCE  
AUTHORS

1 (bases 1 to 165)

## TITLE

Bhattacharya,S., Mapa,K., Prabhavathi,S., Sudhamani,S.R., Menon,P.K., John,K.P., Shivaram,C., Amarnath,S. and Das,S. Phylogenetic conservation of the stem-loop III structure of the 5'untranslated region of Hepatitis C virus RNA among natural variants in samples collected from Southern India Arch. Virol. 149 (5), 1015-1026 (2004)

JOURNAL  
PUBMED

15098115

REFERENCE  
AUTHORS

2 (bases 1 to 165)

## TITLE

Bhattacharya,S., Srinivasan,P., Mapa,K. and Das,S. Direct Submission Submitted (15-JUL-2003) Microbiology & Cell Biology, Indian Institute of Science, C.V. Raman Street, Bangalore, Karnataka 560012, India

## FEATURES

## source

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ORIGIN  
5'UTR

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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148 TTGCGACCCCAACTACTC 129

## RESULT 129

## AF506648/C

166 bp RNA linear VRL 20-MAY-2002  
Hepatitis C virus isolate KGV124 5' untranslated region, partial sequence.

## ACCESSION

AF506648.1 GI:20977992

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepatitis C virus.

REFERENCE  
AUTHORS

1 (bases 1 to 166)

## TITLE

Shustov,A.V., Gavrilova,I.V. and Netesov,S.V. Genetic variability of hepatitis C virus in Western Siberia

## JOURNAL

Unpublished

REFERENCE  
AUTHORS

2 (bases 1 to 166)

## TITLE

Shustov,A.V., Gavrilova,I.V. and Netesov,S.V. Direct Submission Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia

## FEATURES

## source

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/country="Russia"  
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5'UTR

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## RESULT 130

## AF506649/C

166 bp RNA linear VRL 20-MAY-2002  
Hepatitis C virus isolate KGV127 5' untranslated region, partial sequence.

## ACCESSION

AF506649.1 GI:20977993

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepatitis C virus.

REFERENCE  
AUTHORS

1 (bases 1 to 166)

## TITLE

Shustov,A.V., Gavrilova,I.V. and Netesov,S.V. Genetic variability of hepatitis C virus in Western Siberia

## JOURNAL

## REFERENCE

## AUTHORS

Shustov,A.V., Gavrilova,I.V. and Netesov,S.V. Direct Submission Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia

## FEATURES

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1..166  
/organism="Hepatitis C virus"  
/mol\_type="genomic RNA"  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

1 TTGCGACCCCAACTACTC 20  
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159 TTGCGACCCCAACTACTC 140

## RESULT 131

## AF506642/C

167 bp RNA linear VRL 20-MAY-2002  
Hepatitis C virus isolate RIG126 5' untranslated region, partial sequence.

## ACCESSION

AF506642.1 GI:20977986

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepatitis C virus.

REFERENCE  
AUTHORS

1 (bases 1 to 167)

## TITLE

Shustov,A.V., Gavrilova,I.V. and Netesov,S.V. Genetic variability of hepatitis C virus in Western Siberia

## JOURNAL

## REFERENCE

## AUTHORS

Shustov,A.V., Gavrilova,I.V. and Netesov,S.V. Direct Submission Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia

## FEATURES

## source

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OY 1 TTTCGACCCCAACTACTC 20  
161 TTTCGACCCCAACTACTC 142

Db

RESULT 132  
AF506684/c 167 bp RNA linear VRL 20-MAY-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate RIG106 5' untranslated region, partial  
sequence.  
AF506684  
AF506684.1 GI:20978028  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE  
AUTHORS 1 (bases 1 to 167)  
TITLE Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
JOURNAL Genetic variability of hepatitis C virus in Western Siberia  
REFERENCE Unpublished  
AUTHORS 2 (bases 1 to 167)  
TITLE Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
JOURNAL Direct Submission  
Submitted (26-APR-2002) Inst. Molecular Biology, State Research  
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.  
630559, Russia  
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/country="Russia"  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCGACCCCAACTACTC 20  
161 TTTCGACCCCAACTACTC 142

Db

RESULT 133  
AF506682/c 168 bp RNA linear VRL 20-MAY-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate RIG83 5' untranslated region, partial  
sequence.  
AF506682  
AF506682.1 GI:20978026  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
1 (bases 1 to 168)  
TITLE Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
JOURNAL Genetic variability of hepatitis C virus in Western Siberia  
REFERENCE Unpublished  
AUTHORS 2 (bases 1 to 168)  
TITLE Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
JOURNAL Direct Submission  
Submitted (26-APR-2002) Inst. Molecular Biology, State Research  
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.

630559, Russia  
LOCATION/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCGACCCCAACTACTC 20  
162 TTTCGACCCCAACTACTC 143

Db

RESULT 134  
AF506695/c 169 bp RNA linear VRL 20-MAY-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate VO13 5' untranslated region, partial  
sequence.  
AF506695  
AF506695.1 GI:20978039  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
1 (bases 1 to 169)  
TITLE Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
JOURNAL Genetic variability of hepatitis C virus in Western Siberia  
REFERENCE Unpublished  
AUTHORS 2 (bases 1 to 169)  
TITLE Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
JOURNAL Direct Submission  
Submitted (26-APR-2002) Inst. Molecular Biology, State Research  
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.  
630559, Russia  
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ORIGIN 5'UTR

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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTTCGACCCCAACTACTC 20  
162 TTTCGACCCCAACTACTC 143

Db

RESULT 135  
AY146006/c 170 bp RNA linear VRL 12-NOV-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate KGV474 5' UTR, partial sequence.  
AY146006  
AY146006.1 GI:24935134  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
1 (bases 1 to 170)

AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE The prevalence and genetic variability of hepatitis C virus  
isolates in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 170)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (29-AUG-2002) Inst. Molecular Biology, State Research  
Center Vector, SRC VB Vector, Koltsovo, Novosibirskaya obl. 630559,  
Russia

FEATURES  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 125 TTGGGACCCCAACTACTC 106

RESULT 136  
AF506691/C 171 bp RNA linear VRL 20-MAY-2002  
LOCUS Hepatitis C virus isolate RIG96 5' untranslated region, partial  
DEFINITION  
ACCESSION AF506691  
VERSION AF506691  
KEYWORDS AF506691.1 GI:20978035  
SOURCE  
ORGANISM  
Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.  
REFERENCE 1 (bases 1 to 171)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 171)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research  
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.  
630559, Russia  
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QY 1 TTGGGACCCCAACTACTC 20  
DB 165 TTGGGACCCCAACTACTC 146

RESULT 137  
AY545673 172 bp RNA linear VRL 09-MAR-2004  
LOCUS

DEFINITION Hepatitis C virus isolate IR-1269 5' UTR.  
ACCESSION AY545673.1 GI:45120596  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.  
REFERENCE 1 (bases 1 to 172)  
AUTHORS Ahmadipour,M., Keivani Amineh,H., Sabahi,F., Mahboudi,F., Karimi  
Arzenani,M., Adeli,A. and Sarrafi Pouroushani,R.  
TITLE Direct Submission  
JOURNAL Submitted (11-FEB-2004) Biotechnology, Pasteur Institute of Iran,  
12 Farvardin, Tehran 69 13164, Iran  
Location/Qualifiers  
1. .172  
/organism="Hepatitis C virus"  
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/isolate="IR-1269"  
/db\_xref="taxon:11103"  
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/note="genotype: 4"  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 130 TTGGGACCCCAACTACTC 111

RESULT 138  
AY545676 173 bp RNA linear VRL 09-MAR-2004  
LOCUS Hepatitis C virus isolate IR-1806 5' UTR.  
DEFINITION  
ACCESSION AY545676  
VERSION AY545676.1 GI:45120599  
KEYWORDS  
SOURCE  
ORGANISM  
Hepatitis C virus  
Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.  
REFERENCE 1 (bases 1 to 173)  
AUTHORS Ahmadipour,M., Keivani Amineh,H., Sabahi,F., Mahboudi,F., Karimi  
Arzenani,M., Adeli,A. and Sarrafi Pouroushani,R.  
TITLE Direct Submission  
JOURNAL Submitted (11-FEB-2004) Biotechnology, Pasteur Institute of Iran,  
12 Farvardin, Tehran 69 13164, Iran  
Location/Qualifiers  
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/organism="Hepatitis C virus"  
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/db\_xref="taxon:11103"  
/country="Iran"  
/note="genotype: 3a"  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 131 TTGGGACCCCAACTACTC 112

RESULT 139  
AY545676/C

LOCUS AY545678 173 bp RNA linear VRL 09-MAR-2004  
 DEFINITION Hepatitis C virus isolate IR-2026 5' UTR.  
 ACCESSION AY545678  
 VERSION AY545678.1 GI:44975239  
 KEYWORDS Hepatitis C virus  
 SOURCE Hepatitis C virus  
 ORGANISM Hepatitis C virus  
 REFERENCE 1 (bases 1 to 173)  
 AUTHORS Ahmadipour,M., Keivani Amineh,H., Sabahi,F., Mahboudi,F., Karimi Arzamani,M., Adeli,A. and Sarzami Pouroushani,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (11-FEB-2004) Biotechnology, Pasteur Institute of Iran, 12 Farvardin, Tehran 69 13164, Iran  
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 Oy 1 TTCCGACCCCAACTACTC 20  
 DB 131 TTCCGACCCCAACTACTC 112  
 RESULT 140  
 AF506673/c 174 bp RNA linear VRL 20-MAY-2002  
 LOCUS Hepatitis C virus isolate KGV62 5' untranslated region, partial  
 DEFINITION  
 ACCESSION AF506673  
 VERSION AF506673.1 GI:20978017  
 KEYWORDS Hepatitis C virus  
 SOURCE Hepatitis C virus  
 ORGANISM Hepatitis C virus  
 REFERENCE 1 (bases 1 to 174)  
 AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
 TITLE Genetic variability of hepatitis C virus in Western Siberia  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 174)  
 AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia  
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 DB 1 TTCCGACCCCAACTACTC 20

DB 167 TTCCGACCCCAACTACTC 148  
 RESULT 141  
 AF506685/c 174 bp RNA linear VRL 20-MAY-2002  
 LOCUS Hepatitis C virus isolate RI676 5' untranslated region, partial  
 DEFINITION  
 ACCESSION AF506685  
 VERSION AF506685.1 GI:20978029  
 KEYWORDS Hepatitis C virus  
 SOURCE Hepatitis C virus  
 ORGANISM Hepatitis C virus  
 REFERENCE 1 (bases 1 to 174)  
 AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
 TITLE Genetic variability of hepatitis C virus in Western Siberia  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 174)  
 AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia  
 FEATURES  
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 DB 168 TTCCGACCCCAACTACTC 149  
 RESULT 142  
 AF506692/c 174 bp RNA linear VRL 20-MAY-2002  
 LOCUS Hepatitis C virus isolate RI697 5' untranslated region, partial  
 DEFINITION  
 ACCESSION AF506692  
 VERSION AF506692.1 GI:20978036  
 KEYWORDS Hepatitis C virus  
 SOURCE Hepatitis C virus  
 ORGANISM Hepatitis C virus  
 REFERENCE 1 (bases 1 to 174)  
 AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
 TITLE Genetic variability of hepatitis C virus in Western Siberia  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 174)  
 AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia  
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ORIGIN

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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168 TTGGGACCCCAACTACTC 149

Db

RESULT 143

AF506693/C 174 bp RNA linear VRL 20-FEB-2004

LOCUS Hepatitis C virus isolate RIG98 5' untranslated region, partial sequence.

DEFINITION AF506693

ACCESSION AF506693.1 GI:20978037

VERSION

KEYWORDS Hepatitis C virus

SOURCE Hepatitis C virus

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1 (bases 1 to 174)  
Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
Genetic variability of hepatitis C virus in Western Siberia

AUTHORS Unpublished

JOURNAL 2 (bases 1 to 174)  
Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.

REFERENCE Direct Submission  
Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Kolosovo, Novosibirskaya Obl.

AUTHORS

JOURNAL

TITLE

FEATURES

source

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
168 TTGGGACCCCAACTACTC 149

Db

RESULT 144

AY523463/C 174 bp RNA linear VRL 02-FEB-2004

LOCUS Hepatitis C virus isolate IR-1747 5' UTR.

DEFINITION AY523463

ACCESSION AY523463.1 GI:41352544

VERSION

KEYWORDS Hepatitis C virus

SOURCE Hepatitis C virus

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1 (bases 1 to 174)  
Ahmadipour,M.H., Keivani Amineh,H., Sabahi,F., Mahboudi,F., Karimi Arzenani,M., Adeli,A. and Sarrafi Foroushani,R.

AUTHORS Hepatitis C virus 5' untranslated region sequences among Iranian HCV infected subjects

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 174)  
Ahmadipour,M.H., Keivani Amineh,H., Sabahi,F., Mahboudi,F., Karimi Arzenani,M., Adeli,A. and Sarrafi Foroushani,R.

AUTHORS

JOURNAL

TITLE

TITLE Direct Submission

JOURNAL Submitted (08-JAN-2004) Biotechnology, Pasteur of Iran, 12 Farvardin, Tehran, 69 13164, Iran

FEATURES

source

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ORIGIN

5'UTR

Query Match 100.0%; Score 20; DB 14; Length 174;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
133 TTGGGACCCCAACTACTC 114

Db

RESULT 145

AY523464/C 174 bp RNA linear VRL 02-FEB-2004

LOCUS Hepatitis C virus isolate IR-3077 5' UTR.

DEFINITION AY523464

ACCESSION AY523464.1 GI:41352545

VERSION

KEYWORDS Hepatitis C virus

SOURCE Hepatitis C virus

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1 (bases 1 to 174)  
Ahmadipour,M.H., Keivani Amineh,H., Sabahi,F., Mahboudi,F., Karimi Arzenani,M., Adeli,A. and Sarrafi Foroushani,R.

AUTHORS Hepatitis C virus 5' untranslated region sequences among Iranian HCV infected subjects

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 174)  
Ahmadipour,M.H., Keivani Amineh,H., Sabahi,F., Mahboudi,F., Karimi Arzenani,M., Adeli,A. and Sarrafi Foroushani,R.

AUTHORS Direct Submission  
Submitted (08-JAN-2004) Biotechnology, Pasteur of Iran, 12 Farvardin, Tehran, 69 13164, Iran

JOURNAL

TITLE

FEATURES

source

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/organism="Hepatitis C virus"  
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ORIGIN

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Query Match 100.0%; Score 20; DB 14; Length 174;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
133 TTGGGACCCCAACTACTC 114

Db

RESULT 146

AY523465/C 174 bp RNA linear VRL 02-FEB-2004

LOCUS Hepatitis C virus isolate IR-1644 5' UTR.

DEFINITION AY523465

ACCESSION AY523465.1 GI:41352546

VERSION

KEYWORDS

SOURCE  
Hepatitis C virus  
ORGANISM  
Hepatitis C virus  
REFERENCE  
1 (bases 1 to 174)  
AUTHORS  
Ahmadipour, M.H., Keivani Amineh, H., Sabahi, F., Mahboudi, F., Karimi Arzenani, M., Adeli, A. and Sarrafi Pouroushani, R.  
TITLE  
Hepatitis C virus 5' untranslated region sequences among Iranian HCV infected subjects  
JOURNAL  
Unpublished  
REFERENCE  
2 (bases 1 to 174)  
AUTHORS  
Ahmadipour, M.H., Keivani Amineh, H., Sabahi, F., Mahboudi, F., Karimi Arzenani, M., Adeli, A. and Sarrafi Pouroushani, R.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (08-JAN-2004) Biotechnology, Pasteur of Iran, 12 Farvardin, Tehran, 69 13164, Iran  
FEATURES  
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/isolate="IR-1644"  
/db\_xref="taxon:11103"  
/country="Iran"  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 133 TTGGGACCCACACTACTC 114

RESULT 147  
AY523466 174 bp RNA linear VRL 02-FEB-2004  
LOCUS  
DEFINITION  
Hepatitis C virus isolate IR-1411 5' UTR.  
ACCESSION  
AY523466  
VERSION  
AY523466.1 GI:41352547  
KEYWORDS  
Hepatitis C virus  
SOURCE  
Hepatitis C virus  
ORGANISM  
Hepatitis C virus  
REFERENCE  
1 (bases 1 to 174)  
AUTHORS  
Ahmadipour, M.H., Keivani Amineh, H., Sabahi, F., Mahboudi, F., Karimi Arzenani, M., Adeli, A. and Sarrafi Pouroushani, R.  
TITLE  
Hepatitis C virus 5' untranslated region sequences among Iranian HCV infected subjects  
JOURNAL  
Unpublished  
REFERENCE  
2 (bases 1 to 174)  
AUTHORS  
Ahmadipour, M.H., Keivani Amineh, H., Sabahi, F., Mahboudi, F., Karimi Arzenani, M., Adeli, A. and Sarrafi Pouroushani, R.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (08-JAN-2004) Biotechnology, Pasteur of Iran, 12 Farvardin, Tehran, 69 13164, Iran  
FEATURES  
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/organism="Hepatitis C virus"  
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OY  
1 TTGGGACCCACACTACTC 20  
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DB 132 TTGGGACCCACACTACTC 113

RESULT 148  
AY545671 174 bp RNA linear VRL 09-MAR-2004  
LOCUS  
DEFINITION  
Hepatitis C virus isolate IR-0613 5' UTR.  
ACCESSION  
AY545671  
VERSION  
AY545671.1 GI:45120594  
KEYWORDS  
Hepatitis C virus  
SOURCE  
Hepatitis C virus  
ORGANISM  
Hepatitis C virus  
REFERENCE  
1 (bases 1 to 174)  
AUTHORS  
Ahmadipour, M., Keivani Amineh, H., Sabahi, F., Mahboudi, F., Karimi Arzenani, M., Adeli, A. and Sarrafi Pouroushani, R.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (09-FEB-2004) Biotechnology, Pasteur Institute of Iran, 12 Farvardin, Tehran 69 13164, Iran  
FEATURES  
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|||||  
DB 132 TTGGGACCCACACTACTC 113

RESULT 149  
AY545672 174 bp RNA linear VRL 09-MAR-2004  
LOCUS  
DEFINITION  
Hepatitis C virus isolate IR-0652 5' UTR.  
ACCESSION  
AY545672  
VERSION  
AY545672.1 GI:45120595  
KEYWORDS  
Hepatitis C virus  
SOURCE  
Hepatitis C virus  
ORGANISM  
Hepatitis C virus  
REFERENCE  
1 (bases 1 to 174)  
AUTHORS  
Ahmadipour, M., Keivani Amineh, H., Sabahi, F., Mahboudi, F., Karimi Arzenani, M., Adeli, A. and Sarrafi Pouroushani, R.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (11-FEB-2004) Biotechnology, Pasteur Institute of Iran, 12 Farvardin, Tehran 69 13164, Iran  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
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Db 132 TTGGGACCCCACTACTC 113

RESULT 150  
AY545674/c 174 bp RNA linear VRL 09-MAR-2004  
LOCUS Hepatitis C virus isolate IR-1743 5' UTR.  
DEFINITION AY545674  
ACCESSION AY545674.1 GI:45120597  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virusess; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 174)  
AUTHORS Ahmadipour,M., Keivani Amineh,H., Sabahi,F., Mahboudi,F., Karimi Arzenani,M., Adeli,A. and Sarjami Fourooshani,R.  
TITLE Direct Submission  
JOURNAL Submitted (11-FEB-2004) Biotechnology, Pasteur Institute of Iran,  
12 Farvardin, Tehran 69 13164, Iran  
FEATURES  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 132 TTGGGACCCCACTACTC 113

RESULT 151  
AY545675/c 174 bp RNA linear VRL 09-MAR-2004  
LOCUS Hepatitis C virus isolate IR-1743 5' UTR.  
DEFINITION AY545675  
ACCESSION AY545675.1 GI:45120598  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virusess; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 174)  
AUTHORS Ahmadipour,M., Keivani Amineh,H., Sabahi,F., Mahboudi,F., Karimi Arzenani,M., Adeli,A. and Sarjami Fourooshani,R.  
TITLE Direct Submission  
JOURNAL Submitted (11-FEB-2004) Biotechnology, Pasteur Institute of Iran,  
12 Farvardin, Tehran 69 13164, Iran  
FEATURES  
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/country="Iran"  
/note="genotype: 4"  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
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Db 132 TTGGGACCCCACTACTC 113

RESULT 152  
AY545677/c 174 bp RNA linear VRL 09-MAR-2004  
LOCUS Hepatitis C virus isolate IR-1883 5' UTR.  
DEFINITION AY545677  
ACCESSION AY545677.1 GI:45120600  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virusess; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 174)  
AUTHORS Ahmadipour,M., Keivani Amineh,H., Sabahi,F., Mahboudi,F., Karimi Arzenani,M., Adeli,A. and Sarjami Fourooshani,R.  
TITLE Direct Submission  
JOURNAL Submitted (11-FEB-2004) Biotechnology, Pasteur Institute of Iran,  
12 Farvardin, Tehran 69 13164, Iran  
FEATURES  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
|||||  
Db 132 TTGGGACCCCACTACTC 113

RESULT 153  
AF506661/c 175 bp RNA linear VRL 20-MAY-2002  
LOCUS Hepatitis C virus isolate RI81 5' untranslated region, partial  
DEFINITION AF506661  
ACCESSION AF506661.1 GI:20978005  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Virusess; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 175)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 175)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia  
FEATURES  
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/organism="Hepatitis C virus"  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
169 TTGGGACCCCAACTACTC 150

RESULT 154  
AF506645/c 176 bp RNA linear VRL 20-MAY-2002  
LOCUS Hepatitis C virus isolate RIG78 5' untranslated region, partial  
DEFINITION  
ACCESSION AF506645  
VERSION AF506645  
KEYWORDS GI:20977989  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1 (bases 1 to 176)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 176)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
170 TTGGGACCCCAACTACTC 151

RESULT 155  
AF506658/c 176 bp RNA linear VRL 20-MAY-2002  
LOCUS Hepatitis C virus isolate RIG100 5' untranslated region, partial  
DEFINITION  
ACCESSION AF506658  
VERSION AF506658  
KEYWORDS GI:20978002  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1 (bases 1 to 176)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 176)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission

JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia  
FEATURES  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
170 TTGGGACCCCAACTACTC 151

RESULT 156  
AF506694/c 176 bp RNA linear VRL 20-MAY-2002  
LOCUS Hepatitis C virus isolate RIG99 5' untranslated region, partial  
DEFINITION  
ACCESSION AF506694  
VERSION AF506694  
KEYWORDS GI:20978038  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1 (bases 1 to 176)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 176)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia  
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QY 1 TTGGGACCCCAACTACTC 20  
170 TTGGGACCCCAACTACTC 151

RESULT 157  
AY145948/c 176 bp RNA linear VRL 12-NOV-2002  
LOCUS Hepatitis C virus isolate GAY149 5' UTR, partial sequence.  
DEFINITION  
ACCESSION AY145948  
VERSION AY145948  
KEYWORDS GI:24935076  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1 (bases 1 to 176)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 176)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission



Hepatitis C virus.  
1 (bases 1 to 176)  
REFERENCE  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE The prevalence and genetic variability of hepatitis C virus isolates in Western Siberia  
JOURNAL Unpublished  
2 (bases 1 to 176)  
REFERENCE  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (29-AUG-2002) Inst. Molecular Biology, State Research Center Vector, SRC VB Vector, Koltsovo, Novosibirskaya obl. 630559, Russia

FEATURES  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCACTACTC 20  
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131 TTGCGAGCCCACTACTC 112

Db 131 TTGCGAGCCCACTACTC 112

RESULT 158  
AY145951 176 bp RNA linear VRL 12-NOV-2002  
LOCUS Hepatitis C virus isolate GAA236 5' UTR, partial sequence.  
DEFINITION  
ACCESSION AY145951  
VERSION AY145951.1 GI:24935079  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
1 (bases 1 to 176)  
REFERENCE  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE The prevalence and genetic variability of hepatitis C virus isolates in Western Siberia  
JOURNAL Unpublished  
2 (bases 1 to 176)  
REFERENCE  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (29-AUG-2002) Inst. Molecular Biology, State Research Center Vector, SRC VB Vector, Koltsovo, Novosibirskaya obl. 630559, Russia

FEATURES  
source Location/Qualifiers  
1. 176  
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/country="Russia"  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCACTACTC 20  
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131 TTGCGAGCCCACTACTC 112

Db 131 TTGCGAGCCCACTACTC 112

RESULT 159

HCV6329/c  
LOCUS HCV6329 176 bp RNA linear VRL 25-MAY-1998  
DEFINITION Hepatitis C virus type 1b 5'UTR, isolate c94.6, partial.  
ACCESSION AJ006329  
VERSION AJ006329.1 GI:31522994  
KEYWORDS  
SOURCE Hepatitis C virus type 1b  
ORGANISM Hepatitis C virus type 1b  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
1 (bases 1 to 176)  
REFERENCE  
AUTHORS del Campo Terron,S., Moreno Garoz,N., Telleria Oriols,D. and Barcena Marugan,R  
TITLE Virus C de Hepatitis en pacientes transplantados de higado  
JOURNAL Unpublished  
2 (bases 1 to 176)  
REFERENCE  
AUTHORS del Campo Terron,S.  
TITLE Direct Submission  
JOURNAL Submitted (18-MAY-1998) del Campo Terron S., Gastroenterologia, Hospital Ramon y Cajal, CTRA Colmenar Km 9.1 Madrid, E-28034, SPAIN

FEATURES  
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QY 1 TTGCGAGCCCACTACTC 20  
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166 TTGCGAGCCCACTACTC 147

Db 166 TTGCGAGCCCACTACTC 147

RESULT 160  
AF506677 177 bp RNA linear VRL 20-MAY-2002  
LOCUS Hepatitis C virus isolate KGV69 5' untranslated region, partial  
DEFINITION  
ACCESSION AF506677  
VERSION AF506677.1 GI:20978021  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
1 (bases 1 to 177)  
REFERENCE  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
2 (bases 1 to 177)  
REFERENCE  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia

FEATURES  
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/country="Russia"  
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Best Local Similarity 100.0%; Pred. No. 0.14;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 170 TTGGGACCCCACTACTC 151

RESULT 161  
AF506680/c 177 bp RNA linear VRL 20-MAY-2002  
LOCUS Hepatitis C virus isolate KGV70 5' untranslated region, partial  
DEFINITION  
ACCESSION AF506680  
VERSION AF506680  
KEYWORDS AF506680.1 GI:20978024  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 177)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 177)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia  
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/country="Russia"  
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Query Match 100.0%; Score 20; DB 14; Length 177;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 170 TTGGGACCCCACTACTC 151

RESULT 162  
AF506686/c 177 bp RNA linear VRL 20-MAY-2002  
LOCUS Hepatitis C virus isolate RIG75 5' untranslated region, partial  
DEFINITION  
ACCESSION AF506686  
VERSION AF506686  
KEYWORDS AF506686.1 GI:20978030  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 177)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Genetic variability of hepatitis C virus in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 177)  
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.  
TITLE Direct Submission  
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia  
FEATURES  
source Location/Qualifiers  
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/db\_xref="taxon:11103"  
/country="Russia"  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 171 TTGGGACCCCACTACTC 152

RESULT 163  
AY190412/c 177 bp RNA linear VRL 07-NOV-2003  
LOCUS Hepatitis C virus isolate S21 5' noncoding region, partial  
DEFINITION  
ACCESSION AY190412  
VERSION AY190412  
KEYWORDS AY190412.1 GI:37779445  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 177)  
AUTHORS Lole,K.S., Jha,J.A., Shrotri,S.P., Tandon,B.N., Prasad,V.G. and Arankalle,V.A.  
TITLE Comparison of hepatitis C virus genotyping by 5' noncoding region- and core-based reverse transcriptase PCR assay with sequencing and use of the assay for determining subtype distribution in India  
JOURNAL J. Clin. Microbiol. 41 (11), 5240-5244 (2003)  
MEDLINE 22967393  
PUBMED 14605173  
REFERENCE 2 (bases 1 to 177)  
AUTHORS Lole,K.S., Jha,J.A., Shrotri,S.P., Tandon,B.N., Mohan Prasad,V.G. and Arankalle,V.A.  
TITLE Direct Submission  
JOURNAL Submitted (04-DEC-2002) Hepatitis Division, National Institute of Virology, 20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India  
FEATURES  
source Location/Qualifiers  
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/organism="Hepatitis C virus"  
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/isolate="S21"  
/db\_xref="taxon:11103"  
/country="India"

ORIGIN  
5'UTR  
Query Match 100.0%; Score 20; DB 14; Length 177;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 167 TTGGGACCCCACTACTC 148

RESULT 164  
AF463460/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TM37 5'UTR, partial sequence.  
DEFINITION  
ACCESSION AF463460  
VERSION AF463460.1 GI:18390060  
KEYWORDS AF463460.1 GI:18390060  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.

REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi.A. and Triki.H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi.A. and Triki.H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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Db 174 TTCCGACCCCAACTACTC 155

RESULT 165  
AF463462/C 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN25 5'UTR, partial sequence.  
DEFINITION AF463462  
ACCESSION AF463462.1 GI:18390062  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi.A. and Triki.H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi.A. and Triki.H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
Db 171 TTCCGACCCCAACTACTC 152

RESULT 166  
AF463463/C 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN28 5'UTR, partial sequence.  
DEFINITION AF463463  
ACCESSION AF463463.1 GI:18390063  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi.A. and Triki.H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi.A. and Triki.H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
Db 172 TTCCGACCCCAACTACTC 153

RESULT 167  
AF463464/C 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN4 5'UTR, partial sequence.  
DEFINITION AF463464  
ACCESSION AF463464.1 GI:18390064  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi.A. and Triki.H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi.A. and Triki.H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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ORIGIN  
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Db 172 TTTCGACCCCAACACTACTC 153

RESULT 168
AF463466/c 178 bp RNA linear VRL 29-JAN-2002
LOCUS
DEFINITION Hepatitis C virus isolate TN34 5'UTR, partial sequence.
ACCESSION AF463466
VERSION AF463466.1 GI:18390066
KEYWORDS
SOURCE
ORGANISM Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.

REFERENCE
AUTHORS 1 (bases 1 to 178)
          Djebbi, A. and Triki, H.
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates
        from Tunisian Patients
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 178)
AUTHORS Djebbi, A. and Triki, H.
TITLE Direct Submission
SUBMITTED (28-DEC-2001) Laboratoire de Virologie Clinique, Institut
Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002,
Tunisia

FEATURES
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QY 1 TTTCGACCCCAACACTACTC 20
    |||
Db 172 TTTCGACCCCAACACTACTC 153

RESULT 169
AF463467/c 178 bp RNA linear VRL 29-JAN-2002
LOCUS
DEFINITION Hepatitis C virus isolate TN16 5'UTR, partial sequence.
ACCESSION AF463467
VERSION AF463467.1 GI:18390067
KEYWORDS
SOURCE
ORGANISM Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.

REFERENCE
AUTHORS 1 (bases 1 to 178)
          Djebbi, A. and Triki, H.
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates
        from Tunisian Patients
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 178)
AUTHORS Djebbi, A. and Triki, H.
TITLE Direct Submission
SUBMITTED (28-DEC-2001) Laboratoire de Virologie Clinique, Institut
Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002,
Tunisia

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Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002,
Tunisia

FEATURES
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Db 172 TTTCGACCCCAACACTACTC 153

RESULT 170
AF463468/c 178 bp RNA linear VRL 29-JAN-2002
LOCUS
DEFINITION Hepatitis C virus isolate TN20 5'UTR, partial sequence.
ACCESSION AF463468
VERSION AF463468.1 GI:18390068
KEYWORDS
SOURCE
ORGANISM Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.

REFERENCE
AUTHORS 1 (bases 1 to 178)
          Djebbi, A. and Triki, H.
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates
        from Tunisian Patients
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 178)
AUTHORS Djebbi, A. and Triki, H.
TITLE Direct Submission
SUBMITTED (28-DEC-2001) Laboratoire de Virologie Clinique, Institut
Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002,
Tunisia

FEATURES
source Location/Qualifiers
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Db 172 TTTCGACCCCAACACTACTC 153

RESULT 171
AF463469/c 178 bp RNA linear VRL 29-JAN-2002
LOCUS
DEFINITION Hepatitis C virus isolate TN21 5'UTR, partial sequence.
ACCESSION AF463469
VERSION AF463469.1 GI:18390069
KEYWORDS
SOURCE
ORGANISM Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.

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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE  
1 (bases 1 to 178)  
AF463471/C  
AUTHORS  
Djebbi, A. and Triki, H.  
TITLE  
Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL  
Unpublished  
REFERENCE  
2 (bases 1 to 178)  
Djebbi, A. and Triki, H.  
AUTHORS  
Direct Submission  
TITLE  
Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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Qy  
1 TTCCGACCCCACTACTC 20  
173 TTCCGACCCCACTACTC 154

RESULT 172  
AF463470 178 bp RNA linear VRL 29-JAN-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate TN43 5'UTR, partial sequence.  
ACCESSION  
AF463470.1 GI:18390070  
KEYWORDS  
Hepatitis C virus  
SOURCE  
Hepatitis C virus  
ORGANISM  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE  
1 (bases 1 to 178)  
Djebbi, A. and Triki, H.  
AUTHORS  
Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL  
Unpublished  
REFERENCE  
2 (bases 1 to 178)  
Djebbi, A. and Triki, H.  
AUTHORS  
Direct Submission  
TITLE  
Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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Qy  
1 TTCCGACCCCACTACTC 20  
172 TTCCGACCCCACTACTC 153

RESULT 173  
AF463471 178 bp RNA linear VRL 29-JAN-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate TN23 5'UTR, partial sequence.  
ACCESSION  
AF463471  
AF463471.1 GI:18390071  
KEYWORDS  
Hepatitis C virus  
SOURCE  
Hepatitis C virus  
ORGANISM  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE  
1 (bases 1 to 178)  
Djebbi, A. and Triki, H.  
AUTHORS  
Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL  
Unpublished  
REFERENCE  
2 (bases 1 to 178)  
Djebbi, A. and Triki, H.  
AUTHORS  
Direct Submission  
TITLE  
Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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Qy  
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172 TTCCGACCCCACTACTC 153

RESULT 174  
AF463472 178 bp RNA linear VRL 29-JAN-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate TN2 5'UTR, partial sequence.  
ACCESSION  
AF463472  
AF463472.1 GI:18390072  
KEYWORDS  
Hepatitis C virus  
SOURCE  
Hepatitis C virus  
ORGANISM  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE  
1 (bases 1 to 178)  
Djebbi, A. and Triki, H.  
AUTHORS  
Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL  
Unpublished  
REFERENCE  
2 (bases 1 to 178)  
Djebbi, A. and Triki, H.  
AUTHORS  
Direct Submission  
TITLE  
Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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|||||  
Db 172 TTGCGACCCCAACTACTC 153

RESULT 175  
AF463474/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN14 5'UTR, partial sequence.  
DEFINITION AF463474  
ACCESSION AF463474.1 GI:18390074  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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ORIGIN 5'UTR  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
Db 172 TTGCGACCCCAACTACTC 153

RESULT 176  
AF463475/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN24 5'UTR, partial sequence.  
DEFINITION AF463475  
ACCESSION AF463475.1 GI:18390075  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.

TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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ORIGIN 5'UTR  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
|||||  
Db 172 TTGCGACCCCAACTACTC 153

RESULT 177  
AF463476/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN31 5'UTR, partial sequence.  
DEFINITION AF463476  
ACCESSION AF463476.1 GI:18390076  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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ORIGIN 5'UTR  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
Db 172 TTGCGACCCCAACTACTC 153

RESULT 178  
AF463477/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN33 5'UTR, partial sequence.  
DEFINITION AF463477  
ACCESSION AF463477.1 GI:18390077  
VERSION  
KEYWORDS

SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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Oy 1 TTGGGACCCCACTACTC 20  
Db 171 TTGGGACCCCACTACTC 152

RESULT 179  
AF463478 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN15 5'UTR, partial sequence.  
DEFINITION AF463478  
ACCESSION AF463478.1 GI:18390078  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCACTACTC 20  
Db 171 TTGGGACCCCACTACTC 152

Db 172 TTGGGACCCCACTACTC 153

RESULT 180  
AF463479 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN42 5'UTR, partial sequence.  
DEFINITION AF463479  
ACCESSION AF463479.1 GI:18390079  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCACTACTC 20  
Db 173 TTGGGACCCCACTACTC 154

RESULT 181  
AF463480 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN18 5'UTR, partial sequence.  
DEFINITION AF463480  
ACCESSION AF463480.1 GI:18390080  
VERSION  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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/country="Tunisia"  
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OY 1 TTCCGACCCCAACTACTC 20  
172 TTCCGACCCCAACTACTC 153

Db 172 TTCCGACCCCAACTACTC 153

RESULT 182  
AF463486/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate TN5 5'UTR, partial sequence.  
ACCESSION AF463486  
VERSION AF463486.1 GI:18390086  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.

REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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172 TTCCGACCCCAACTACTC 153

Db 172 TTCCGACCCCAACTACTC 153

RESULT 183  
AF463487/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate TN36 5'UTR, partial sequence.  
ACCESSION AF463487  
VERSION AF463487.1 GI:18390087  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.

REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished

2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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172 TTCCGACCCCAACTACTC 153

Db 172 TTCCGACCCCAACTACTC 153

RESULT 184  
AF463488/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate TN7 5'UTR, partial sequence.  
ACCESSION AF463488  
VERSION AF463488.1 GI:18390088  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepadnavirus.

REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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172 TTCCGACCCCAACTACTC 153

Db 172 TTCCGACCCCAACTACTC 153

RESULT 185  
AF463489/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS  
DEFINITION Hepatitis C virus isolate TN1 5'UTR, partial sequence.  
ACCESSION AF463489



VERSION AF463489.1 GI:18390089  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

FEATURES  
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OY 1 TTCCGACCCCAACTACTC 20  
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Db 173 TTCCGACCCCAACTACTC 154

RESULT 186  
AF463491/c 178 bp RNA linear VRL 29-JAN-2002  
LOCUS Hepatitis C virus isolate TN22 5'UTR, partial sequence.  
DEFINITION AF463491  
ACCESSION AF463491  
VERSION AF463491.1 GI:18390091  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Genotyping and Phylogenetic Analysis of Hepatitis C Virus Isolates from Tunisian Patients  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 178)  
AUTHORS Djebbi, A. and Triki, H.  
TITLE Direct Submission  
JOURNAL Submitted (28-DEC-2001) Laboratoire de Virologie Clinique, Institut Pasteur de Tunis, 13, Place Pasteur BP74, Belvedere, Tunis 1002, Tunisia

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OY 1 TTCCGACCCCAACTACTC 20  
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Db 171 TTCCGACCCCAACTACTC 152

RESULT 187  
AY145950/c 179 bp RNA linear VRL 12-NOV-2002  
LOCUS Hepatitis C virus isolate GAI195 5' UTR, partial sequence.  
DEFINITION AY145950  
ACCESSION AY145950  
VERSION AY145950.1 GI:24935078  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1 (bases 1 to 179)  
AUTHORS Shustov, A. V., Gavrilova, I. V. and Neresov, S. V.  
TITLE The prevalence and genetic variability of hepatitis C virus isolates in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 179)  
AUTHORS Shustov, A. V., Gavrilova, I. V. and Neresov, S. V.  
TITLE Direct Submission  
JOURNAL Submitted (29-AUG-2002) Inst. Molecular Biology, State Research Center Vector, SRC VB Vector, Koltsovo, Novosibirskaya obl. 630559, Russia

FEATURES  
source Location/Qualifiers  
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OY 1 TTCCGACCCCAACTACTC 20  
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Db 134 TTCCGACCCCAACTACTC 115

RESULT 188  
AY145973/c 180 bp RNA linear VRL 12-NOV-2002  
LOCUS Hepatitis C virus isolate KGV299 5' UTR, partial sequence.  
DEFINITION AY145973  
ACCESSION AY145973  
VERSION AY145973.1 GI:24935101  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
REFERENCE 1 (bases 1 to 180)  
AUTHORS Shustov, A. V., Gavrilova, I. V. and Neresov, S. V.  
TITLE The prevalence and genetic variability of hepatitis C virus isolates in Western Siberia  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 180)  
AUTHORS Shustov, A. V., Gavrilova, I. V. and Neresov, S. V.  
TITLE Direct Submission  
JOURNAL Submitted (29-AUG-2002) Inst. Molecular Biology, State Research Center Vector, SRC VB Vector, Koltsovo, Novosibirskaya obl. 630559, Russia

FEATURES  
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LOCUS	180 bp	RNA	linear	VR1_07-NOV-2003
DEFINITION	Hepatitis C virus isolate S38 5' noncoding region, partial sequence.			

ACCESSION	AY190502	GI:37779535
VERSION	AY190502.1	
KEYWORDS		
SOURCE	Hepatitis C virus	
ORGANISM	Hepatitis C virus	

REFERENCE  
AUTHORS  
1 (bases 1 to 180)  
Iole, K.S., Jha, J.A., Shrotri, S.P., Tandon, B.N., Prasad, V.G. and  
Aravindan, V.

TITLE	Comparison of hepatitis C virus genotyping by 5' noncoding region- and core-based reverse transcriptase PCR assay with sequencing and use of the assay for determining subtype distribution in India
JOURNAL	J. Clin. Microbiol. 41 (11) 5240-5244 (2003)
DOI	10.1128/JCM.41.11.5240-5244.2003

REFERENCE	AUTHORS	TITLE
2 (bases 1 to 180)	Loie, K.S., Jha, J.A., Shrotri, S.P., Tandon, B.N., Mohan Prasad, V.G. and Arankalle, V.A.	Direct Substitution

SOURCE	1	180	location/Qualifiers
JOURNAL			
Submitted	(04-DEC-2002)	Hepatitis Division, National Institute of Virology, 20-A, Dr. Ambedkar Road, Pune, Maharashtra 411 001, India	
FEATURES			

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Db      170 TTGCGACCCACACTACTC 151

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RESULT	190
AF134750/c	
LOCUS	181 bp RNA linear VRL 01-SEP-2000
DEFINITION	Hepatitis C virus isolate NY-1 5' non-coding region.
ACCSSION	M33476D

VERSION	AF134750.1	GI:9956918
KEYWORDS	.	
SOURCE	Hepatitis C virus	
ORGANISM	Hepatitis C virus	

REFERENCE

1 Hepacivirus.  
1 (bases 1 to 181)

DEFINITION Hepatitis C virus isolate NIV-5 5' non-coding region.  
ACCESSION AF134754  
VERSION AF134754.1 GI:9956922  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
JOURNAL Phylogenetic Analysis of Indian HCV Indian Isolates  
REFERENCE 2 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
TITLE Direct Submission  
SUBMITTED (12-MAR-1999) Hepatitis Department, National Institute of Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune, Maharashtra 411001, India  
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QY 1 TTGGGACCCCAACTACTC 20  
Db 170 TTGGGACCCCAACTACTC 151  
RESULT 193  
AF134756 181 bp RNA linear VRL 01-SEP-2000  
LOCUS AF134756  
DEFINITION Hepatitis C virus isolate NIV-7 5' non-coding region.  
ACCESSION AF134756  
VERSION AF134756.1 GI:9956924  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
JOURNAL Phylogenetic Analysis of Indian HCV Indian Isolates  
REFERENCE 2 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
TITLE Direct Submission  
SUBMITTED (12-MAR-1999) Hepatitis Department, National Institute of Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune, Maharashtra 411001, India  
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Db 170 TTGGGACCCCAACTACTC 151  
RESULT 194  
AF134757 181 bp RNA linear VRL 01-SEP-2000  
LOCUS AF134757  
DEFINITION Hepatitis C virus isolate NIV-8 5' non-coding region.  
ACCESSION AF134757  
VERSION AF134757.1 GI:9956925  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
JOURNAL Phylogenetic Analysis of Indian HCV Indian Isolates  
REFERENCE 2 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
TITLE Direct Submission  
SUBMITTED (12-MAR-1999) Hepatitis Department, National Institute of Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune, Maharashtra 411001, India  
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Db 170 TTGGGACCCCAACTACTC 151  
RESULT 195  
AF134758 181 bp RNA linear VRL 01-SEP-2000  
LOCUS AF134758  
DEFINITION Hepatitis C virus isolate NIV-9 5' non-coding region.  
ACCESSION AF134758  
VERSION AF134758.1 GI:9956926  
KEYWORDS Hepatitis C virus  
SOURCE Hepatitis C virus  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.  
REFERENCE 1 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
JOURNAL Phylogenetic Analysis of Indian HCV Indian Isolates  
REFERENCE 2 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
TITLE Direct Submission  
SUBMITTED (12-MAR-1999) Hepatitis Department, National Institute of Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune, Maharashtra 411001, India  
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/isolate="NIV-9"  
misc\_feature 1..181  
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QY 1 TTGGCGACCCCAACACTACTC 20  
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170 TTGGCGACCCCAACACTACTC 151

Db 170 TTGGCGACCCCAACACTACTC 151

RESULT 196  
AF134759/c 181 bp RNA linear VRL 01-SEP-2000  
LOCUS Hepatitis C virus isolate NIV-10 5' non-coding region.  
DEFINITION AF134759  
ACCESSION AF134759  
VERSION AF134759.1 GI:9956927  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
JOURNAL Phylogenetic Analysis of Indian HCV Indian Isolates  
TITLE Unpublished  
AUTHORS 2 (bases 1 to 181)  
Jha,J. and Arankalle,V.A.  
REFERENCE Direct Submission  
TITLE Submitted (12-MAR-1999) Hepatitis Department, National Institute of  
Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune,  
Maharashtra 411001, India  
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170 TTGGCGACCCCAACACTACTC 151

Db 170 TTGGCGACCCCAACACTACTC 151

RESULT 197  
AF134760/c 181 bp RNA linear VRL 01-SEP-2000  
LOCUS Hepatitis C virus isolate NIV-11 5' non-coding region.  
DEFINITION AF134760  
ACCESSION AF134760  
VERSION AF134760.1 GI:9956928  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
JOURNAL Phylogenetic Analysis of Indian HCV Indian Isolates  
TITLE Unpublished  
AUTHORS 2 (bases 1 to 181)  
Jha,J. and Arankalle,V.A.  
REFERENCE Direct Submission  
TITLE Submitted (12-MAR-1999) Hepatitis Department, National Institute of  
Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune,  
Maharashtra 411001, India  
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QY 1 TTGGCGACCCCAACACTACTC 20  
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170 TTGGCGACCCCAACACTACTC 151

Db 170 TTGGCGACCCCAACACTACTC 151

RESULT 198  
AF158605/c 181 bp RNA linear VRL 31-AUG-2000  
LOCUS Hepatitis C virus isolate NIV-12 5' non-coding region.  
DEFINITION AF158605  
ACCESSION AF158605  
VERSION AF158605.1 GI:9954158  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 181)  
AUTHORS Jha,J.A. and Arankalle,V.A.  
JOURNAL Phylogenetic Analysis of Indian HCV Isolates  
TITLE Unpublished  
AUTHORS 2 (bases 1 to 181)  
Jha,J.A. and Arankalle,V.A.  
REFERENCE Direct Submission  
TITLE Submitted (11-JUN-1999) Hepatitis Department, National Institute of  
Virology, 20-A, Dr. Ambedkar Road, Pune, Maharashtra 411001, India  
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ORIGIN

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QY 1 TTGGCGACCCCAACACTACTC 20  
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170 TTGGCGACCCCAACACTACTC 151

Db 170 TTGGCGACCCCAACACTACTC 151

RESULT 199  
AF158607/c 181 bp RNA linear VRL 31-AUG-2000  
LOCUS Hepatitis C virus isolate NIV-34 5' non-coding region.  
DEFINITION AF158607  
ACCESSION AF158607  
VERSION AF158607.1 GI:9954160  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
JOURNAL Phylogenetic Analysis of Indian HCV Indian Isolates  
TITLE Unpublished  
AUTHORS 2 (bases 1 to 181)  
Jha,J. and Arankalle,V.A.  
REFERENCE Direct Submission  
TITLE Submitted (12-MAR-1999) Hepatitis Department, National Institute of  
Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune,  
Maharashtra 411001, India  
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Query Match 100.0%; Score 20; DB 14; Length 181;  
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QY 1 TTGGCGACCCCAACACTACTC 20  
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170 TTGGCGACCCCAACACTACTC 151

Db 170 TTGGCGACCCCAACACTACTC 151

RESULT 199  
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DEFINITION AF158607  
ACCESSION AF158607  
VERSION AF158607.1 GI:9954160  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
JOURNAL Phylogenetic Analysis of Indian HCV Indian Isolates  
TITLE Unpublished  
AUTHORS 2 (bases 1 to 181)  
Jha,J. and Arankalle,V.A.  
REFERENCE Direct Submission  
TITLE Submitted (12-MAR-1999) Hepatitis Department, National Institute of  
Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune,  
Maharashtra 411001, India  
FEATURES  
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170 TTGGCGACCCCAACACTACTC 151

Db 170 TTGGCGACCCCAACACTACTC 151

TITLE Direct Submission  
JOURNAL Submitted (12-MAR-1999) Hepatitis Department, National Institute of  
Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune,  
Maharashtra 411001, India  
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Db 170 TTGGCGACCCCAACACTACTC 151

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ACCESSION AF158605  
VERSION AF158605.1 GI:9954158  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 181)  
AUTHORS Jha,J.A. and Arankalle,V.A.  
JOURNAL Phylogenetic Analysis of Indian HCV Isolates  
TITLE Unpublished  
AUTHORS 2 (bases 1 to 181)  
Jha,J.A. and Arankalle,V.A.  
REFERENCE Direct Submission  
TITLE Submitted (11-JUN-1999) Hepatitis Department, National Institute of  
Virology, 20-A, Dr. Ambedkar Road, Pune, Maharashtra 411001, India  
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QY 1 TTGGCGACCCCAACACTACTC 20  
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170 TTGGCGACCCCAACACTACTC 151

Db 170 TTGGCGACCCCAACACTACTC 151

RESULT 199  
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LOCUS Hepatitis C virus isolate NIV-34 5' non-coding region.  
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ACCESSION AF158607  
VERSION AF158607.1 GI:9954160  
KEYWORDS  
SOURCE Hepatitis C virus  
ORGANISM Hepatitis C virus  
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
Hepacivirus.  
REFERENCE 1 (bases 1 to 181)  
AUTHORS Jha,J. and Arankalle,V.A.  
JOURNAL Phylogenetic Analysis of Indian HCV Indian Isolates  
TITLE Unpublished  
AUTHORS 2 (bases 1 to 181)  
Jha,J. and Arankalle,V.A.  
REFERENCE Direct Submission  
TITLE Submitted (12-MAR-1999) Hepatitis Department, National Institute of  
Virology, 20-A, Dr. Ambedkar Road, Post Box No. 11, Pune,  
Maharashtra 411001, India  
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170 TTGGCGACCCCAACACTACTC 151

Db 170 TTGGCGACCCCAACACTACTC 151

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

Hepacivirus.

1 (bases 1 to 181)

Jha,J.A. and Arankalle,V.A.

Phylogenetic Analysis of Indian HCV Isolates

Unpublished

2 (bases 1 to 181)

Jha,J.A. and Arankalle,V.A.

Direct Submission

Submitted (11-JUN-1999) Hepatitis Department, National Institute of

Virology, 20-A, Dr. Ambedkar Road,, Pune, Maharashtra 411001, India

Location/Qualifiers

1..181

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/mol\_type="genomic RNA"

/isolate="NIV-34"

/db\_xref="taxon:11103"

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1..181

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Best Local Similarity 100.0%; Pred. No. 0.14;

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DB

170 TTGGGACCCACACTACTC 151

RESULT 200

AF158608/C

LOCUS

AF158608 181 bp RNA linear VRL 31-AUG-2000

DEFINITION Hepatitis C virus isolate NIV-35 5' non-coding region.

ACCESSION

AF158608

VERSION

AF158608.1 GI:9954161

KEYWORDS

Hepatitis C virus

Hepatitis C virus

Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

ORGANISM

Hepacivirus.

1 (bases 1 to 181)

Jha,J.A. and Arankalle,V.A.

Phylogenetic Analysis of Indian HCV Isolates

Unpublished

2 (bases 1 to 181)

Jha,J.A. and Arankalle,V.A.

Direct Submission

Submitted (11-JUN-1999) Hepatitis Department, National Institute of

Virology, 20-A, Dr. Ambedkar Road,, Pune, Maharashtra 411001, India

Location/Qualifiers

1..181

/organism="Hepatitis C virus"

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1..181

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# ORIGIN

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

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DB

170 TTGGGACCCACACTACTC 151

Search completed: April 25, 2005, 13:37:23  
Job time : 871.789 secs

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C	105	14	70.0	668	7	CF351064	r166h11.y
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C	138	14	70.0	768	2	BM172443	Danio rer
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C	143	14	70.0	783	8	BZ822648	PUFMB95TD
C	144	14	70.0	783	8	BZ822648	PUFMB95TD
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C	146	14	70.0	791	8	BZ468932	Mus muscu
C	147	14	70.0	793	5	BZ477400	BONDF31TR
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C	152	14	70.0	806	9	CG155334	PUIRKS9TB
C	153	14	70.0	809	2	BF696995	602130174
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977 13 65.0 786 8 BH465051 BH465051 BOGH086TF
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982 13 65.0 788 9 AG575010 AG575010 Mus muscu
983 13 65.0 789 4 BJ742507 BJ742507 B742507
984 13 65.0 789 6 CB169580 CB169580 RUC603000
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986 13 65.0 791 7 CO245229 CO245229 AGENCOURT
c 987 13 65.0 791 8 BZ695278 BZ695278 SP_Ba006
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## ALIGNMENTS

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RESULT 1
LOCUS CV350260 597 bp mRNA linear EST 27-SEP-2004
DEFINITION MR2-SN0006-050600-002-b11 SN0006 Homo sapiens cDNA, mRNA sequence.
ACCESSION CV350260
VERSION CV350260.1 GI:52700315
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 597) Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Negal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Coes, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

```

```

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. http://www.ludwig.org.br.
Location/Qualifiers
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Site 2: SmaI: A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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DEFINITION NL1-DJ12C Human NotI clones Homo sapiens genomic, genomic survey
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ACCESSION AQ938853
VERSION AQ938853.1 GI:7215231
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 144) Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Zabarovskiy, E.R., Gizatullin, R., Podowski, R.M., Zabarovska, V.V.,
Kie, L., Muravenko, O.V., Kozyrev, S., Petrenko, L., Skobeleva, N.,
Li, J., Protolopov, A., Kashuba, V., Ernberg, I., Winberg, G. and
Wahlestedt, C.
NotI clones in the analysis of the human genome
Nucleic Acids Res. 28 (7), 1635-1639 (2000)
20175728
PUBMED 10710430
COMMENT Contact: Podowski RM
Center for Genomics Research
Karolinska Institute
17177 Stockholm, Sweden
Tel: +46-8-728-6372
Fax: +46-8-337983
Email: Raf.Podowski@cgr.ki.se
Class: NotI site.
Location/Qualifiers
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QY 3 CGGACCCCACTACTC 18
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RESULT 3
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DEFINITION rswp0_002823.y1 swp Bombyx mori cDNA, mRNA sequence.
ACCESSION CK560425
VERSION CK560425.1 GI:40944879
KEYWORDS EST.
SOURCE Bombyx mori (domestic silkworm)
ORGANISM Bombyx mori
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
Bombycoidea; Bombycidae; Bombyx.  
1 (bases 1 to 586)

REFERENCE  
AUTHORS  
Xia, Q., Zhou, Z., Lu, C., Cheng, D., Dai, F., Li, B., Zhao, P., Zha, X.,  
Cheng, T., Chai, C., Pan, G., Xu, J., Liu, C., Lin, Y., Qian, D., Hou, Y.,  
Wu, Z., Li, G., Pan, M., Li, C., Shen, Y., Lan, X., Yuan, L., Li, T.,  
Xu, H., Yang, G., Wan, Y., Zhu, Y., Yu, M., Shen, W., Wu, D., Xiang, Z.,  
Yu, J., Wang, J., Li, R. Q., Shi, J. P., Li, H., Li, G. Y., Su, J. N.,  
Wang, X. L., Li, G. Q., Zhang, Z. J., Wu, Q. F., Li, J., Zhang, Q. P., Wei, N.,  
Xu, J. Z., Sun, H. B., Dong, L., Liu, D. Y., Zhao, S. L., Zhao, X. L.,  
Meng, Q. S., Lan, F. D., Huang, X. G., Li, Y. Z., Fang, F., Li, C. F.,  
Li, D. W., Sun, Y. Q., Zhang, Z. P., Yang, Z., Huang, Y. Q., Xi, Y., Qi, Q. H.,  
He, D. D., Huang, H. Y., Zhang, X. W., Wang, Z. Q., Li, W. J., Cao, Y. Z.,  
Wang, J., Ye, J., Ji, H., Li, S. T., Ni, P. X., Zhang, J. G., Zhang, Y.,  
Zheng, H. K., Ye, C., Wang, J., Wong, G. K. S. and Yang, H. M.  
A draft sequence for the genome of the domesticated silkworm  
(Bombyx mori)  
Unpublished (2004)  
Contact: Zhonghui Xiang  
Southwest Agricultural University  
Chongqing Baibei  
Tel: 86-23-68251123  
Fax: 86-23-68251128  
Email: xzh@swau.cq.cn.  
Location/Qualifiers

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGGGACCCCAACTA 17  
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Db 217 TTGGGACCCCAACTA 232

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DEFINITION genomic survey sequence.  
ACCESSION CC876242  
VERSION CC876242.1 GI:33306164  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
Clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 293)  
Yu, Y., Kim, H. R., Hatfield, J., Soderlund, C., Bharti, A. K., Messing, J.  
and Wing, R.  
Sequencing of the maize genome  
Unpublished (2003)  
Contact: Rod Wing  
Arizona Genomics Institute  
University of Arizona  
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ  
85721-0088 USA  
Tel: 520 626 3967  
Fax: 520 621 9288  
Email: http://genome.arizona.edu  
PCR Primers  
FORWARD: T7

BACKWARD: M13r  
Plate: 0194 row: M column: 08  
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Class: BAC ends.  
Location/Qualifiers

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Db 251 TTGGGACCCCAACAC 237

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DEFINITION ZMMBB0625L20 5', genomic survey sequence.  
ACCESSION CU283937  
VERSION CU283937.1 GI:42498324  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
Clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 328)  
Bharti, A. K., Young, S., Kavchok, S., Keltner, G., Bronzino, A. C.,  
Zohovetz, V., Fuks, G., Yu, Y., Wing, R. and Messing, J.  
Sequencing of the maize genome at PCR (2003c)  
Unpublished (2003)  
Contact: Bharti, A. K.  
Dr. Joachim Messing's lab  
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
University  
190 Freilichuysen Road, Piscataway, NJ 08854, USA  
Tel: 732 445 3801  
Fax: 732 445 5735  
Email: bharti@waksman.rutgers.edu  
Seq primer: T7  
Class: BAC ends  
High quality sequence start: 126.  
Location/Qualifiers

FEATURES  
source  
1..328  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBB0625L20"  
/lab\_host="E. coli DH10B"  
/clone\_lib="ZMMBB (HindIII)"  
/note="Vector: pCUG1; Site\_1: HindIII; Site\_2: HindIII"

ORIGIN  
Query Match 75.0%; Score 15; DB 9; Length 328;  
Best Local Similarity 100.0%; Pred. No. 11e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACAC 15  
|||||

DB 244 TTCGGACCCACACTA 230

RESULT 6  
LOCUS AG306140/c  
DEFINITION Mus musculus molossinus DNA, clone:MSM901-086P16.T7, genomic survey sequence.  
ACCESSION AG306140  
VERSION AG306140.1 GI:47879094  
KEYWORDS GSS.  
SOURCE Mus musculus molossinus  
ORGANISM Mus musculus molossinus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
TITLE BAC end Sequences of Library MSM901  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 395)  
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: hattori@gsc.riken.jp URL: http://ngp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
JOURNAL Clones are derived from the mouse BAC library MSM901. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).  
Tsubura Institute, Bio Resource Center,  
The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
Koyadai, Tsukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@rtc.riken.jp  
PRIMERS

COMMENT  
Sequencing : T7  
LIBRARY  
Vector : PBACe3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI

FEATURES  
source  
1..395  
/organism="Mus musculus molossinus"  
/mol\_type="genomic DNA"  
/sub\_species="molossinus"  
/db\_xref="taxon:57486"  
/clone="MSM901-086P16.T7"  
/sex="male"  
/tissue\_type="mixture of kidney and spleen"  
/clone\_lib="MSM901 Mouse Male BAC Library"

ORIGIN  
Query Match 75.0%; Score 15; DB 9; Length 395;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCGGACCCACACTA 17  
DB 336 CCGGACCCACACTA 322

RESULT 7  
LOCUS AI891392/c  
DEFINITION 457 bp mRNA linear EST 27-JUL-1999  
AI891392 614021B04.x1 614 - root cDNA library from Walbot Lab Zea mays cDNA,  
mRNA sequence.  
ACCESSION AI891392  
VERSION AI891392.1 GI:5597294  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

REFERENCE  
1 (bases 1 to 457)  
AUTHORS Walbot, V.  
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University  
JOURNAL Unpublished (1999)  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 614021 row: E column: 04.

FEATURES  
source  
1..457  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="W23"  
/db\_xref="taxon:4577"  
/tissue\_type="root"  
/dev\_stage="3-4 days old"  
/lab\_host="XLOIR"  
/clone\_lib="614 - root cDNA library from Walbot Lab"  
/note="Organ: root; Vector: pBluescriptII SK+; Site: 1: EcoRI; Site 2: XhoI; 3-4 days old root tissue from Walbot Lab (LM)"

ORIGIN  
Query Match 75.0%; Score 15; DB 1; Length 457;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCGGACCCACACTA 17  
DB 298 CCGGACCCACACTA 284

RESULT 8  
LOCUS AZ170379  
DEFINITION 468 bp DNA linear GSS 29-AUG-2000  
SP 0116 Al G11 T7A Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=116 Col=21 Row=M, genomic survey sequence.  
ACCESSION AZ170379  
VERSION AZ170379.1 GI:8340747  
KEYWORDS GSS.  
SOURCE Strongylocentrotus purpuratus  
ORGANISM Strongylocentrotus purpuratus  
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinoidea;  
Strongylocentrotidae; Strongylocentrotus.  
1 (bases 1 to 468)  
Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray, G.A., Ertensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. and Hood, L.  
A sea urchin genome project: sequence scan, virtual map, and additional resources  
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)  
JOURNAL MEDLINE  
PUBMED 20402566  
10920195  
CONTACT: Cameron, RA, Davidson, EH, Hood, L  
Division of Biology 156-29  
California Institute of Technology  
Pasadena California 91125, USA  
Tel: (626) 395-8421  
Fax: (626) 793-3047  
Email: acameron@caltech.edu  
Plate: 116 row: M column: 21  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 468.



## FEATURES

source

## Location/Qualifiers

1..468  
/organism="Strongylocentrotus purpuratus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7668"  
/clone\_lib="Plate=116 Col=21 Row=M"  
/clone\_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"  
/note="Organ: sperm; Vector: BAC3.6; BAC clones in E-Coli DH10B"

## ORIGIN

Query Match 75.0%; Score 15; DB 8; Length 468;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCACACTACTC 20  
DB 407 GACCCACACTACTC 421

## RESULT 9

BF610107/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BF610107 479 bp mRNA linear EST 07-MAY-2003  
NXSI\_054\_G10\_F NXSI (Nef Xylem Side wood Inclined) Pinus taeda CDNA  
clone NXSI\_054\_G10\_5', mRNA sequence.  
BF610107  
BF610107.1 GI:11778429  
EST.  
Pinus taeda (loblolly pine)  
Pinus taeda  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
1 (bases 1 to 479)  
Sederoff, R.  
Molecular Basis of Wood Formation in the Pine Megagenome  
Unpublished (2000)  
Contact: Sederoff, Ron  
Forest Biotechnology  
North Carolina State University  
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,  
NC 27695, USA  
Tel: 919 515 7800  
Fax: 919 515 7801  
Email: ron\_sederoff@ncsu.edu, jerri\_johnson@ncsu.edu  
Please see <http://web.ahc.umn.edu/biodata/nsfpine/> for further  
information.  
Seq primer: T3.

COMMENT

## FEATURES

source

## Location/Qualifiers

1..479  
/organism="Pinus taeda"  
/mol\_type="mRNA"  
/strain="Coastal plain loblolly pine from North Carolina"  
/db\_xref="taxon:3352"  
/clone="NXSI\_054\_G10"  
/tissue\_type="Xylem"  
/cell\_type="Side"  
/dev\_stage="Juvenile"  
/lab\_host="XLI-Blue"  
/clone\_lib="NXSI (Nef Xylem Side wood Inclined)"  
/note="Vector: Bluescript SK; Site 1: Eco RI; Site 2:  
XhoI. The library is from early (spring) wood, taken from  
three six-year old trees (three different genotypes), in  
the juvenile phase. These trees were induced to form side  
wood by bending to a 45 degree angle and tying them to the  
ground. Differentiating xylem was harvested from the sides  
of the inclined stems, and a mixture of all three  
genotypes was used for the library. oligo-dt primed cDNA  
was directionally cloned into the EcoRI-XhoI Bluescript SK  
vector arms. NOTE: The sequences contain a 'cDNA adapter'  
between the EcoRI site and the start of the EST. The  
adapter sequence is 'AATTCGCGACGAG'."

ORIGIN

Query Match 75.0%; Score 15; DB 2; Length 479;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCACACTACTC 20  
DB 18 GACCCACACTACTC 4

## RESULT 10

AM037206

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AM037206 496 bp mRNA linear EST 15-SEP-1999  
614021B04.y1 614 - root cDNA library from Walbot Lab Zea mays CDNA,  
mRNA sequence.  
AM037206  
AM037206.1 GI:5895960  
EST.  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
Clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 496)  
Walbot, V.  
Maize ESTs from various cDNA libraries sequenced at Stanford  
University  
Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 614021 row: B column: 04.

COMMENT

## FEATURES

source

## Location/Qualifiers

1..496  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="W23"  
/db\_xref="taxon:4577"  
/tissue\_type="root"  
/dev\_stage="3-4 days old"  
/lab\_host="XLOLR"  
/clone\_lib="614 - root cDNA library from Walbot Lab"  
/note="Organ: root; Vector: pBluescriptII SK+; Site 1:  
EcoRI; Site 2: XhoI; 3-4 days old root tissue from Walbot  
Lab (LM) "

## ORIGIN

Query Match 75.0%; Score 15; DB 2; Length 496;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGGACCCACACTCA 17  
DB 168 CGGACCCACACTCA 182

## RESULT 11

AZ170708

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AZ170708 549 bp DNA linear GSS 29-AUG-2000  
SP 0117.AL.H09.T7A Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=117 Col=17 Row=0, genomic survey sequence.  
AZ170708  
AZ170708.1 GI:8341076  
GSS.  
Strongylocentrotus purpuratus  
Strongylocentrotus purpuratus  
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
Echinoidea; Euechinoidea; Echinacea; Echinoida;

REFERENCE 1 (bases 1 to 549)  
 AUTHORS Cameron, R.A., Mahairas, G., Raat, J.P., Martinez, P., Blondi, T.R., Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H., and Hood, L.  
 TITLE A sea urchin genome project: Sequence scan, virtual map, and additional resources  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)  
 MEDLINE 20402566  
 PUBMED 10920195  
 COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L  
 Division of Biology 156-29  
 California Institute of Technology  
 Pasadena California 91125, USA  
 Tel: (626) 395-8421  
 Fax: (626) 793-3047  
 Email: acameron@caltech.edu  
 Plate: 117 row: O column: 17  
 Seq primer: 17  
 Class: BAC ends  
 High quality sequence stop: 549.  
 Location/Qualifiers  
 1..549  
 /organism="Strongylocentrotus purpuratus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7668"  
 /clone="Plate:117 Col:17 Row:O"  
 /clone\_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"  
 /note="Organ: sperm; Vector: BAC3.6; BAC clones in E-Coli DH10B"

ORIGIN  
 Query Match 75.0%; Score 15; DB 8; Length 549;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 394 GACCCACACTACTC 408  
 |||||  
 |||||

RESULT 12  
 CA772709/c 599 bp mRNA linear EST 03-DEC-2002  
 LOCUS 1083102.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6133106 5',  
 DEFINITION mRNA sequence.  
 CA772709  
 VERSION CA772709.1 GI:26009976  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 599)  
 Melton, P., Brown, J., Kenney, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scarsce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blisstein, A., Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tesgareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.  
 Endocrine Pancreas Consortium  
 Unpublished (2000)  
 Other ESTs: 1083102.x1  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biohp.harvard.edu

TITLE  
 JOURNAL  
 COMMENT

REFERENCE 1  
 AUTHORS Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@wustl.edu)  
 TITLE  
 JOURNAL  
 COMMENT

FEATURES  
 source  
 1..599  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6133106"  
 /tissue\_type="Purified pancreatic islet"  
 /lab\_host="DH10B"  
 /clone\_lib="HR85 islet"  
 /note="Organ: Pancreas; Vector: phagescript SK(-); Site\_1: NotI, Site\_2: XhoI, cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110. E-mail: hinoue@ingate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN  
 Query Match 75.0%; Score 15; DB 6; Length 599;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 80 CGCGACCCACACTA 66  
 |||||  
 |||||

RESULT 13  
 CL934496 616 bp DNA linear GSS 14-SEP-2004  
 LOCUS OA\_ABA0044F03.r OA\_ABA Oryza australiensis genomic clone  
 DEFINITION OA\_ABA0044F03 3', genomic survey sequence.  
 CL934496  
 VERSION CL934496.1 GI:52063100  
 KEYWORDS GSS.  
 SOURCE Oryza australiensis  
 ORGANISM Oryza australiensis  
 Eukaryota; Viridiplantae; Striptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 616)  
 Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.  
 OMAP Project  
 Unpublished (2004)  
 Contact: Rod A. Wing  
 Arizona Genomics Institute  
 University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9595  
 Fax: 520 621 1259  
 Email: http://genome.arizona.edu  
 PCR Primers  
 FORWARD: TAA TAC GAC TCA CTA TAG GG  
 BACKWARD: CAC TCA TTA GGC ACC CCA  
 Plate: 0044 row: F column: 03  
 Seq primer: CAC TCA TTA GGC ACC CCA  
 Class: BAC ends.  
 Location/Qualifiers  
 1..616  
 /organism="Oryza australiensis"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:4532"  
 /clone="OA\_ABA0044F03"  
 /tissue\_type="young leaves"

FEATURES  
 source

ORIGIN  
 /lab host="DH10B T1 phage resistant"  
 /clone\_lib="OA\_Aba"  
 /note="Vector: pAGIBAC1, Site\_1: HindIII, Site\_2: HindIII"

Query Match 75.0%; Score 15; DB 9; Length 616;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCAACTACTC 20  
 Db 140 GACCCAACTACTC 154

RESULT 14  
 A0325164/c 624 bp DNA linear GSS 08-JAN-1999  
 LOCUS mgxb0020P04r CUGI Rice Blast BAC library Magnaporthe grisea genomic  
 DEFINITION clone mgxb0020P04r, genomic survey sequence.

ACCESSION A0325164.1 GI:4117016  
 VERSION A0325164.1  
 KEYWORDS GSS.  
 SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
 ORGANISM Magnaporthe grisea  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Magnaporthe grisea

REFERENCE 1 (bases 1 to 624)  
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,  
 Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.  
 A BAC End Sequencing Framework to Sequence the Magnaporthe grisea  
 Genome

JOURNAL Unpublished (1998)

COMMENT Contact: Dean RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson University, Clemson, SC 29634  
 Tel: 864 656 5737  
 Fax: 864 656 4293  
 Email: rdean@clemson.edu  
 Seq primer: GGAAACAGCTATGACCATG  
 Class: BAC ends  
 High quality sequence stop: 395.  
 Location/Qualifiers

FEATURES  
 source 1..624

/organism="Magnaporthe grisea"  
 /mol\_type="genomic DNA"  
 /strain="70-15"  
 /db\_xref="taxon:148305"  
 /clone="mgxb0020P04r"  
 /issue\_type="Protoplasts"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="CUGI Rice Blast BAC library"  
 /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;  
 Rice blast is one of the most devastating fungal diseases  
 of rice world wide. It is a filamentous ascomycete with  
 a haploid genome (n=7) of approximately 40 Mbp. Rice  
 blast is an important model fungal pathogen for studying  
 numerous aspects of the fungal-host interaction. In  
 order to facilitate genome wide analysis, a BAC library  
 containing 9216 clones with an average insert size of 130  
 kbp was constructed. This library represents greater  
 than 25X genome coverage. High density colony filters  
 are available upon request."

ORIGIN

Query Match 75.0%; Score 15; DB 8; Length 624;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCAACTACTC 20  
 Db 248 GACCCAACTACTC 234

RESULT 15  
 A0286947/c 635 bp DNA linear GSS 03-DEC-1998  
 LOCUS mgxb0015C17r CUGI Rice Blast BAC library Magnaporthe grisea genomic

DEFINITION clone mgxb0015C17r, genomic survey sequence.

ACCESSION A0286947  
 VERSION A0286947.1 GI:3948033  
 KEYWORDS GSS.  
 SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
 ORGANISM Magnaporthe grisea  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Magnaporthe grisea

REFERENCE 1 (bases 1 to 635)  
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,  
 Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.  
 A BAC End Sequencing Framework to Sequence the Magnaporthe grisea  
 Genome

JOURNAL Unpublished (1998)

COMMENT Contact: Dean RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson University, Clemson, SC 29634  
 Tel: 864 656 5737  
 Fax: 864 656 4293  
 Email: rdean@clemson.edu  
 Seq primer: GGAAACAGCTATGACCATG  
 Class: BAC ends  
 High quality sequence start: 18  
 High quality sequence stop: 464.  
 Location/Qualifiers

FEATURES  
 source 1..635

/organism="Magnaporthe grisea"  
 /mol\_type="genomic DNA"  
 /strain="70-15"  
 /db\_xref="taxon:148305"  
 /clone="mgxb0015C17r"  
 /issue\_type="Protoplasts"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="CUGI Rice Blast BAC library"  
 /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII;  
 Rice blast is one of the most devastating fungal diseases  
 of rice world wide. It is a filamentous ascomycete with  
 a haploid genome (n=7) of approximately 40 Mbp. Rice  
 blast is an important model fungal pathogen for studying  
 numerous aspects of the fungal-host interaction. In  
 order to facilitate genome wide analysis, a BAC library  
 containing 9216 clones with an average insert size of 130  
 kbp was constructed. This library represents greater  
 than 25X genome coverage. High density colony filters  
 are available upon request."

ORIGIN

Query Match 75.0%; Score 15; DB 8; Length 635;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCAACTACTC 20  
 Db 271 GACCCAACTACTC 257

RESULT 16

LOCUS B2247695 650 bp DNA linear GSS 12-OCT-2002  
 DEFINITION CH230-408D6, TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone

ACCESSION B2247695

VERSION B2247695.1 GI:23908877

KEYWORDS GSS.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus  
1 (bases 1 to 650)  
Zhao, S., Shetty, U., Shatsman, S., Tsagaye, G., Geer, K.,  
Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,  
Ri998, F., de Jong, P. and Fraser, C.M.  
Rat BAC End Sequences from Library CHORI-230 MboI segment  
Unpublished (1999)  
Other GSSs: CH230-408D6.TVB  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0208  
Fax: 301 838 0208  
Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230  
(http://www.chori.org/bacpac/rat230.htm). For BAC library  
availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/or\_ering\_information.htm). BAC end  
page: http://www.tigr.org/cdb/bac\_ends/rat/bac\_end\_intro.html  
Plate: 408 row: D column: 6  
Seq primer: SP6  
Class: BAC ends.

#### FEATURES

source

Location/Qualifiers  
1..650  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/strain="BN/SnHsd/MCw"  
/db\_xref="taxon:10116"  
/clone="CH230-408D6"  
/sex="Female"  
/cell\_type="Brain"  
/clone\_lib="CHORI-230 Segment 2"  
/note="Vector: pPARAC1.3; Site\_1: MboI; Site\_2: MboI;  
CHORI-230 Rat (BN/SnHsd/MCw) BAC library produced by  
Pieter de Jong"

#### ORIGIN

Query Match 75.0%; Score 15; DB 8; Length 650;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 GACCCAACTACTC 20  
Db 423 GACCCAACTACTC 437

RESULT 17  
LOCUS CG19811 721 bp DNA linear GSS 26-AUG-2003  
DEFINITION OGEV51TV\_ZM\_0.7.1.5\_Zea mays genomic clone ZMEMA0523105,  
genomic survey sequence.  
ACCESSION CG19811.  
VERSION CG19811.1 GI:34237077  
KEYWORDS GSS  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 721)  
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,  
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, V.A., Rohlfing, T.,  
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other GSSs: OGEV51TV  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TP  
Class: sheared ends.  
Location/Qualifiers  
1..721  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_lib="ZM\_0.7.1.5\_KB"  
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

#### ORIGIN

Query Match 75.0%; Score 15; DB 9; Length 721;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 GACCCAACTACTC 20  
Db 41 GACCCAACTACTC 55

RESULT 18  
LOCUS CV435578/c 784 bp mRNA linear EST 29-SEP-2004  
DEFINITION 59138.1 Suspension culture Solanum tuberosum cDNA clone 59138 5',  
mRNA sequence.  
ACCESSION CV435578  
VERSION CV435578.1 GI:52844868  
KEYWORDS EST.  
SOURCE Solanum tuberosum (potato)  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamiales; Solanales; Solanaceae; Solanum.  
1 (bases 1 to 784)  
Pilm, B., Rochwell, C., Sardana, R., Griffiths, R., Laque, M., De  
Koeyer, D., Audy, P., Goyer, C., Li, X.-Q., Mang-Pruski, G. and Regan, S.  
Generation of ESTs from potato suspension cultures  
Unpublished (2004)  
Contact: Barry Pilm  
The Canadian Potato Genome Project - BioAtlantech  
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA  
Email: bfilin@bioatlantech.nb.ca  
Seq primer: T3.

#### FEATURES

source

Location/Qualifiers  
1..784  
/organism="Solanum tuberosum"  
/mol\_type="mRNA"  
/culturiv="Shepody"  
/db\_xref="taxon:4113"  
/clone="59138"  
/issue\_type="Callus-derived suspension culture"  
/lab\_host="XL10-Gold"  
/clone\_lib="Suspension culture"

/note="Vector: plusscript II SK(+) XR; Site\_1: EcoRI;  
Site\_2: XhoI; supplier: Developmental series. Callus was  
induced from Shepody, Clone 1756, sterile stem sections by  
culture on Callus Induction Medium (CIM), comprised of MS  
medium (pH 5.6) containing 10 mg/L thiamine-HCl, .01 mg/L  
kinetin and 3 mg/L 2,4-D solidified with .8% (w/v)  
Phytagar. Suspensions were induced by placing callus from  
the plates into 125 ml Erlenmeyer flasks with liquid CIM  
(no Phytagar) at a density of 10% (w/v) in volumes of  
approximately 30-35 ml. Cells were subcultured weekly by  
transfer to fresh media, with the density remaining at 10%  
(w/v) and the volume remaining around 30 ml. Cells were  
collected for RNA isolations and library construction 5  
days after subculture."

#### ORIGIN

Query Match 75.0%; Score 15; DB 7; Length 784;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCAACTACT 19  
 |||||  
 Db 632 CGACCAACTACT 618

RESULT 19  
 CL907067 787 bp DNA linear GSS 14-SEP-2004  
 LOCUS OA\_ABA0005M21.f OA\_ABA Oryza australiensis genomic clone  
 DEFINITION OA\_ABA0005M21.5, genomic survey sequence.  
 ACCESSION CL907067  
 VERSION CL907067.1 GI:52015946  
 KEYWORDS GSS.  
 SOURCE Oryza australiensis  
 ORGANISM Oryza australiensis  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriocarpaceae; Oryzaceae; Oryza.  
 1 (bases 1 to 787)  
 REFERENCE Kilm.H., Yu.Y., Stum.D., Yost.D., Rao.K., Luo.M., Jetty.R.,  
 Kildra.D., Muller.C., Hatfield.J., Soderlund.C. and Wing.R.  
 OMAP Project  
 TITLE OMAP Project  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Rod A. Wing  
 Arizona Genomics Institute  
 University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9595  
 Fax: 520 621 1259  
 Email: http://genome.arizona.edu  
 PCR Primers  
 FORWARD: TAA TAC GAC TCÀ CTA TAG GG  
 BACKWARD: CAC TCA TTA GGC ACC CCA  
 Plate: 0005 ROW: M column: 21  
 Seq primer: TAA TAC GAC TCA CTA TAG GG  
 Class: BAC ends.

FEATURES  
 source  
 1..787  
 /organism="Oryza australiensis"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:4532"  
 /clone="OA\_ABA0005M21"  
 /issue\_type="young leaves"  
 /lab\_host="DH10B T1 phage resistant"  
 /clone\_lib="OA\_ABA"  
 /note="Vector: pGIBAC1, Site\_1: HindIII, Site\_2: HindIII"

ORIGIN  
 Query Match 75.0%; Score 15; DB 9; Length 787;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCAACTACTC 20  
 |||||  
 Db 731 GACCAACTACTC 745

RESULT 20  
 BG299847 798 bp mRNA linear EST 18-OCT-2001  
 LOCUS HVSME0022B19f Hordeum vulgare seedling shoot EST library  
 DEFINITION HVSME0022B19f, mRNA sequence.  
 ACCESSION BG299847  
 VERSION BG299847.2 GI:16256940  
 KEYWORDS EST.  
 SOURCE Hordeum vulgare subsp. vulgare  
 ORGANISM Hordeum vulgare subsp. vulgare

REFERENCE  
 AUTHORS Wing.R., Close.T.J., Kleinhofs.A., Wise.R., Begum.D., Friesch.D.,  
 Yu.Y., Henry.D., Palmer.M., Rambo.T., Simmons.J., Oates.R.,  
 Choi.D.W., Fenton.R.D. and Main.D.  
 Development of a genetically and physically anchored EST resource  
 for barley genomics: Morex cold-stressed seedling shoot cDNA  
 library  
 TITLE Unpublished (2001)  
 JOURNAL On Feb 21, 2001 this sequence version replaced gi:13087684.  
 COMMENT Contact: Wing RA  
 Clemson University Genomics Institute  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu  
 Total hg bases = 280  
 Seq primer: AATTACCTCCTCAAGG  
 High quality sequence stop: 628.

FEATURES  
 source  
 1..798  
 /organism="Hordeum vulgare subsp. vulgare"  
 /mol\_type="mRNA"  
 /culivar="Morex"  
 /sub\_species="vulgare"  
 /db\_xref="taxon:112509"  
 /clone="HVSME0022B19f"  
 /issue\_type="Seedling shoot"  
 /lab\_host="TTC121"  
 /clone\_lib="Hordeum vulgare seedling shoot EST library  
 HVCDA0001 (Cold stress)"  
 /note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;  
 Seeds were surface sterilized then germinated under aseptic  
 conditions in the dark at room temperature on filter paper  
 with water, nystatin and cefotaxime in covered  
 crystallization dishes. Five-day old seedlings were  
 incubated at 50C for 2 days. Shoots were then harvested,  
 total RNA was prepared, poly(A) RNA was purified, one  
 primary unamplified cDNA library was made, and 600000 pfu  
 were in vivo excised to give plasmid SK(-) cDNA  
 phagemids. These steps were performed in the TU Close  
 Laboratory at the University of California, Riverside  
 (Choi, Close, Fenton). Phagemids were plated and picked at  
 the Clemson University Genomics Institute (CUGI) (Begum,  
 Palmer, Friesch, Atkins and Wing). Plasmid DNA  
 preparations, DNA sequencing and sequence analysis were  
 performed at CUGI (Wing, Yu, Friesch, Henry, Simmons,  
 Oates, Rambo, Main). The sequence has been trimmed to  
 remove vector sequence and contains a minimum of 100 bases  
 of phred value 20 or above. For more details on library  
 preparation and sequence analysis see  
 http://www.genome.clemson.edu/projects/barley. To order  
 this clone see http://www.genome.clemson.edu/orders also  
 see Close.TU, Wing.R., Kleinhofs.A., Wise.R. (2001)  
 Genetically and physically anchored EST resources for  
 barley genomics. Barley Genetics Newsletter 31:29-30.  
 (http://wheat.pw.usda.gov/gsgpages/bgn/31/cover.html)"

ORIGIN  
 Query Match 75.0%; Score 15; DB 4; Length 798;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TCGGACCAACT 16  
 |||||  
 Db 206 TCGGACCAACT 220

RESULT 21  
 BG441796/c

LOCUS BG441796 854 bp mRNA linear EST 15-MAR-2001  
 DEFINITION GA\_Ea0014L03f Gossypium arboreum 7-10 dpa fiber library Gossypium  
 arboreum cDNA clone GA\_Ea0014L03f, mRNA sequence.  
 ACCESSION BG441796  
 VERSION BG441796.1 GI:13351448  
 KEYWORDS EST.  
 SOURCE Gossypium arboreum  
 ORGANISM Gossypium arboreum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
 1 (bases 1 to 854)  
 Wing, R.A., Fritsch, D., Yu, Y., Main, D., Rambo, T., Simmons, J.,  
 Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.  
 An integrated analysis of the genetics, development, and evolution  
 of the cotton fiber  
 Unpublished (2000)  
 JOURNAL Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7286  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu  
 Seq primer: TAATACGACTCACTATAGG  
 High quality sequence start: 2  
 High quality sequence stop: 734.  
 Location/Qualifiers  
 1..854  
 /organism="Gossypium arboreum"  
 /mol\_type="mRNA"  
 /strain="AKA"  
 /cultivar="8400"  
 /db\_xref="taxon:29729"  
 /clone="GA\_Ea0014L03f"  
 /issue\_type="Fibers isolated from bolls harvested 7-10  
 dpa"  
 /lab\_host="E. coli"  
 /clone\_lib="Gossypium arboreum 7-10 dpa fiber library"  
 /note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"  
 ORIGIN  
 Query Match 75.0%; Score 15; DB 4; Length 854;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTCCGCGACCCGACAC 15  
 Db 596 TTCCGCGACCCGACAC 582  
 RESULT 22  
 CG463371 871 bp DNA linear GSS 17-SEP-2003  
 LOCUS PUJ099DB\_ZM\_0.6\_1.0\_KB\_Zea mays genomic clone ZMMBTa0598A18,  
 DEFINITION genomic survey sequence.  
 ACCESSION CG463371  
 VERSION CG463371.1 GI:34848358  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 1 (bases 1 to 871)  
 Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
 Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J., and  
 Benneken, J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 JOURNAL Other\_GSSs: PUJ099TBB  
 COMMENT Contact: Cathy Whitelaw  
 TIGR

FEATURES  
 source  
 1..871  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBTa0598A18"  
 /clone\_lib="ZM\_0.6\_1.0\_KB"  
 /note="Vector: pCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 Cor selected genomic DNA library"  
 ORIGIN  
 Query Match 75.0%; Score 15; DB 9; Length 871;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GACCAACACTACTC 20  
 Db 434 GACCAACACTACTC 420  
 RESULT 23  
 CC096047 873 bp DNA linear GSS 16-APR-2003  
 LOCUS CSU-K34.114P10\_SPE CSU-K34 Aedes aegypti genomic clone  
 DEFINITION CSU-K34.114P10, genomic survey sequence.  
 ACCESSION CC096047  
 VERSION CC096047.1 GI:25959126  
 KEYWORDS GSS.  
 SOURCE Aedes aegypti (yellow fever mosquito)  
 ORGANISM Aedes aegypti  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes;  
 Stegomyia.  
 1 (bases 1 to 873)  
 Loftus, B., Shetty, J., Severson, D., Brown, S. and Knudson, D.  
 End sequencing of Aedes aegypti BACS  
 Unpublished (2003)  
 JOURNAL Other\_GSSs: CSU-K34.114P10.T7  
 COMMENT Contact: Brendan Loftus  
 Department of Eukaryotic Genomics  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-3543  
 Fax: 301-838-0208  
 Email: emna@tigr.org  
 Library was provided by Susan Brown and Dennis Knudson at Colorado  
 State University.  
 Seq primer: SP6  
 Class: BAC ends.  
 Location/Qualifiers  
 1..873  
 /organism="Aedes aegypti"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7159"  
 /clone="CSU-K34.114P10"  
 /clone\_lib="CSU-K34"  
 /note="Vector: pBAC3.6; Site\_1: EcoRI; Source DNA: Aedes  
 aegypti; strain unknown [derived from freshly hatched  
 larvae at the Virus Research Centre, Poona, India.  
 Reference: SINGH, K. R. P., 1967 Cell cultures derived  
 from larvae of Aedes albopictus (Skuse) and Aedes aegypti  
 (L.). Current Science 36: 506-508]; ATC-10 cell line ATCC  
 CCL-125"  
 ORIGIN  
 Query Match 75.0%; Score 15; DB 8; Length 873;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 GACCCACACTACTC 20  
|||||  
742 GACCCACACTACTC 728

Db 455 GACCCACACTACTC 469

RESULT 24  
CG117887 876 bp DNA linear GSS 20-AUG-2003  
LOCUS PUPOP4STD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa0697H18,  
DEFINITION genomic survey sequence.  
ACCESSION CG117887  
VERSION CG117887.1 GI:34001324  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 876)  
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
Bennerzen,J.  
Bennetzen,J.  
TITLE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other GSSs: PUPOP45TB  
Contact: Cathy WhiteLaw  
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteLaw@tigr.org  
Seq primer: TF  
Class: sheared ends.  
FEATURES  
source location/Qualifiers  
1..876  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBTa0697H18"  
/clone\_lib="ZM\_0.6\_1.0\_KB"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
Cot selected genomic DNA library"

ORIGIN

Query Match 75.0%; Score 15; DB 9; Length 876;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 GACCCACACTACTC 20  
|||||  
455 GACCCACACTACTC 469

Db 455 GACCCACACTACTC 469

RESULT 25  
BG422240 879 bp mRNA linear EST 14-MAR-2001  
LOCUS 602446874P1 NIH\_MGC\_14 Homo sapiens cDNA clone IMAGE:4565315 5',  
DEFINITION mRNA sequence.  
ACCESSION BG422240  
VERSION BG422240.1 GI:13328746  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 879)  
Mammalia http://mgc.ncl.nih.gov/.  
NHLBI National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: DCTD/DTP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.lnl.gov  
Plate: LILCM1312 row: d column: 20  
High quality sequence stop: 668.  
location/Qualifiers  
1..879  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4565315"  
/clone\_lib="NIH\_MGC\_14"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: Kidney; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 75.0%; Score 15; DB 4; Length 879;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCCGACCCACAC 15  
|||||  
856 TTCCGACCCACAC 870

Db 856 TTCCGACCCACAC 870

RESULT 26  
CC438014 942 bp DNA linear GSS 20-MAY-2003  
LOCUS PUHGJ10TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa445A20,  
DEFINITION genomic survey sequence.  
ACCESSION CC438014  
VERSION CC438014.1 GI:30936685  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 942)  
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
Bennerzen,J.  
Bennetzen,J.  
TITLE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other GSSs: PUHGJ10TB  
Contact: Cathy WhiteLaw  
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteLaw@tigr.org  
Seq primer: TF  
Class: sheared ends.  
FEATURES  
source location/Qualifiers  
1..942  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"

ORIGIN  
 Query Match 75.0%; Score 15; DB 8; Length 942;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 713 GACCCACACTACTC 727  
 /clone="ZM08TA445A20"  
 /note=Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

ORIGIN  
 Query Match 75.0%; Score 15; DB 8; Length 942;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 713 GACCCACACTACTC 727  
 /clone="ZM08TA445A20"  
 /note=Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

RESULT 27  
 BZ697242 945 bp DNA linear GSS 19-FEB-2003  
 LOCUS PUBM020TD ZM 0.6.1.0\_KB Zea mays genomic clone ZM08TA089D15,  
 DEFINITION genomic survey sequence.  
 ACCESSION BZ697242  
 VERSION BZ697242.1 GI:28417089  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 1 (bases 1 to 945)  
 Whitehead, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,  
 Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and  
 Bennetzen, J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Contact: Cathy Whitelaw  
 TIGR

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitelaw@tigr.org  
 Seq primer: TF  
 Class: sheared ends.  
 Location/Qualifiers  
 1..945  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZM08TA089D15"  
 /note=Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

FEATURES  
 source  
 1..945  
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 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZM08TA089D15"  
 /note=Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

ORIGIN  
 Query Match 75.0%; Score 15; DB 8; Length 945;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 844 GACCCACACTACTC 858  
 /clone="ZM08TA445A20"  
 /note=Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

ORIGIN  
 Query Match 75.0%; Score 15; DB 8; Length 945;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 844 GACCCACACTACTC 858  
 /clone="ZM08TA445A20"  
 /note=Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

RESULT 28  
 CG117886/c 955 bp DNA linear GSS 20-AUG-2003  
 LOCUS PUF0P45TB ZM 0.6.1.0\_KB Zea mays genomic clone ZM08TA0697H18,  
 DEFINITION genomic survey sequence.  
 ACCESSION CG117886  
 VERSION CG117886.1 GI:34001323  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 1 (bases 1 to 955)  
 Whitehead, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,  
 Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and  
 Bennetzen, J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Contact: Cathy Whitelaw  
 TIGR

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitelaw@tigr.org  
 Seq primer: TR  
 Class: sheared ends.  
 Location/Qualifiers  
 1..955  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZM08TA0697H18"  
 /note=Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

ORIGIN  
 Query Match 75.0%; Score 15; DB 9; Length 955;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 540 GACCCACACTACTC 526  
 /clone="ZM08TA445A20"  
 /note=Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

FEATURES  
 source  
 1..955  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZM08TA0697H18"  
 /note=Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

ORIGIN  
 Query Match 75.0%; Score 15; DB 9; Length 955;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 540 GACCCACACTACTC 526  
 /clone="ZM08TA445A20"  
 /note=Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

ORIGIN  
 Query Match 75.0%; Score 15; DB 9; Length 955;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 540 GACCCACACTACTC 526  
 /clone="ZM08TA445A20"  
 /note=Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 COT selected genomic DNA library"

RESULT 29  
 CC438010/c 968 bp DNA linear GSS 20-MAY-2003  
 LOCUS PUF0J10TB ZM 0.6.1.0\_KB Zea mays genomic clone ZM08TA445A20,  
 DEFINITION genomic survey sequence.  
 ACCESSION CC438010  
 VERSION CC438010.1 GI:30936679  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 1 (bases 1 to 968)  
 Whitehead, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,  
 Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and  
 Bennetzen, J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Contact: Cathy Whitelaw  
 TIGR

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitelaw@tigr.org  
 Seq primer: TR  
 Class: sheared ends.  
 Location/Qualifiers  
 1..968  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"

FEATURES  
 source  
 1..968  
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 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"

FEATURES  
 source  
 1..968  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"



/clone="ZM8BTA445A20"  
/note="Vector: PCR4-TOPO, Site 1: EcoRI, 0.6-1.0 kb high  
Cot selected genomic DNA library"

ORIGIN

Query Match 75.0%; Score 15; DB 8; Length 968;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCACACTACTC 20  
|||||  
Db 621 GACCCACACTACTC 607

RESULT 30  
BG962370 989 bp mRNA linear EST 12-JUN-2001  
LOCUS 602827180P1\_NCI\_CGAP\_C024 Mus musculus cDNA clone IMAGE:4982250 5',  
DEFINITION mRNA sequence.  
ACCESSION BG962370.1 GI:14350007  
VERSION BG962370.1  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 989)  
NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov  
Plate: L1AM10984 row: 0 column: 19  
High quality sequence stop: 616.  
Location/Qualifiers

FEATURES  
source 1..989  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:4982250"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_1lb="NCI\_CGAP\_C024"  
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.6 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

ORIGIN

Query Match 75.0%; Score 15; DB 4; Length 989;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCGACCCACACTAC 18  
|||||  
Db 841 GCGACCCACACTAC 855

RESULT 31  
CG757040 1192 bp DNA linear GSS 24-OCT-2003  
LOCUS P052-1-H01.2a Ppa EcoRI BAC library Pristionchus pacificus genomic,  
DEFINITION genomic survey sequence.  
ACCESSION CG757040  
VERSION CG757040.1 GI:37985205

KEYWORDS  
SOURCE GSS.  
ORGANISM Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.  
1 (bases 1 to 1192)  
Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolle,L., Jansen,K.,  
Buntjer,J., van der Meulen,M. and Sommer,R.J.  
An integrated physical and genetic map of the nematode Pristionchus  
pacificus  
Mol. Genet. Genomics 269 (5), 715-722 (2003)  
MEDLINE 22835951  
PUBMED 12884007  
COMMENT Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany.  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
Class: BAC ends.  
Location/Qualifiers

FEATURES  
source 1..1192  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="california"  
/db\_xref="taxon:54126"  
/clone\_1lb="Ppa EcoRI BAC Library"  
/note="The library was generated by a partial digest of  
the genomic DNA with EcoRI and cloning into the BAC  
vector."

ORIGIN

Query Match 75.0%; Score 15; DB 9; Length 1192;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCACACTACTC 20  
|||||  
Db 597 GACCCACACTACTC 611

RESULT 32  
B1561676 1633 bp mRNA linear EST 05-SEP-2001  
LOCUS 603255804P1\_NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:5298097 5',  
DEFINITION mRNA sequence.  
ACCESSION B1561676  
VERSION B1561676.1 GI:15448990  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1633)  
NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki  
Toshiyuki and Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov  
Plate: L1AM11754 row: h column: 02  
High quality sequence stop: 126.  
Location/Qualifiers

FEATURES  
source 1..1633  
/organism="Homo sapiens"

Query Match	75.0%	Score 15	DB 4	Length 1633
Best Local Similarity	100.0%	Pred. No. 1e+02		
Matches	15	Conservative	0	Mismatches 0; Indels 0; Gaps 0;
Qy	1	TTTCGGACCCCAACAC	15	
Db	673	TTTCGGACCCCAACAC	687	

TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	Proc. Natl. Acad. Sci. U.S.A.	97 (7)	3491-3496 (2000)	
20202663				
10737800				
Contact: Simpson A.J.G.				
Laboratory of Cancer Genetics				
Ludwig Institute for Cancer Research				
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil				
Tel: +55-11-27049922				
Fax: +55-11-2707001				
Email: asimpson@ludwig.org.br				
This sequence was derived from the FADESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL				
( <a href="http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM2&amp;t2=CM2-GN0295-020101-656-cl0&amp;t3=2001-01-02&amp;t4=1">http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM2&amp;t2=CM2-GN0295-020101-656-cl0&amp;t3=2001-01-02&amp;t4=1</a> )				
Seq primer: puc 18 forward				
High quality sequence start: 30				
High quality sequence stop: 180.				
Location/Qualifiers				
1..183				

	70.0%;	Score 14;	DB 4;	Length 183;
Query Match	Best Local Similarity	100.0%;	Pred. No. 4.7e+02;	
Matches	14;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	6	GACCCAACACTACT	19	
Dd	151	GACCCAACACTACT	164	

RESULT	34
BG988270	
LOCUS	BG988270          267 bp        mRNA       linear    EST 13-JUN-2001
DEFINITION	PMO-Htt167-120101-001-G07 Htt167 Homo sapiens cDNA, mRNA sequence.
ACCESSION	BG988270
VERSION	BG988270.1    GI:14392340
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
Eukaryota; Metazoa;	Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria;	Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 267)	
Dias Neto,E., Silva Correa,R., Verjowski-Almeida,S., Britones,M.R., Nagai,M.A., da Silva M., Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsushima,A., Balz,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.	
Title	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
PubMed	10737800
COMMENT	Contact: Simpson A.J.G.

JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 10737800  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 103, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM0&t=PM0-HT167>)  
 120101-001-G07&ct=2001-01-12&f4=1)  
 Seq. primer: puc 18 forward  
 High quality sequence start: 8  
 High quality sequence stop: 77.  
 Location/Qualifiers  
 1..267  
 source

```

FEATURES
source
location/Qualifiers
1..267
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1b="HT1167"
/note="Organ: head neck; Vector: puc18; Site 1: Smal;
Site 2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig; Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

Query Match	70.0%	Score 14;	DB 4;	Length 267;
Best Local Similarity	100.0%	Pred. NO. 4.6e+02;		
Matches 14; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	3	CGGACCCCACT 16 
Dd	3	CGGACCCCACT 16
RESULT 35		
LOCUS	AV269536	
DEFINITION	AV269536 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 493054J09 3', mRNA sequence.	276 bp mRNA linear EST 05-NOV-1998
ACCESSION	AV269536	
VERSION	AV269536.1 GI:6257573	
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionathii; Muridae; Murinae; Mus. 1 (bases 1 to 276)	
AUTHORS	Komno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., Fukuda,S., Fukuishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibaek,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Takahashi,F., Tateono,M., Tomihaga,N., Tsunoda,Y., Wataniki,A., Watanabe,S., Yamamura,T., Yeanishi,A., Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.	
TITLE	RIKEN Mouse ESTs (Komno,H., et al. 1999)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Yoshihide Hayashizaki	

```

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4930543J09"
/sex="male"
/cleanse_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="Riken full-length enriched, adult male testis
(DH10B)"
/notes="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was

```

primed with a primer [5'  
GAGGAGAGAGATCCAGAGCTCTTTTTTTTTTTN 3'], cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. Second strand cDNA was prepared with the  
primer adapter of sequence [5'  
GAGAGAGATTCCTCGATTAAATTAATCCCCCCCCC 3']. cDNA  
was cloned into the XhoI and BamHI sites. Vector: a  
modified pluescript KS(+) after bulk excision from Lambda  
FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

	70.0%;	Score 14;	DB 1;	Length 276;
Query Match	Best Local Similarity	100.0%;	Pred. No.	4.6e+02;
Matches 14;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Oy	6 GACCCACACTACT	19		
Dd	92 GACCCACACTACT	105		

SOURCE ORGANISM	
<i>Picea engelmannii</i>	x <i>Picea sitchensis</i>
<i>Picea engelmannii</i>	x <i>Picea sitchensis</i>

/mol\_type="mRNA"  
/cultivar="Fal-1028"  
/db\_xref="taxon:273280"  
/cloname="MS09028\_124"  
/sex="Hermaphrodite"  
/lab\_host="E. coli DH10B cells"  
/cloname\_1lb="S-B-N-A-10"  
/note="Organ: Bark (with phloem and cambium attached) from  
one year old clonal trees grown under greenhouse  
conditions in standard potting soil mixture; Vector:  
pBluescript II SK (+) XR; Site\_1: EcoRI (5' end of cDNA) ;  
Site\_2: XhoI (3' end of cDNA) ; Bark was wounded using  
razor blades along the entire length of the tree at 5 mm  
intervals on opposite sides of the trunk. The same trees  
were also sprayed with a 0.01% (v/v) methyl jamonate  
solution resuspended in 0.1% (v/v) tween 20 (~50mls per  
tree). Bark tissue with phloem attached was harvested 3

hours, 6 hours, 12 hours, 24 hours, 2 days, 4 days and 8 days after initiating the treatment. Untreated control dark was also harvested at time 0 hours. mRNA was isolated from each tissue source independently and equal quantities of mRNA from each tissue were then pooled. cDNA was prepared from 5 micrograms of mRNA and directionally ligated into the pBluescript II SK (+) XR vector using the pBluescript II XR cDNA Library Construction Kit according to manufacturer's instructions with modifications (Stratagene). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation. Normalization was applied according to published methods [Bonaldo M.F. et al. (1996) Genome Research 6(9):791] in order to reduce the abundance of highly expressed transcripts."

Query Match 70.0%; Score 14; DB 7; Length 281;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TCGCAGCCCAACAC 15  
|||||  
191 TCGCAGCCCAACAC 178

Db

RESULT 37  
BBI09364 302 bp mRNA linear EST 27-JUN-2000  
DEFINITION BBI09364 RIKEN full-length enriched, adult male urinary bladder Mus musculus CDNA 9530018G08 3', mRNA sequence.  
LOCUS BBI09364  
ACCESSION BBI09364  
VERSION BBI09364.1 GI:8761932  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 302)  
REFERENCE 1 (bases 1 to 302)  
AUTHORS Komno, H., Alizawa, K., Akahira, S., Akiyama, J., Aragawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Horii, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Iizawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shimagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tegawa, A., Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watanabe, S., Yamamura, T., Yamana, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Komno, H., et al.)  
Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/  
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagakura, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Thermolabile and thermolabile enzymes by CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh, M., Kiteunai, T., Akiyama, J., Shibata, K., Iizawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.

## FEATURES

source

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

Location/Qualifiers  
1. 302

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="9530018G08"

/sex="male"

/tissue\_type="urinary bladder"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_1b="RIKEN full-length enriched, adult male urinary bladder"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTWN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTATTAATTAATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from lambda FLC I."

## ORIGIN

Query Match 70.0%; Score 14; DB 2; Length 302;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCAGACTACT 19  
|||||  
28 GACCCAGACTACT 41

RESULT 38  
BUE40525

LOCUS BUE40525 315 bp mRNA linear EST 06-MAY-2003  
DEFINITION BUE40525 RCM lambda Zap Express Library Magnaporthe grisea  
CDNA clone mgcw019x123 5', mRNA sequence.

ACCESSION BUE40525

VERSION BUE40525.2 GI:30395847

KEYWORDS EST.

SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)

ORGANISM Magnaporthe grisea

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

1 (bases 1 to 315)  
Bhobole, D., J., Yuan, J., Thomas, T. L., Bobrowicz, P., Lu, G.,

Bhatterai, K., and Dean, R. A.

Expressed sequence tags from the rice blast fungus, Magnaporthe

grisea

Unpublished (2002)

On Sep 30, 2002 this sequence version replaced gi:23352851.

Contact: Bhobole DJ

Department of Plant Pathology & Microbiology

Texas A&M University

Peterson Bldg, MS2132, College Station, TX 77843-2132, USA

Tel: 979 845 4831

Fax: 979 845 6483

Email: d-bhobole@tamu.edu

Chromatogram file of this sequence is available, see contact

person;  
PCR Primers

FEATURES  
source  
Location/Qualifiers

1..315

/organism="Magnaporthe grisea"

/mol\_type="rRNA"

/strain="CP987"

/db\_xref="taxon:148305"

/clone="mgcw019x123"

/sex="Mati-1 hermaphrodite"

/tissue\_type="Mycelium"

/dev\_stage="Day 5 post-inoculation"

/clone\_lib="RCM Lambda Zap Express Library"

/note="Vector: pBluescript excised from Lambda Zap

Express; Site\_1: EcoRI; Site\_2: XhoI; Day 5

post-inoculation mRNAs prepared from Magnaporthe grisea

grown at 23C in the dark with constant gyratory shaking

100 rpm in Vogel's minimal medium containing 0.5% isolated

rice cell walls as the sole carbon source. Library

provided by Sheng-Cheng Wu. Sequences were processed by

one of two methods. Where a full-length alignment to the

M. grisea genome sequence was available, the EST sequence

was trimmed according to the alignment, otherwise sequence

quality was assessed using phredphrap version 991019 and

trimmed according to phd files (0.05) and for vector

seqs."

## ORIGIN

Query Match

Best Local Similarity 70.0%; Score 14; DB 5; Length 315;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCACACTACT 19

Db 289 GACCCACACTACT 302

RESULT 39  
CG124493/c

LOCUS 319 bp DNA linear GSS 20-AUG-2003

DEFINITION PUGG62TD ZM 0.6 1.0 KB zea mays genomic clone ZMMBT0660L03,

genomic survey sequence.

ACCESSION CG124493

VERSION CG124493.1 GI:34007930

KEYWORDS GSS.

SOURCE

ORGANISM

Ze mays

Ze mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

1 (bases 1 to 319)

Whiteaw,C.A., Quackenbush,J., Van Aken,S., Uteerback,T.,

Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and

Bennetzen,J.

Maize Genomics Consortium

Unpublished (2003)

Other GSSs: PUGG62TB

Contact: Cathy Whiteaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whiteaw@tigr.org

Seq primer: TP

Class: sheared ends.

location/Qualifiers

1..319

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

FEATURES

source

/clone="ZMMBT0660L03"

/clone\_lib="ZM 0.6 1.0 KB"

/note="Vector: pCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high

Cot selected genomic DNA library"

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCACACACTACTC 20

Db 202 ACCACACACTACTC 189

RESULT 40  
CL957629/c

LOCUS 336 bp DNA linear GSS 21-SEP-2004

DEFINITION OsIFCC036262 Oryza sativa Express Library Oryza sativa (Indica

cultivar-group) genomic, genomic survey sequence.

ACCESSION CL957629

VERSION CL957629.1 GI:52370011

KEYWORDS GSS.

SOURCE

ORGANISM

Oryza sativa (Indica cultivar-group)

Oryza sativa (Indica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Embaricoidae; Oryzaceae; Oryza.

1 (bases 1 to 336)

Ma,L., Wang,C.J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,

Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,

Mong,G.K.S., Deng,X.W. and Wang,J.

An analysis of transcriptional regulation of the rice genome and

its comparison to Arabidopsis

Unpublished (2004)

Contact: Chen Chen

Department of Bioinformatic

Chinese Academy of Genomics

Tel: 86-10-80481559

Fax: 86-10-80488676

Email: chenchen@genomics.org.cn

Rice genomic sequence.

Class: exon-trapped.

location/Qualifiers

1..336

/organism="Oryza sativa (Indica cultivar-group)"

/mol\_type="genomic DNA"

/db\_xref="taxon:39946"

/clone\_lib="Oryza sativa Express Library"

/note="Oryza sativa exon trapped genomic sequences "

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GACCCACACTACT 18

Db 150 GACCCACACTACT 137

RESULT 41  
CA652219/c

LOCUS 337 bp mRNA linear EST 24-NOV-2002

DEFINITION wreln.pk0112.f12 wreln Triticum aestivum cDNA clone

wreln.pk0112.f12 5' end, mRNA sequence.

ACCESSION CA652219

VERSION CA652219.1 GI:25230744

KEYWORDS EST.

SOURCE

ORGANISM

Triticum aestivum (bread wheat)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.  
 1 (bases 1 to 337)  
 Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,  
 Mafo, G., Caraher, N. and Hanafey, M.K.  
 DuPont Wheat CNA and Hanafey, M.K.  
 DuPont Wheat CNA Sequence  
 Unpublished (2002)  
 Contact: Scott V. Tingey  
 Crop Genetics  
 E. I. DuPont de Nemours and Company  
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
 Tel: 302-631-2602  
 Fax: 302-631-2607  
 Email: Scott.V.Tingey@usa.dupont.com  
 Seq primer: M13

FEATURES  
 source  
 1. .337  
 /location/Qualifiers  
 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4565"  
 /clone\_lib="wheat.pk0112.f12"  
 /tissue\_type="root"  
 /clone\_lib="wheat"  
 /note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:  
 XhoI; Wheat (Triticum aestivum L.) root; normalized from  
 wrel library"

ORIGIN  
 Query Match 70.0%; Score 14; DB 6; Length 337;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 ACCCAACTACTCTC 20  
 |||||||||  
 221 ACCCAACTACTCTC 208

Db

RESULT 42  
 CF435681 347 bp mRNA linear EST 04-SEP-2003  
 LOCUS EST672026 normalized cDNA library of onion Allium cepa cDNA clone  
 ACAB249, mRNA sequence.  
 CF435681  
 CF435681.1 GI:34458371  
 EST:  
 Allium cepa (onion)  
 Allium cepa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;  
 Allium.  
 1 (bases 1 to 347)  
 Hevey, M.J., Cheung, F., Van Aken, S., Uterback, T. and Town, C.D.  
 Expressed Sequence Tags from a normalized library of mixed onion  
 tissues (Allium cepa)  
 Unpublished (2003)  
 Contact: Hevey MJ  
 Department of Horticulture  
 USDA-ARS and University of Wisconsin  
 1575 Linden Drive, Madison, WI 53706, USA  
 Tel: 608-262-1830  
 Fax: 608-262-4743  
 Email: mhavey@facstaff.wisc.edu  
 TIGR sequence name ACAB249TR. For more information:  
 http://havey1ab.hort.wisc.edu  
 Seq primer: CAG GAA ACA GCT ATG ACC.  
 Location/Qualifiers  
 1. .347  
 /organism="Allium cepa"  
 /mol\_type="mRNA"  
 /cultiVar="Red Creole(bulbs), unknown(callus), Ebano &  
 Texas Legend(root8)"  
 /db\_xref="taxon:4679"  
 /clone="ACAB249"

FEATURES  
 source

/tissue\_type="Callus, roots, and young bulbs"  
 /clone\_lib="normalized cDNA library of onion"  
 /note="Vector: PCW5port6.1-ccdb (Invitrogen); Site 1:  
 EcoRV (5'); Site 2: NotI (3'); Equal molar amounts of mRNA  
 from callus, roots, and young bulbs were combined to  
 synthesize the library. Normalization to enrich for  
 low-copy transcripts was performed by proprietary  
 techniques of Invitrogen."

ORIGIN  
 Query Match 70.0%; Score 14; DB 7; Length 347;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 ACCCAACTACTCTC 20  
 |||||||||  
 145 ACCCAACTACTCTC 158

Db

RESULT 43  
 CG845406 351 bp DNA linear GSS 13-NOV-2003  
 LOCUS CG845406/c  
 DEFINITION CG845406 ZM 0.7.1.5\_KB Zea mays genomic clone ZMMBMA0803E20,  
 genomic survey sequence.  
 ACCESSION CG845406  
 VERSION CG845406.1 GI:38306110  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 351)  
 White, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
 Resnick, A., Nunberg, A., Robbins, D. and Lakey, N.  
 Citek, R.W., Consortium for Maize Genomics  
 Unpublished (2002)  
 Other\_GSSs: OG4AB34TH  
 Contact: Cathy White  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitec@tigr.org  
 Seq primer: TF  
 Class: sheared ends.  
 Location/Qualifiers  
 1. .351  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBMA0803E20"  
 /clone\_lib="ZM 0.7.1.5\_KB"  
 /note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb  
 methylation filtered genomic DNA library"

FEATURES  
 source

ORIGIN  
 Query Match 70.0%; Score 14; DB 9; Length 351;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGCGACCCCAACA 14  
 |||||||||  
 89 TTGCGACCCCAACA 76

Db

RESULT 44  
 BH282705 362 bp DNA linear GSS 30-NOV-2001  
 LOCUS BH282705/c  
 DEFINITION CH230-166L20.7U CHORI-230 Segment 1 Ratius norvegicus genomic clone  
 CH230-166L20, genomic survey sequence.

ACCESSION BH282705  
VERSION GI:17195107  
KEYWORDS GSS.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 362)  
Shao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,  
Shahrabegyn,A., Gebregorgis,E., Overton,L., Russell,D., Chen,D.,  
Riggs,F., de Jong,P. and Fraser,C.M.  
Rat BAC End Sequences from Library CHORI-230 EcoRI segment  
Unpublished (1999)  
Other\_GSSs: CH230-166L20.TV  
COMMENT Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhaot@tigr.org  
Clones are derived from the rat BAC library CHORI-230  
(http://www.chori.org/bacpac/rat230.htm). For BAC library  
availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/or\_ering\_information.htm). BAC end  
page: http://www.tigr.org/tdb/bac\_ends/rat/bac\_end\_intro.html  
Plate: 166 row: L column: 20  
Seq primer: SP6  
Class: BAC ends.  
FEATURES  
Source Location/Qualifiers  
1..362  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/strain="BN/SsNHsd/MCM"  
/db\_xref="taxon:10116"  
/clone="CH230-166L20"  
/sex="Female"  
/cell\_type="Brain"  
/clone\_id="CHORI-230 Segment 1"  
/note="Vector: PTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;  
CHORI-230 Rat (BN/SsNHsd/MCM) BAC library produced by  
Pieter de Jong"  
ORIGIN  
Query Match 70.0%; Score 14; DB 8; Length 362;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGACCCACACA 14  
|||||  
Db 39 TTCCGACCCACACA 26  
RESULT 45  
LOCUS BP752355 365 bp mRNA linear EST 15-JUN-2004  
DEFINITION BP752355 partially normalized diploid tobacco CDNA library  
Nicotiana sylvestris cDNA clone R-111\_F03, mRNA sequence.  
ACCESSION BP752355  
VERSION BP752355.1 GI:48761959  
KEYWORDS EST.  
SOURCE Nicotiana sylvestris (wood tobacco)  
ORGANISM Nicotiana sylvestris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamiales; Solanales; Solanaceae; Nicotiana.  
REFERENCE 1 (bases 1 to 365)  
Katoh,A., Yamaguchi,Y., Sano,H. and Hashimoto,T.  
Analysis of expression sequence tags from Nicotiana sylvestris  
Proc. Jpn. Acad. Ser. B 79, 151-154 (2003)  
COMMENT Contact: Takashi Hashimoto

Graduate School of Biological Sciences  
Nara Institute of Science and Technology  
Takayama 8916-5, Ikoma, Nara 630-0192, Japan  
Tel: 81-743-72-5520  
Fax: 81-743-72-5529  
Email: hashimoto@bs.naist.jp.  
FEATURES  
Source Location/Qualifiers  
1..365  
/organism="Nicotiana sylvestris"  
/mol\_type="mRNA"  
/db\_xref="taxon:4096"  
/clone="R-111\_F03"  
/tissue\_type="mixture of wounded and un-wounded leaf"  
/dev\_stage="2-month-old plant"  
/clone\_id="partially normalized diploid tobacco CDNA  
library"  
ORIGIN  
Query Match 70.0%; Score 14; DB 5; Length 366;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 ACCCAACACTACTC 20  
|||||  
Db 169 ACCCAACACTACTC 182  
RESULT 46  
LOCUS BP751956 366 bp mRNA linear EST 15-JUN-2004  
DEFINITION BP751956 partially normalized diploid tobacco CDNA library  
Nicotiana sylvestris cDNA clone R-101\_G09, mRNA sequence.  
ACCESSION BP751956  
VERSION BP751956.1 GI:48761560  
KEYWORDS EST.  
SOURCE Nicotiana sylvestris (wood tobacco)  
ORGANISM Nicotiana sylvestris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamiales; Solanales; Solanaceae; Nicotiana.  
REFERENCE 1 (bases 1 to 366)  
Katoh,A., Yamaguchi,Y., Sano,H. and Hashimoto,T.  
Analysis of expression sequence tags from Nicotiana sylvestris  
Proc. Jpn. Acad. Ser. B 79, 151-154 (2003)  
COMMENT Contact: Takashi Hashimoto  
Graduate School of Biological Sciences  
Nara Institute of Science and Technology  
Takayama 8916-5, Ikoma, Nara 630-0192, Japan  
Tel: 81-743-72-5520  
Fax: 81-743-72-5529  
Email: hashimoto@bs.naist.jp.  
FEATURES  
Source Location/Qualifiers  
1..366  
/organism="Nicotiana sylvestris"  
/mol\_type="mRNA"  
/db\_xref="taxon:4096"  
/clone="R-101\_G09"  
/tissue\_type="mixture of wounded and un-wounded leaf"  
/dev\_stage="2-month-old plant"  
/clone\_id="partially normalized diploid tobacco CDNA  
library"  
ORIGIN  
Query Match 70.0%; Score 14; DB 5; Length 366;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 ACCCAACACTACTC 20  
|||||  
Db 169 ACCCAACACTACTC 182  
RESULT 47

AA310704  
 LOCUS AA310704 385 bp mRNA linear EST 19-APR-1997  
 DEFINITION EST181516 Jurkat T-cells V Homo sapiens CDNA 5' end, mRNA sequence.  
 ACCESSION AA310704  
 VERSION AA310704.1 GI:1963053  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 385)  
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clifton,R.A., Cline,T.R., Cotton,M.D., Barle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geisler,N.S., Glodex,A., Gnehm,C.L., Hanna,M.C., Hedblom,B., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Springs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bedarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferris,A., Fischer,C., Hastings,G.A., He,W.W., Hu,Y.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weisner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M., and Venter,J.C.  
 TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
 JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)  
 MEDLINE 96026280  
 PUBMED 7566098  
 COMMENT Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 FEATURES  
 source  
 1.385  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="ATCC (Inhost):156734"  
 /db\_xref="taxon:9606"  
 /cell\_type="T-lymphocyte"  
 /clone\_lib="Jurkat T-cells V"  
 /note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI"  
 ORIGIN  
 Query Match 70.0%; Score 14; DB 1; Length 385;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GACCCACACTACT 19  
 |||||  
 60 GACCCACACTACT 73  
 RESULT 48  
 CA370296 418 bp mRNA linear EST 06-NOV-2002  
 LOCUS CA370296 650428 NCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT22A11\_A\_A06 5',  
 DEFINITION mRNA sequence.  
 ACCESSION CA370296  
 VERSION CA370296.1 GI:24682780  
 KEYWORDS EST.

SOURCE  
 ORGANISM Oncorhynchus mykiss (rainbow trout)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 REFERENCE 1 (bases 1 to 418)  
 Rexroad,C.E. 3rd, Lee,Y., Keele,J.W., Karamyheva,S., Brown,G., Koop,B., Gahr,S.A., Palti,Y. and Quackenbush,J.  
 TITLE Sequence analysis of a rainbow trout cDNA library and creation of a gene index  
 JOURNAL Cytogenet. Genome Res. 102 (1-4), 347-354 (2003)  
 COMMENT Contact: Rexroad CE  
 USDA, ARS, National Center for Cool and Cold Water Aquaculture  
 11876 Leetown Road, Kearneysville, WV 25430, USA  
 Tel: 304 724 8340 x2129  
 Fax: 304 725 0351  
 Email: crexroad@nccwa.ars.usda.gov  
 Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim\_alt option. Vector identified by cross match v0.990329.  
 Seq primer: AGCGATACAAATTTCACACAGA.  
 FEATURES  
 source  
 1.418  
 /organism="Oncorhynchus mykiss"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8022"  
 /clone="1RT22A11\_A\_A06"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="NCCWA 1RT"  
 /note="Vector: pCMV SPORT6; Site\_1: NotI; Site\_2: SalI; library made from pooled tissue from brain, gill, liver, spleen, muscle, and kidney."  
 ORIGIN  
 Query Match 70.0%; Score 14; DB 6; Length 418;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GACCCACACTACT 19  
 |||||  
 269 GACCCACACTACT 282  
 RESULT 49  
 BZ787299 432 bp DNA linear GSS 17-MAR-2003  
 LOCUS BZ787299 432 bp DNA linear GSS 17-MAR-2003  
 DEFINITION PUFK39TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMB7A357G05,  
 genomic survey sequence.  
 ACCESSION BZ787299  
 VERSION BZ787299.1 GI:28980896  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 432)  
 WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Reenick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennerzen,J.  
 TITLE Maize Genomics Consortium  
 JOURNAL Unpublished (2003)  
 COMMENT Other\_GSSs: PUFK39TB  
 Contact: Cathy WhiteLaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteLaw@tigr.org  
 Seq primer: TF  
 Class: sheared ends.  
 FEATURES  
 Location/Qualifiers



source

1..432  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBTA357G05"  
/clone\_lib="ZM 0.6.1.0 KB"  
/note="Vector: pCR4-TOPO, Site 1: EcoRI, 0.6-1.0 kb high  
cor selected genomic DNA library"

ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 432;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 GCGACCCACACTA 17  
|||||  
158 GCGACCCACACTA 171

RESULT 50  
CF350979 447 bp mRNA linear EST 20-AUG-2003  
LOCUS r165g10.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
DEFINITION cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN. ;, mRNA  
sequence.  
CF350979.1 GI:33953561

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

McCartner, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,  
Wyle, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,  
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,  
Taagaraihu, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
Harvey, N., Schurk, R., Kohn, M., Allen, M., Person, B., Swaller, T.,  
McCann, R., Waterston, R. and Wilson, R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)  
Contact: McCartner JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: east@wustl.edu  
Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified  
using Dynabeads (Dyna1) and mRNA eluted for first strand synthesis.  
First strand cDNA was created using MMLV RT (Powerscript, Clontech)  
and primed with oligo(dT) with XhoI site and 5'SMART 'anchor' added  
using chimeric DNA-RNA oligo. 12 PCR cycles were done using first  
strand and primers specific to SMART oligo and 3' end. Double  
stranded cDNA was digested using XhoI/NotI, fractionated on  
Chroma-spin 400 columns (Clontech) and ligated to digested  
pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as  
host cells. Library materials provided by Dr. David Bird of North  
Carolina State University. Library construction by Jeff Rousch. See  
www.nematode.net for additional project information.  
Seq primer: Sp6  
High quality sequence stop: 446.  
Location/Qualifiers  
1..447  
/organism="Meloidogyne javanica"  
/mol\_type="mRNA"  
/db\_xref="taxon:6303"  
/clone\_lib="J2"  
/dev\_stage="J2"  
/lab\_host="DH10B"  
/clone\_lib="Meloidogyne javanica J2 SMART pGEM"

/note="Vector: plasmid (ampicillin resistant); Site 1:  
XhoI, Site 2: NotI; Cloned unidirectionally. Poly(A)+ RNA  
was concentrated and purified using Dynabeads (Dyna1) and  
mRNA eluted for first strand synthesis. First strand cDNA  
was created using MMLV RT (Powerscript, Clontech) and  
primed with oligo(dT) with XhoI site and 5'SMART 'anchor'  
added using chimeric DNA-RNA oligo. 12 PCR cycles were  
done using first strand and primers specific to SMART  
oligo and 3' end. Double stranded cDNA was digested using  
XhoI/NotI, fractionated on Chroma-spin 400 columns  
(Clontech) and ligated to digested pGEM-11zf(+) plasmid.  
Chemically competent DH10B cells were used as host cells.  
Library materials provided by Dr. David Bird of North  
Carolina State University. Library construction by Jeff  
Rousch. See www.nematode.net for additional project  
information."

ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 447;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGCGACCCACACA 14  
|||||  
118 TTGCGACCCACACA 131

RESULT 51  
A1706594 455 bp mRNA linear EST 03-JUN-1999  
LOCUS UI-R-AE1-zf-c-12-0-UI s1 UI-R-AE1 Rattus norvegicus cDNA clone  
DEFINITION UI-R-AE1-zf-c-12-0-UI 3', mRNA sequence.  
A1706594.1 GI:4994494

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Soares, M.B.  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Oligo-dT track not found. Not 1 site shown in beginning of sequence  
is likely internal to the message. cDNA library Preparation: M.B.  
Soares Lab Clone Distribution: Clones will be available through  
Research Genetics (www.resgen.com) The following repetitive  
elements were found in this cDNA sequence: 289-374,  
>(CGG)nSimple repeat  
Seq primer: M13 Forward  
POLYA=NO.  
Location/Qualifiers  
1..455  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-AE1-zf-c-12-0-UI"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="UI-R-AE1"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site\_1: Not I; Site\_2: Eco RI; The UI-R-ARI library is a normalized library constructed from 15 dpc rat ventricle. The tag is a string of 5 nucleotides present between the Not I site and the oligo-dt track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996. Tissue provided by Jim Lin, Department of Biology, University of Iowa.  
TAG\_SEQ=None found"

## ORIGIN

Query Match 70.0%; Score 14; DB 1; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGCGACCCACACTA 14  
|||||  
DB 435 TTCGCGACCCACACTA 448

## RESULT 52

CG059179/c 457 bp DNA linear GSS 19-AUG-2003  
DEFINITION PUCW72TD ZM 0.6.1.0\_Zea mays genomic clone ZMMBTa0639L23,  
genomic survey sequence.

ACCESSION CG059179  
VERSION CG059179.1 GI:33931359  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
1 (bases 1 to 457)  
White, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennett, J.

## AUTHORS

TITLE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other GSSs: PUCW72TD  
Contact: Cathy White, 9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitec@tigr.org  
Seq primer: TR  
Class: sheared ends.

## FEATURES

source Location/Qualifiers  
1..457

/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_lib="ZMMBTa0639L23"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high  
Cot selected genomic DNA library"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 457;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCGACCCACACTA 17  
|||||  
DB 262 GCGACCCACACTA 249

## RESULT 53

CG059181 457 bp DNA linear GSS 19-AUG-2003  
LOCUS CG059181  
DEFINITION PUCW72TD ZM 0.6.1.0\_Zea mays genomic clone ZMMBTa0639L23,

genomic survey sequence.

ACCESSION CG059181  
VERSION CG059181.1 GI:33931361  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
1 (bases 1 to 457)  
White, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennett, J.

## AUTHORS

TITLE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other GSSs: PUCW72TD  
Contact: Cathy White, 9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitec@tigr.org  
Seq primer: TR  
Class: sheared ends.

FEATURES source Location/Qualifiers  
1..457

/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_lib="ZMMBTa0639L23"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high  
Cot selected genomic DNA library"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 457;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCGACCCACACTA 17  
|||||  
DB 194 GCGACCCACACTA 207

## RESULT 54

AZ650597 462 bp DNA linear GSS 14-DEC-2000  
LOCUS IM0520D24R Mouse 10kb plasmid U0CCIM library Mus musculus genomic  
DEFINITION clone U0CCIM0520D24 R, genomic survey sequence.

ACCESSION AZ650597  
VERSION AZ650597.1 GI:11785244  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 462)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tinsley, A., von Niederhausern, A. and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

## AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0520 row: D column: 24

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 462.  
Location/Qualifiers

1. 462

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="U9C1M0520D24"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid U9C1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1473214[g1473214]AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 462;

Best Local Similarity 100.0%; Pred. No. 4.5e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACCTACTC 20

Db 369 ACCCAACCTACTC 382

## RESULT 55

CG845394

LOCUS

DEFINITION CG845394 475 bp DNA linear GSS 13-NOV-2003

genomic survey sequence.

CG845394

VERSION CG845394.1 GI:38306098

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

1 (bases 1 to 475)

Whitehead, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,

Reinick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,

Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: OG4AB34TV

Contact: Cathy Whitehead

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitehead@tigr.org

Seq primer: TR

Class: sheared ends.

## FEATURES

### SOURCE

Location/Qualifiers

1. 475

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone="ZM0803820"

/clone\_lib="ZM 0.7-1.5\_KB"

/note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb

methylation filtered genomic DNA library"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 475;

Best Local Similarity 100.0%; Pred. No. 4.5e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCACACA 14

Db 263 TTCCGACCCACACA 276

## RESULT 56

B0741880/c

LOCUS

DEFINITION B0741880 482 bp mRNA linear EST 02-JUL-2004

Gm-c1045-4254 5', mRNA sequence.

ACCESSION B0741880

VERSION B0741880.1 GI:21888667

KEYWORDS EST.

SOURCE Glycine max

ORGANISM Glycine max

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

Glycine.

1 (bases 1 to 482)

Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V.,

Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,

Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,

Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,

Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,

McCann, R., Waterson, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

When it has been determined, an EST from the other end of this

clone is listed in the 'Other ESTs on clone' field. This clone is

available through: Biogenetic Services, 801 32nd Ave. Brookings, SD

57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)

Seq primer: -40RP from Gibco

High quality sequence stop: 431.

Location/Qualifiers

1. 482

/organism="Glycine max"

/mol\_type="mRNA"

/cultivar="Williams 82"

/db\_xref="taxon:3847"

/clone="SOYBEAN CLONE ID: Gm-c1045-4254"

/tissue\_type="Hypocotyl, 9-10 day old etiolated seedlings"

/lab\_host="Gm-c1045"

/note="Vector: pBluescriptII SK+; Site 1: EcoRI; Site 2:

XhoI; This cDNA library was constructed from mRNA isolated

from etiolated hypocotyl tissue of 9-10 day old seedlings

of the cultivar Williams 82. Complementary DNA was

synthesized from mRNA using a primer consisting of a

poly(dT) primer with a XhoI restriction site. EcoRI

adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and XhoI. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 482;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCAACTACTCT 19  
|||||  
184 GACCAACTACTCT 171

RESULT 57  
LOCUS B29191/c  
DEFINITION T28D21TF TAMU Arabidopsis thaliana genomic clone T28D21, genomic survey sequence.  
ACCESSION B29191  
VERSION B29191.1 GI:2515157  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 490)  
Rounsley, S.D., Kelley, J.M., Field, C.E., Craven, M.B., Adams, M.D. and Venter, J.C.  
Use of a BAC End Sequence Database To Identify Minimal Overlaps for Unpublished (1997)  
Other\_GSSs: T28D21TR  
Contact: Steve Rounsley  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: rounsley@tigr.org  
Seq primer: M13-21  
Class: BAC ends  
High quality sequence stop: 490.

JOURNAL COMMENT  
Location/Qualifiers  
1..490  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Columbia"  
/db\_xref="taxon:3702"  
/clone="T28D21"  
/sex="hermaphrodite"  
/clone\_lib="TAMU"  
/note="Vector: pBluescript, Site 1: HindIII, Site 2: HindIII; Produced by Rod Wing"

FEATURES  
source  
Location/Qualifiers  
1..490  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/ecotype="Columbia"  
/db\_xref="taxon:3702"  
/clone="T28D21"  
/sex="hermaphrodite"  
/clone\_lib="TAMU"  
/note="Vector: pBluescript, Site 1: HindIII, Site 2: HindIII; Produced by Rod Wing"

ORIGIN  
Query Match 70.0%; Score 14; DB 8; Length 490;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ACCCAACTACTCT 20  
|||||  
429 ACCCAACTACTCT 416

RESULT 58  
LOCUS BH219227/c  
BH219227 491 bp DNA linear GSS 08-NOV-2001

DEFINITION 1006085D03.x1 1006 - Rescuedu Grid G Zea mays genomic, genomic survey sequence.  
ACCESSION BH219227  
VERSION BH219227.1 GI:16813010  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE 1 (bases 1 to 491)  
Walbot, V.  
Maize genomic sequences found using engineered Rescuedu transposon  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 723 8221  
Email: walbot@stanford.edu  
Very probable ligation site found so sequence was trimmed.  
Post-ligation sequence submitted separately.  
Plate: 1006085 row: 20  
Class: transposon-tagged.

LOCATION/QUALIFIERS  
1..491  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A188/B73"  
/db\_xref="taxon:4577"  
/issue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1006 - Rescuedu Grid G"  
/note="Organ: leaf; Vector: Rescuedu (engineered from pBluescript backbone); Site 1: BamHI, Site 2: BglII; Rescuedu is a 4.9 Kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuedu, go to the web site 'www.zmbd.iastate.edu' and follow the links for 'Rescuedu', 'Grid G' was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

## FEATURES

source

ORIGIN  
Query Match 70.0%; Score 14; DB 8; Length 491;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ACCCAACTACTCT 20  
|||||  
103 ACCCAACTACTCT 90

RESULT 59  
LOCUS CK148694/c  
DEFINITION AGT-30-G10 Suppressive subtractive hybridization library Cicer arietinum cDNA clone AGT-30-G10 5', mRNA sequence.  
ACCESSION CK148694  
VERSION CK148694.1 GI:47832382  
KEYWORDS EST.  
SOURCE Cicer arietinum (chickpea)  
ORGANISM Cicer arietinum

REFERENCE 1 (bases 1 to 496)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.  
Cicer.

**AUTHORS** Buhariwalla, H.K., Jayashree, B. and Crouch, J.H.  
**TITLE** Characterization of ESTs associated with drought tolerance from chickpea (*C. arietinum*) root tissue  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Buhariwalla HK  
 Swaminathan Applied Genomics Laboratory  
 International Crops Research Institute for the Semi-arid Tropics (ICRISAT)  
 Patancheru 502 324, Andhra Pradesh, India  
 Tel: +91 40 23296161  
 Fax: +91 40 23241239  
 Email: Buhariwalla@ICRISAT.EXCH.cgiar.org  
 Seq primer: T7

**FEATURES**  
**Source** High quality sequence stop: 496.  
 Location/Qualifiers

```

1..496
/organism="Cicer arietinum"
/mol_type="mRNA"
/cultivar="ICC 4958"
/db_xref="taxon:3827"
/clone="ACT-30-G10"
/lisue_type="Root"
/lab_host="E.coli DH10B"
/clone_lib="Suppressive subtractive hybridization library"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Site 2: EcoRI;
The suppression subtractive hybridization process was
carried out using ICC 4958 as the tester and Amigari as
the driver, the PCR products of the subtraction were
cloned into the PCR4-TOPO cloning vector. The c-DNA
inserts were amplified with M13 forward and reverse
primers and subsequently sequenced with T7 primer from the
3' end."

```

**ORIGIN**

Query Match 70.0%; Score 14; DB 7; Length 496;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 7 ACCCAACTACTCTC 20  
 |||||  
**Db** 83 ACCCAACTACTCTC 70

**RESULT** 60  
**LOCUS** CK747642 504 bp mRNA linear EST 24-FEB-2004  
**DEFINITION** nad03-6c84-d09 Nad03 Nuphar advena cDNA clone nad03-6c84-d09 5',  
 mRNA sequence.  
**ACCESSION** CK747642  
**VERSION** CK747642.1 GI:42638065  
**KEYWORDS** EST.  
**SOURCE** Nuphar advena  
**ORGANISM** Nuphar advena  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; stem Magnoliophyta; Nymphaeales;  
 Nymphaeaceae; Nuphar.  
 1 (bases 1 to 504)  
 Leebens-Mack, J., Carlson, J., Ma, H., Frohlich, M., Tanksley, S.,  
 Leebens-Mack, J., Field, D., Arrington, J., Zahn, L., Kong, H.,  
 Druckenmiller, M., Landherr, L., Hu, Y., Iluc, D., Wall, K.,  
 Pluck, S., Chioresan, S., Albert, V., Doyle, J., Miller, W.,  
 Oppenheimer, D., Soltis, D., Soltis, P. and Rhesissen, G.  
 Generation of ESTs from early flower buds of Nuphar advena  
 Unpublished (2002)  
**TITLE** Contact: Claude Leebens-Mack  
**JOURNAL** Mueller Laboratory  
**COMMENT** Penn State University  
 208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn  
 State University, University Park, PA 16802, USA  
 Tel: 814 865 6413  
 Fax: 814 865 9131  
 Email: cwl3@psu.edu or jh100@psu.edu  
 The sequence provided is trimmed of vector and low quality regions.

**FEATURES**  
**source** Location/Qualifiers

Full sequence and original trace file are available from the Plant  
 Genome Network website (<http://pgn.cornell.edu>)  
 Plate: nad03-6c84 row: d column: 09  
 Seq primer: M13F.

```

1..504
/organism="Nuphar advena"
/mol_type="mRNA"
/db_xref="taxon:77108"
/clone="nad03-6c84-d09"
/lisue_type="flower buds"
/dev_stage="<= 2.5mm"
/lab_host="SOLR"
/clone_lib="nad03"
/notes="Vector: pBluescript SK (+/-); Site 1: EcoRI;
Site 2: XhoI; Only floral buds with diameter of 2.5 mm of
less were used for RNA isolation. This is a directionally
cloned, non-normalized library. Avg. insert length: 1134;
Primers: M13F and M13R; Antibiotic: 50 ug/ml Ampicillin;
Primary filter: 286 pfu total; Amplified filter: 3.2E10
pfu/ml; Mass Excised filter: 5E10 total; This library has
been generated by the floral genome project (FGP). The
floral genome project is funded by NSF's Plant Genome
Research Program (DBI-0115684). More information about the
project can be obtained at http://fgp.bio.psu.edu"

```

**ORIGIN**

Query Match 70.0%; Score 14; DB 7; Length 504;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 7 ACCCAACTACTCTC 20  
 |||||  
**Db** 255 ACCCAACTACTCTC 268

**RESULT** 61  
**LOCUS** BU964885 507 bp mRNA linear EST 01-JUL-2004  
**DEFINITION** sat03h04.y1 Gm-c1036 Glycine max cDNA clone SOYBRAN CLONE ID:  
 Gm-c1036-12656 5', mRNA sequence.  
**ACCESSION** BU964885  
**VERSION** BU964885.1 GI:24205632  
**KEYWORDS** EST.  
**SOURCE** Glycine max (soybean)  
**ORGANISM** Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.  
 1 (bases 1 to 507)  
 Shoemaker, R., Keim, P., Vodkin, L., Erpelidg, J., Coryell, V.,  
 Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,  
 Beck, C., Wylie, T., Underwood, K., Stepec, M., Theising, B., Allen, M.,  
 Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N.,  
 Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
 McCann, R., Waterston, R. and Wilson, R.  
 Public Soybean EST Project  
 Unpublished (1999)  
**TITLE** Contact: Shoemaker R/Public Soybean EST Project  
**JOURNAL** Public Soybean EST Project  
**COMMENT** Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 When it has been determined, an EST from the other end of this  
 clone is listed in the 'other ESTs on clone' field. This clone is  
 available through: Biogenetic Services, 801 32nd Ave. Brookings, SD  
 57006 USA (phone: 800 423 4163; email: [info@biogeneticservices.com](mailto:info@biogeneticservices.com))  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 450.  
 Location/Qualifiers

## source

1. 507  
 /organism="glycine max"  
 /mol\_type="mRNA"  
 /cultivar="JACK"  
 /db\_xref="taxon:3847"  
 /clone="SOYBEAN CLONE ID: Gm-c1036-12656"  
 /tissue\_type="somatic embryos cultured on MSD 20"  
 /lab\_host="DH10B"  
 /clone\_lib="Gm-c1036"  
 /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; This cDNA library was constructed from mRNA isolated from somatic embryos (age ranging from 2 months to 9 months) cultured on MSD 20. The library was prepared using the life Technologies superscript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a NotI restriction site. SalI linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This library was constructed in the laboratory of Dr. Lila Vodkin by Anu Khanna at the University of Illinois at Urbana-Champaign. e-mail: l-vodkin@uiuc.edu"

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 507;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACCCAACACTACTC 20  
 |||||  
 Db 442 ACCCAACACTACTC 455

## RESULT 62

BE474398/c

LOCUS

BE474398 512 bp mRNA linear EST 13-JUL-2004  
 sp63h05.y1 Gm-c1044 glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
 Gm-c1044-658 5', mRNA sequence.

ACCESSION

BE474398

VERSION

BE474398.1

KEYWORDS

GI:9564889

SOURCE

EST.

ORGANISM

Glycine max (soybean)

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.

REFERENCE

1 (bases 1 to 512)

AUTHORS

Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Corryell, V.,  
 Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,  
 Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M.,  
 Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pepe, D., Harvey, N.,  
 Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
 McCann, R., Waterson, R. and Wilson, R.

TITLE

Public Soybean EST Project

UNPUBLISHED (1999)

CONTACT: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.wustl.edu

When it has been determined, an EST from the other end of this  
 clone is listed in the 'Other ESTs on clone' field. This clone is  
 available through: Biogenetic Services, 801 32nd Ave. Brookings, SD  
 57006 USA (phone: 800.423.4163; email: info@biogeneticservices.com)  
 Insert Length: 854 Std Error: 0.00  
 High quality sequence stop: 363.  
 Location/Qualifiers  
 1. 512

## ORIGIN

Query Match 70.0%; Score 14; DB 2; Length 512;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCACACTACT 19  
 |||||  
 Db 23 GACCCACACTACT 10

## RESULT 63

BU039555

LOCUS

BU039555 513 bp mRNA linear EST 26-AUG-2002  
 PP LEA0003C22F Peach developing fruit mesocarp Prunus persica cDNA  
 clone PP LEA0003C22F, mRNA sequence.

ACCESSION

BU039555

VERSION

BU039555.1

KEYWORDS

GI:22478309

SOURCE

EST.

ORGANISM

Prunus persica (peach)

Prunus persica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.

REFERENCE

1 (bases 1 to 513)

AUTHORS

Callahan, A., Palmer, M., Main, D., Wing, R. and Abbott, A.

TITLE

Peach Model genome for Rosaceae

UNPUBLISHED (2002)

CONTACT: Abbott, A.

Dept of Genetics and Biochemistry

Clemson University

122 Long Hall, Clemson University, Clemson, SC 29634, USA

Tel: 864 656 3060

Fax: 864 656 6879

Email: aalbert@clemson.edu

Total High Quality bases = 13;

Seq primer: TATACGACTGACTATGAGG

High quality sequence stop: 513.  
 Location/Qualifiers  
 1. 513  
 /organism="Prunus persica"  
 /mol\_type="mRNA"  
 /cultivar="Loring"  
 /db\_xref="taxon:3760"  
 /clone="PP\_LEA0003C22F"  
 /tissue\_type="Mesocarp"  
 /lab\_host="E. coli"  
 /clone\_lib="Peach developing fruit mesocarp"  
 /note="Vector: pBluescript II SK(-); Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from etiolated hypocotyl tissue of 9-10 day old seedlings of the cultivar Williams. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) primer with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and XhoI. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."

Sequence has been trimmed to remove vector sequence and  
 contains a minimum of 100 bases of phred value 20 or

## ORIGIN

above. For more details on library preparation and sequence analysis go to <http://www.genome.clemson.edu/projects/peach>. To order this clone go to <http://www.genome.clemson.edu/orders>

Query Match 70.0%; Score 14; DB 5; Length 513;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 GACCCCAACTACT 18  
|||||  
DB 280 GACCCCAACTACT 293

RESULT 64  
B1786794/c 525 bp mRNA linear EST 08-JUL-2004  
LOCUS sa153409.y1 Gm-cl068 Glycine max cDNA clone GENOME SYSTEMS CLONE  
DEFINITION ID: Gm-cl068-2465 5', mRNA sequence.  
ACCESSION B1786794  
VERSION B1786794.1 GI:15814519  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max

REFERENCE  
AUTHORS Shoenmaker, R., Kaim, P., Vockin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurr, R., Ritzer, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
TITLE Public Soybean EST Project  
JOURNAL Unpublished (1999)  
COMMENT Contact: Shoenmaker R./Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: eest@wustl.edu

When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: [info@biogeneticservices.com](mailto:info@biogeneticservices.com))  
Seq primer: -40RP from Gibco  
High quality sequence stop: 428.  
Location/Qualifiers  
1..525  
/organism="Glycine max"  
/mol\_type="mRNA"  
/culti\_var="Williams 82"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl068-2465"  
/tissue\_type="leaf, drought stressed, 1 month old plants, greenhouse grown"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl068"  
/note="Vector: pluescript II SK+, Site\_1: EcoRI, Site\_2: XhoI; The cDNA library was constructed from mRNA isolated from drought stressed leaf tissue of the cultivar Williams 82. The month old greenhouse grown plants were deprived of water for 3 days prior to harvesting the stressed leaf tissue. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pluescript vector. The

FEATURES  
source

## ORIGIN

ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoenmaker."

Query Match 70.0%; Score 14; DB 4; Length 525;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCCAACTACT 19  
|||||  
DB 439 GACCCCAACTACT 426

RESULT 65  
CF350940 534 bp mRNA linear EST 20-AUG-2003  
LOCUS r165d01.y1 Meloidogyne javanica J2 SMART cDNA Meloidogyne javanica  
DEFINITION cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN. ;, mRNA sequence.  
ACCESSION CF350940  
VERSION CF350940.1 GI:33953484  
KEYWORDS EST.  
SOURCE Meloidogyne javanica (root-knot nematode)  
ORGANISM Meloidogyne javanica

REFERENCE  
AUTHORS Eukaryote; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.  
1 (bases 1 to 534)  
McCarter, J., Clifton, S., Chiappelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritzer, E., Bennett, J., Franklin, C., Tsagaris, B., R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurr, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
TITLE The Washington Univ. Nematode EST Project, 1999  
JOURNAL Unpublished (1999)  
COMMENT Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: eest@wustl.edu

Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (Dynal) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5'SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11ze(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See [www.nematode.net](http://www.nematode.net) for additional project information.  
Seq primer: Sp6  
High quality sequence stop: 534.  
Location/Qualifiers  
1..534  
/organism="Meloidogyne javanica"  
/mol\_type="mRNA"  
/db\_xref="taxon:6303"  
/tissue\_type="whole organism"  
/dev\_stage="J2"  
/lab\_host="DH10B"  
/clone\_lib="Meloidogyne javanica J2 SMART pGEM"  
/note="Vector: plasmid (ampicillin resistant); Site\_1: XhoI; Site\_2: NotI; Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (Dynal) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5'SMART 'anchor'

FEATURES  
source

added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractioned on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See [www.nemacode.net](http://www.nemacode.net) for additional project information."

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 534;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCGCGACCCCAACA 14  
71 TTCGCGACCCCAACA 84

## RESULT 66

AL913399/c AL913399 539 bp mRNA linear EST 06-JUN-2004  
DEFINITION AL913399 PUR-Z1+Z2 Danio rerio cDNA clone 172-B03-2, mRNA sequence.  
ACCESSION AL913399  
VERSION AL913399.1 GI:23178669  
KEYWORDS EST.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

Lo, J., Lee, S., Xu, M., Liu, F., Ruan, H., Eun, A., He, Y., Ma, W., Wang, W., Wen, Z. and Peng, J.  
15000 unique zebrafish EST clusters and their future use in microarray for profiling gene expression patterns during embryogenesis  
Genome Res. 13 (3), 455-466 (2003)  
12618176  
Contact: Peng J  
Lab of Functional Genomics  
Institute of Molecular and Cell Biology  
30 Medical Drive, Singapore, 117609, Singapore  
Email: pengj@imcb.a-star.edu.sg  
Clone requests: info@openbiosystems.com  
Open Biosystems,  
6705 Odysey Drive, Huntsville, AL 35806.  
Location/Qualifiers  
1. 539  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/strain="local\_wildtype"  
/db\_xref="taxon:7955"  
/clone="172-B03-2"  
/issue\_type="whole embryo or fish"  
/dev\_stage="mixed stages"  
/clone\_1b="PUR-Z1+Z2"

## FEATURES

## source

## ORIGIN

Query Match 70.0%; Score 14; DB 1; Length 539;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## OY

3 CGGACCCCAACT 16  
496 CGGACCCCAACT 483

## RESULT 67

CO210460/c

LOCUS CO210460 540 bp mRNA linear EST 22-JUN-2004  
DEFINITION WS00918.B21 E20 IS-B-N-A-10 Picea engelmannii x Picea sitchensis  
cDNA clone WS00918\_E20 3', mRNA sequence.  
ACCESSION CO210460  
VERSION CO210460.1 GI:49022990  
KEYWORDS EST.

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

Ralph, S., Kolosova, N., Cooper, D., Butterfield, Y., Kirkpatrick, R., Liu, J., Palmquist, D., Scott, J., Barber, S., Yang, G., Babakelf, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A., Mayo, M., Moran, J., Olson, T., Wong, D., Friedmann, M.F., Ritland, C.E., Siddiqui, A., Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and Bohlmann, J.  
The spruce transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries  
Unpublished (2004)  
Contact: Joerg Bohlmann  
Genome BC forest genomics program  
University of British Columbia  
UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237,  
Vancouver, British Columbia, Canada, V6T 1Z3  
Tel: 1-604-822-0282  
Fax: 1-604-822-6097  
Email: bohlmann@interchange.ubc.ca  
Plate: WS00918 row: E column: 20  
High quality sequence stop: 540  
POLA=yes

## JOURNAL

## COMMENT

## TITLE

## FEATURES

## source

Location/Qualifiers  
1. 540  
/organism="Picea engelmannii x Picea sitchensis"  
/mol\_type="mRNA"  
/cultivar="Fal-1028"  
/db\_xref="taxon:273280"  
/clone="WS00918\_E20"  
/sex="Hermaphrodite"  
/lab\_host="E. coli DH10B cells"  
/clone\_1b="IS-B-N-A-10"  
/note="Organ: Bark (with phloem and cambium attached) from one year old clonal trees grown under greenhouse conditions in standard potting soil mixture; Vector: Bluescript II SK (+) XR; Site: 1: EcoRI (5' end of cDNA); Site 2: XhoI (3' end of cDNA); Bark was wounded using razor blades along the entire length of the tree at 5 mm intervals on opposite sides of the trunk. The same trees were also sprayed with a 0.01% (v/v) methyl jasmonate solution resuspended in 0.1% (v/v) tween 20 (50mls per tree). Bark tissue with phloem attached was harvested 3 hours, 6 hours, 12 hours, 24 hours, 2 days, 4 days and 8 days after initiating the treatment. Untreated control bark was also harvested at time 0 hours. mRNA was isolated from each tissue source independently and equal quantities of RNA from each tissue were then pooled. cDNA was prepared from 5 micrograms of mRNA and directionally ligated into the Bluescript II SK (+) XR vector using the phluescript II XR cDNA Library Construction Kit according to manufacturer's instructions with modifications (Stratagene). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation. Normalization was applied according to published methods [Bonaldi M.F. et al. (1996) Genome Research 6(9):791] in order to reduce the abundance of highly expressed transcripts."

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 540;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## OY

6 GACCAACTACT 19



Db 413 GACCCACACTACT 400

RESULT 68  
BG593673/c

LOCUS CA225879 541 bp mRNA linear EST 25-SEP-2003

DEFINITION SCRLFL3004E02.b Saccharum officinarum FL3 Saccharum officinarum

ACCESSION CA225879

VERSION CA225879.1

KEYWORDS GI:35284679

SOURCE EST

ORGANISM Saccharum officinarum  
Saccharum officinarum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum  
complex.

REFERENCE

1 (bases 1 to 541)  
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.  
The libraries that made SUCEST

JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

COMMENT

Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parida@unicamp.br  
Clone distribution: clone distribution information can be found  
through the Brazilian Clone Collection Center (BCCC) at  
http://www.bcccenter.fcav.unesp.br  
Plate: 004 row: E column: 02  
Seq primer: SP6 Promoter primer.

FEATURES

source

1..541  
/organism="Saccharum officinarum"

/mol\_type="mRNA"

/db\_xref="taxon:4547"

/clone="SCRLFL3004E02"

/lab\_host="DH10B"

/clone\_1lb="Saccharum officinarum FL3"

/note="Organ: Base of developing inflorescence (5cm-long);  
Vector: pspori1, Site 1: Salt, Site 2: Nocti. An  
unidirectional cDNA library generated from (base of  
developing inflorescence (5cm-long)). cDNA was prepared  
from polyA+ mRNA using Superscript Plasmid System Kit  
(Invitrogen). The double-strand cDNAs were fractionated  
in a sepharose CL-2B 40cm-columns and fragments sizing  
between 0.8 and 1.5 kb were directionally cloned into the  
vector. Details of each source of RNA and library  
construction can be obtained at  
http://sucest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 70.0%; Score 14; DB 6; Length 541;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCACACTACT 19

Db 481 GACCCACACTACT 468

RESULT 69

BG593673/c

LOCUS BG593673 556 bp mRNA linear EST 07-MAR-2003

DEFINITION

ACCESSION BG593673

VERSION BG593673.1

KEYWORDS

Solanum tuberosum (potato)

ORGANISM

Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamiales; Solanales; Solanaceae; Solanum.

REFERENCE

1 (bases 1 to 556)  
Van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemiango,A.,  
Bongri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.

Generations of ESTs from sprouting potato eyes

JOURNAL Unpublished (2000)

COMMENT The Institute for Genomic Research  
Contact: Robin Buell  
7712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potaro-array@tigr.org

This clone can be obtained from the University of Arizona Genomics  
Institute. Orders can be made through URL:  
http://genome.arizona.edu/orders/  
Seq primer: M13P-R.

FEATURES

source

1..556  
/organism="Solanum tuberosum"

/mol\_type="mRNA"

/cultivar="Kennebec"

/db\_xref="taxon:4113"

/clone="CSTS515"

/issue\_type="sprouting eyes from tubers"

/dev\_stage="12-14 weeks post harvest"

/lab\_host="SOLR"

/clone\_1lb="CSTS"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:  
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were  
taken from tubers. The tubers were incubated at 26C in the  
dark for 2-3 weeks prior to sprouting. The eyes were  
frozen in liquid nitrogen immediately upon removal from  
tubers."

ORIGIN

Query Match 70.0%; Score 14; DB 4; Length 556;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCACACTACT 19

Db 514 GACCCACACTACT 501

RESULT 70

BM307732/c

LOCUS BM307732 564 bp mRNA linear EST 06-JUL-2004

DEFINITION Gm-cl075-y1 Gm-cl075 Glycine max cDNA clone SOYBEAN CLONE ID:  
Gm-cl075-4651 5' similar to TR:Q9XHS Q9XHS MICROTUBULE-ASSOCIATED  
PROTEIN. (1) ; mRNA sequence.

ACCESSION BM307732

VERSION BM307732.1

KEYWORDS GI:18039438

SOURCE EST

ORGANISM Glycine max (soybean)  
Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

REFERENCE 1 (bases 1 to 564)

AUTHORS

Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V.,  
Knappa,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,  
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M.,  
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N.,  
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCann,R., Waterston,R. and Wilson,R.

Public Soybean EST Project

Unpublished (1999)

JOURNAL

COMMENT Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: [esc@watson.wustl.edu](mailto:esc@watson.wustl.edu)  
 When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: [info@biogeneticservices.com](mailto:info@biogeneticservices.com))  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 421.  
 Location/Qualifiers  
 1..564

/organism="Glycine max"  
 /mol\_type="mRNA"  
 /cultivar="Jack"  
 /db\_xref="taxon:3847"  
 /clone="SOYBEAN CLONE ID: Gm-cl075-4651"  
 /tissue\_type="differentiating somatic embryos cultured on MSM6AC"  
 /lab\_host="DH10B"  
 /clone\_id="Gm-cl075"

/note="vector: pBluescript II SK+, Site 1: EcoRI, Site 2: XhoI; The cDNA library was constructed from mRNA isolated from differentiating somatic embryos cultured on MSM6AC. The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E. coli Electromax DH10B host cells. Tissue culture and library construction were performed by Françoise Thibaud-Nissen and Anu Khanna (Lila Vodkin lab, University of Illinois)."

## ORIGIN

Query Match 70.0%; Score 14; DB 4; Length 564;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCACACTACT 19  
 |||||  
 Db 212 GACCCACACTACT 199

## RESULT 71

CE261393/c

LOCUS CE261393 566 bp DNA linear GSS 26-SEP-2003  
 DEFINITION tigr-gss-dog-17000346569937 Dog Library Canis familiaris genomic,  
 genomic survey sequence.

ACCESSION

CE261393

VERSION

KEYWORDS

SOURCE

ORGANISM

Canis familiaris (dog)

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

The dog genome: survey sequencing and comparative analysis  
 Science 301 (5641), 1898-1903 (2003)  
 Contact: Kirkness BP  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: [ekirkness@tigr.org](mailto:ekirkness@tigr.org)

Class: Shotgun.  
 Location/Qualifiers  
 1..566

/organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_id="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from peripheral blood"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 566;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACACTACTC 20  
 |||||  
 Db 184 ACCCAACACTACTC 171

## RESULT 72

CK435227/c

LOCUS CK435227 572 bp mRNA linear EST 08-JAN-2004  
 DEFINITION glauca cDNA clone GQ0063\_P07 3', mRNA sequence.

ACCESSION

CK435227

VERSION

KEYWORDS

SOURCE

ORGANISM

Picea glauca (white spruce)

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Seq primer: PolyTplus Primer.

Location/Qualifiers

1..572

/organism="Picea glauca"

/mol\_type="mRNA"

/strain="Two trees of provenance 5333 and one from 5208"

/db\_xref="taxon:3330"

/clone="GQ0063\_P07"

/sex="Hermaphrodite"

/tissue\_type="Cambium and phloem region from normal vertical trees"

/dev\_stage="Cambium and phloem tissue scraped from inside of bark from trees harvested 2.5 hours, 6 hours and 11 hours after day break were pooled"

/lab\_host="E. coli DH10B cells"

/clone\_id="GQ0063\_P07"

/note="Organ: Stem from ground to lower part of live crown, on 33 year old tree; Vector: pBluescript II SK (+) mid-June, during formation of early wood. cDNA was prepared from 5 mg of poly A+ selected RNA and was

directionally ligated into the pBluescript II SK (+) XR vector (Stratagene), transformed by electroporation into DH10B cells (in vitro) for propagation"

Query Match 70.0%; Score 14; DB 7; Length 572;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCCACTACT 19

Db 477 GACCCCACTACT 464

RESULT 73  
LOCUS CO207163 575 bp mRNA linear EST 21-JUN-2004  
DEFINITION WS00913.B21 F10 IS-B-N-A-10 Picea engelmannii x Picea sitchensis  
CDNA clone WS00913\_F10 3', mRNA sequence.

ACCESSION CO207163  
VERSION CO207163.1 GI:49018338

KEYWORDS EST.  
ORGANISM Picea engelmannii x Picea sitchensis  
Picea engelmannii x Picea sitchensis  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.

REFERENCE 1 (bases 1 to 575)  
AUTHORS Ralph, S., Kolosova, N., Cooper, D., Butterfield, Y., Kirkpatrick, R.,  
Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G., Babakoff, R.,  
Brown-John, M., Chand, S., Featherstone, R., Masson, A., Mayo, M.,  
Moran, J., Olson, T., Wong, D., Friedmann, M.F., Ritzland, C.E.,  
Siddiqui, A., Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C.,  
Ritzland, K. and Bohlmann, J.

TITLE The spruce transcriptome: Analysis of expressed sequence tags from  
multiple cDNA libraries  
JOURNAL Unpublished (2004)  
COMMENT Contact: Joerg Bohlmann  
Genome BC forest genomics program  
University of British Columbia  
UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237,  
Vancouver, British Columbia, Canada, V6T 1Z3  
Tel: 1-604-822-0282  
Fax: 1-604-822-6097  
Email: bohlmann@interchange.ubc.ca  
Plate: WS00913 row: F column: 10  
High quality sequence stop: 575  
POLYA=yes.

FEATURES Location/Qualifiers

SOURCE

1. 575  
/organism="Picea engelmannii x Picea sitchensis"  
/mol\_type="mRNA"  
/cultivar="Fal-1028"  
/db\_xref="taxon:273280"  
/clone="WS00913\_F10"  
/sex="Hermaphrodite"  
/lab\_host="E. coli DH10B cells"  
/clone\_1b="IS-B-N-A-10"  
/note="Organ: Bark (with phloem and cambium attached) from  
one year old clonal trees grown under greenhouse  
conditions in standard potting soil mixture; Vector:  
pBluescript II SK (+) XR; Site 1: EcoRI (5' end of cDNA);  
Site 2: XhoI (3' end of cDNA); Bark was wounded using  
razor blades along the entire length of the tree at 5 mm  
intervals on opposite sides of the trunk. The same trees  
were also sprayed with a 0.01% (v/v) methyl jasmonate  
solution resuspended in 0.1% (v/v) tween 20 (~50mls per  
tree). Bark tissue with phloem attached was harvested 3  
hours, 6 hours, 12 hours, 24 hours, 2 days, 4 days and 8  
days after initiating the treatment. Untreated control  
bark was also harvested at time 0 hours. mRNA was isolated  
from each tissue source independently and equal quantities  
of mRNA from each tissue were then pooled. cDNA was  
prepared from 5 micrograms of mRNA and directionally

ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 575;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCCACTACT 19

Db 378 GACCCCACTACT 365

RESULT 74  
LOCUS CF351038 579 bp mRNA linear EST 20-AUG-2003  
DEFINITION r166f04.y1 Meloidogyne javanica J2 SMART PGM Meloidogyne javanica  
cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN. ;, mRNA  
sequence.

ACCESSION CF351038  
VERSION CF351038.1 GI:33953680

KEYWORDS EST.  
ORGANISM Meloidogyne javanica (root-knot nematode)  
Meloidogyne javanica  
Eukaryote; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
Tylenchoidea; Heterodermidae; Meloidogyninae; Meloidogyne.

REFERENCE 1 (bases 1 to 579)  
AUTHORS McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,  
Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,  
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,  
Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
Harvey, N., Schurk, R., Allen, M., Peterson, B., Swaller, T.,  
Haderwood, K., Steptoe, M., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
McCann, R., Waterston, R. and Wilson, R.

TITLE The Washington Univ. Nematode EST Project, 1999  
JOURNAL Unpublished (1999)  
COMMENT Contact: McCarter, JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

Cloned unidirectionally. Poly(A)<sup>+</sup> RNA was concentrated and purified  
using Dynabeads (Dyna) and mRNA eluted for first strand synthesis.  
First strand cDNA was created using MMV RT (PowerScript, Clontech)  
and primed with oligo(dT) with xhoi site and 5'SMART 'anchor' added  
using chimeric DNA-RNA oligo. 12 PCR cycles were done using first  
strand and primers specific to SMART oligo and 3' end. Double  
stranded cDNA was digested using XhoI/NotI, fractionated on  
Chroma-spin 400 columns (Clontech) and ligated to digested  
pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as  
host cells. Library materials provided by Dr. David Bird of North  
Carolina State University. Library construction by Jeff Rousch. See  
www.nematode.net for additional project information.  
Seq primer: Sp6.

FEATURES Location/Qualifiers

SOURCE

1. 579  
/organism="Meloidogyne javanica"  
/mol\_type="mRNA"  
/db\_xref="taxon:6303"  
/tissue\_type="whole organism"  
/dev\_stage="J2"  
/lab\_host="DH10B"  
/clone\_1b="Meloidogyne javanica J2 SMART PGM"  
/note="Vector: plasmid (ampicillin resistant); site\_1:

XhoI, Site 2: NotI; Cloned unidirectionally. Poly(A)<sup>+</sup> RNA was concentrated and purified using Dynabeads (DynaI) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See [www.nemacode.net](http://www.nemacode.net) for additional project information.

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 579;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCACACA 14  
118 TTCCGACCCACACA 131

## RESULT 75

LOCUS CLJ233606/c 579 bp DNA linear GSS 19-AUG-2004  
DEFINITION RPT14\_458D12.f RPT1-44 Sus scrofa genomic clone RPT14\_458D12,  
genomic survey sequence.

ACCESSION CLJ233606  
VERSION CLJ233606.1 GI:51375577  
KEYWORDS GSS.

SOURCE Sus scrofa (pig)  
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
1 (bases 1 to 579)

AUTHORS Rogatcheva, M.B., Meyers, S., He, W., Larkin, D.M., Marron, B.M.,  
Piggy-BACing the Human Genome: Constructing a Porcine Physical Map  
Through Comparative Genomics

TITLE Unpublished (2004)  
JOURNAL Other GSSs: RPT14\_458D12.r

COMMENT Contact: Lawrence B. Schook  
Department of Animal Sciences  
University of Illinois at Urbana Champaign  
1201 W. Gregory Dr., Urbana, IL 61801, USA  
Tel: 217 265 5326  
Fax: 217 244 5617  
Email: [schook@uiuc.edu](mailto:schook@uiuc.edu)

Clones are derived from the porcine BAC library RPT1-44  
(<http://www.bacpac.chori.org/mporcine44.htm>). For BAC library  
availability, please contact Pieter de Jong ([pdejong@chori.org](mailto:pdejong@chori.org)).  
Clones may be purchased from BACPAC Resources  
(<http://BACPACResources.chori.org>). This work was undertaken as part  
of the International Swine Genome Sequencing Consortium by  
University of Illinois at Urbana Champaign, USA with funds provided  
by grant No. AG2002-34480-11828 from USDA-CSREES and  
AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing  
Initiative)

Plate: 458 row: D column: 12  
Seq primer: T7  
Class: BAC ends.

## FEATURES

source Location/Qualifiers  
1..579  
/organism="Sus scrofa"  
/mol\_type="genomic DNA"  
/strain="four pigs (breed: 37.5% Yorks Landrace and 25%  
Meishan)"  
/db\_xref="taxon:9823"  
/clone="RPT14\_458D12"

/sex="male"  
/cell\_type="blood"  
/clone\_lib="RPT1-44"  
/note="Vector: pTARBAC2; Site 1: EcoRI; Site 2: EcoRI;  
porcine male BAC library produced by Pieter de Jong"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 579;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCAACTACT 19  
280 GACCCAACTACT 267

## RESULT 76

LOCUS CG810144 586 bp DNA linear GSS 13-NOV-2003  
DEFINITION FSAJB1R LargeInsertGenomicLibrary Fusarium virguliforme genomic  
clone KMFV1M18, genomic survey sequence.

ACCESSION CG810144  
VERSION CG810144.1 GI:38263618  
KEYWORDS GSS.

SOURCE Fusarium virguliforme  
ORGANISM

REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
1 (bases 1 to 586)

AUTHORS Meksem, K., Ishihara, H., Koo, H., Shultz, J., Ali, S., Iqbal, J.,  
Lightfoot, D.A. and Town, C.D.  
End sequencing of BACs from a fingerprint physical map of the  
causative agent of soybean sudden death syndrome, *Fusarium  
virguliforme*

Unpublished (2003)  
JOURNAL Other GSSs: FSAJB1R

COMMENT Contact: Chris Town and K. Meksem  
The Center of Excellence in Soybean Research, Teaching and  
Outreach, Southern Illinois University at Carbondale and Plant  
Genomics, The Institute for Genomic Research  
Room 176, Ag. Building, Mail Code 4415, Carbondale, IL 62901-4415,  
USA and 9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 618 453-7457 and 301-838-3523  
Fax: 618 453-7457 and 301-838-0208  
Email: [meksem@siu.edu](mailto:meksem@siu.edu); [cdtown@tigr.org](mailto:cdtown@tigr.org) (URL:  
<http://Fusariumvirguliforme.siu.edu>)  
Seq primer: CAGGAAACAGCTATGACC  
Class: BAC ends.

## FEATURES

source Location/Qualifiers  
1..586  
/organism="Fusarium virguliforme"  
/mol\_type="genomic DNA"  
/cultivar="Monticello"  
/db\_xref="taxon:232082"  
/clone="KMFV1M18"  
/note="Organ: Hypnae; Vector: pINDIGOBACs; A single spore  
derived culture was used. Hypnae were grown in an  
incubator for four days. Nuclei were isolated and embedded  
in agarose, restriction digested with Hind III. Large size  
DNA fragments were ligated in vector pINDIGOBACs and  
electro-transformed into DH10B cells."

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 586;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCAACACTAC 18  
242 CGACCAACACTAC 255

RESULT 77  
LOCUS CO209937 593 bp mRNA linear EST 21-JUN-2004  
DEFINITION WS00916.B21.1\_J14 IS-B-N-A-10 Picea engelmannii x Picea sitchensis  
CDNA clone WS00916\_J14 3', mRNA sequence.  
ACCESSION CO209937  
VERSION CO209937  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
Ralph, S., Kolosova, N., Cooper, D., Butterfield, Y., Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G., Babakait, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A., Mayo, M., Moran, J., Olson, T., Wong, D., Friedmann, M.F., Ritzland, C.E., Siddiqui, A., Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritzland, K. and Bohlmann, J.  
The spruce transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries  
TITLE  
JOURNAL  
COMMENT  
Contact: Joerg Bohlmann  
Genome BC forest genomics program  
University of British Columbia  
UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237, Vancouver, British Columbia, Canada, V6T 1Z3  
Tel: 1-604-822-0282  
Fax: 1-604-822-6097  
Email: bohlmann@interchange.ubc.ca  
Plate: WS00916 row: J column: 14  
High quality sequence stop: 593.  
Location/Qualifiers  
1. 593  
/organism="Picea engelmannii x Picea sitchensis"  
/mol\_type="mRNA"  
/culivar="Pal-1028"  
/db\_xref="taxon:273280"  
/clone="WS00916\_J14"  
/sex="Hermaphrodite"  
/lab\_host="E. coli DH10B cells"  
/clone\_1ib="IS-B-N-A-10"  
/note="Organ: Bark (with phloem and cambium attached) from one year old clonal trees grown under greenhouse conditions in standard potting soil mixture; Vector: pBluescript II SK (+) XR; Site 1: EcoRI (5' end of cDNA); Site 2: XhoI (3' end of cDNA); Bark was wounded using razor blades along the entire length of the tree at 5 mm intervals on opposite sides of the trunk. The same trees were also sprayed with a 0.01% (v/v) methyl jasmonate solution resuspended in 0.1% (v/v) tween 20 (~50mls per tree). Bark tissue with phloem attached was harvested 3 hours, 6 hours, 12 hours, 24 hours, 2 days, 4 days and 8 days after initiating the treatment. Untreated control bark was also harvested at time 0 hours. mRNA was isolated from each tissue source independently and equal quantities of mRNA from each tissue were then pooled. cDNA was prepared from 5 micrograms of mRNA and directionally ligated into the pBluescript II SK (+) XR vector using the pBluescript II XR cDNA Library Construction Kit according to manufacturer's instructions with modifications (Stratagene). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for published methods [Bonaldo M.F. et al. (1996) Genome Research 6(9):791] in order to reduce the abundance of highly expressed transcripts."

ORIGIN  
Query Match 70.0%; Score 14; DB 7; Length 593;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCCAACTACT 19  
|||||  
Db 382 GACCCCAACTACT 395  
|||||

RESULT 78  
LOCUS FR0049660 597 bp DNA linear GSS 05-SEP-2001  
DEFINITION Fugu rubripes GSS sequence, clone B29C07e1, genomic survey sequence.  
ACCESSION AL605469  
VERSION AL605469.1 GI:15487270  
KEYWORDS  
SOURCE  
ORGANISM  
Takiugu rubripes (Fugu rubripes)  
Takiugu rubripes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Takiugu.  
1 (bases 1 to 597)  
REFERENCE  
AUTHORS  
Clark, M.S.  
TITLE  
JOURNAL  
COMMENT  
Direct Submission  
Submitted (04-SEP-2001) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB, UK Email: biohelp@hmp.mrc.ac.uk  
Vector: pBluescript II KS  
V\_type: phagemid  
PRIMER: KS  
DESCR:  
One pass dye-terminator sequencing of BAC (pBelobAC11) cloned genomic sequence  
The BACs can be obtained from <http://www.incyte.com>.  
Location/Qualifiers  
1. 597  
/organism="Takiugu rubripes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:31033"  
/clone="B29C07e1"  
/clone\_1ib="BAC B29C07"

ORIGIN  
Query Match 70.0%; Score 14; DB 9; Length 597;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GACCCCAACTACT 18  
|||||  
Db 216 GACCCCAACTACT 229  
|||||

RESULT 79  
LOCUS CF629503 599 bp mRNA linear EST 02-OCT-2003  
DEFINITION zmrw48 OA20-002-b10.83 zmrw48 Zea mays cDNA 3', mRNA sequence.  
ACCESSION CF629503  
VERSION CF629503.1 GI:37384806  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 599)  
REFERENCE  
AUTHORS  
Bohner, H., Sharp, R.E., Springer, G.K., Poroyko, V., Fredricksen, M., Sharp, L.G., Spollen, W.G., Ries, J., Guillen, A., Khambati, A., Topinka, C., Davis, G.E., Schachtman, D., Wu, Y. and Nguyen, H.T.  
NSF Grant DBI-0211842; Functional Genomics of Root Growth and Root Signaling Under Drought  
Unpublished (2003)  
JOURNAL  
COMMENT  
Contact: Hans Bohner  
University of Illinois, Urbana-Champaign  
1201 West Gregory Drive, Urbana, IL 61801, USA  
Tel: 217-265-5475

FEATURES  
SOURCE

Fax: 217-333-5574  
Email: bohnert@life.uiuc.edu  
POLYA=yes

Location/Qualifiers  
1. 599  
/organism="Zea mays"  
/mol\_type="mRNA"  
/db\_xref="taxon:4577"  
/clone\_lib="zmrw848"  
/note="Samples were collected in Robert E. Sharp's lab (University of Missouri-Columbia) to construct three normalized cDNA libraries. Dark-grown maize seedlings with primary roots 12-20 mm in length were transplanted to high (-0.03 MPa) or low water potential (-1.6 MPa) vermiculite, and harvested at 5 h and 48 h after transplanting. About 1,000 roots were used for each of the low water potential libraries (zmrw805 and zmrw848) while 500 roots were combined from each of the two time points at high water potential (zmrw00). Each root was divided into 4 segments (distances are from the junction of the root apex and root cap): segment 1, 0-3 mm plus the root cap; segment 2, 3-7 mm; segment 3, 7-12 mm; segment 4, 12-20 mm. (For details of conditions see (1) with nutrient modifications as in (2)). The three normalized cDNA libraries were constructed in the lab of Hans Bohnert (University of Illinois-UC). Total RNA was extracted by the 'hot phenol' method (Plant Molecular Biology manual, D5: 1-13, 2nd ed., 1997). This method worked in eliminating carbohydrate material present in the root tips. The integrity of the RNA was verified by denaturing agarose gels and spectrophotometry (ratio A260/280). Poly(A)+mRNA was isolated twice from total RNA using the Oligotex Direct mRNA kit (Qiagen). Poly(A)+mRNA was converted to double-stranded cDNA and tagged by using modified Oligo(dT) primers. One of 4 sequence tags corresponding to a different segment of the root was added to the 3'-end of the modified Oligo(dT) primers, including a NotI site and used to reverse transcribe the segment-specific mRNAs into cDNAs. Each library contains all four tags. A suffix (s1, s2, s3, or s4) has been added to each sequence identifier to designate which region of the root (Root segment 1, 2, 3, or 4) the sequence was found in based on the identification of the tag. A suffix of s0 indicates that the sequence tag, and hence the source segment, could not be identified. The double stranded cDNAs were size-selected (>450 bp). Size selected cDNAs were adapted with EcoRI adaptors at both ends, and then digested with NotI. The cDNA was directionally cloned into EcoRI-NotI digested pBS II SK(+) phagemid vector (Stratagene) and electroporated into E.coli DH10B. The total number of white colony forming units (cfu) in the primary libraries before amplification was as follows: zmrw805: 3.37 x 10<sup>6</sup>; zmrw848: 4.87 x 10<sup>6</sup>; zmrw00: 3 x 10<sup>6</sup>. The background of empty clones was less than 1%. Inserts ranged from -0.5 kb to >2.5 kb, as determined by PCR. Plasmid DNA from the primary libraries then was converted to single-stranded circles and used as a template for PCR amplification using the T7 and T3 priming sites that flank the cloned cDNA inserts. The purified PCR products, representing the entire cDNA population cloned in each library, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 300C. Non-hybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B. The total number of clones with insert was: zmrw805: 2.0x10<sup>7</sup>; zmrw848: 4.2x10<sup>7</sup>; zmrw00: 1.1x10<sup>7</sup>. The background of empty clones was less than 2%. Insert size, determined by PCR of the entire library, ranged from 0.5 kb to 2.5 kb. (1) Sharp R E, Silk W K, Heiao T C. Growth of the Maize Primary Root at Low Water Potentials I. Spatial Distribution of Expansive Growth. Plant Physiology (Rockville). 87(1). 1988. 50-57. (2) Spoilen W G, Lehnoble M E, Samuels T D, Bernstein N, Sharp

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 599;  
Best Local Similarity 100.0%; Pred No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

2 TCCTGACCCACAC 15  
|||||  
583 TCCTGACCCACAC 596

## RESULT 80

## AZ808200/c

LOCUS 600 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0071E18R Mouse 10kb plasmid UGCG1M library Mus musculus genomic

ACCESSION AZ808200  
clone UGCG2M0071E18 R, genomic survey sequence.

VERSION AZ808200.1 GI:12973498  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus. 1 (bases 1 to 600)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0071 row: E column: 18  
Seq primer: CACACGAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 600.

## FEATURES

## SOURCE

1. 600  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCG2M0071E18"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCG1M library"  
/note="Vector: pMD22nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrolytically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD22 (GI14732114|GB|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 600;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 GACCAACACTACT 19  
|||||  
Db 555 GACCAACACTACT 542

RESULT 81  
BMS81700/c 602 bp mRNA linear EST 31-AUG-2004  
LOCUS BMS81700 Yutaka Satou unpublished cDNA library (csefl) ciona  
DEFINITION BMS81700 Yutaka Satou unpublished cDNA library (csefl) ciona  
BMS81700  
BMS81700.1 GI:51762375  
EST.  
Ciona savignyi  
Ciona savignyi  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Cionidae; Ciona.  
1 (bases 1 to 602)  
Yamada, L., Satoh, N. and Satou, Y.  
Expressed genes in *Ciona savignyi* (Yamada, Satoh, Satou)  
Unpublished (2004)  
Contact: Yutaka Satou  
Department of Zoology  
Kyoto University  
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4095  
Fax: 81-75-705-1113  
Email: yutaka@ascidian.zool.kyoto-u.ac.jp.  
Location/Qualifiers

FEATURES  
source  
1..602  
/organism="Ciona savignyi"  
/mol\_type="mRNA"  
/db\_xref="taxon:51511"  
/clone="csefl015j23"  
/dev\_stage="egg"  
/clone\_lib="Yutaka Satou unpublished cDNA library (csefl)"

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 602;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGCGACCCACACA 14  
|||||  
Db 477 TTGCGACCCACACA 464

RESULT 82  
BZ878744/c 604 bp DNA linear GSS 18-MAR-2003  
LOCUS BZ878744 CH240\_293M13.TJ CHORI-240 Bos taurus genomic clone CH240\_293M13,  
DEFINITION BZ878744 genomic survey sequence.  
BZ878744  
BZ878744.1 GI:29106146  
GSS.  
Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 604)

## AUTHORS

Zhao, S., Shetty, J., Shatsman, S., Tsagaye, G., Geer, K.,  
Shvartsbeyn, A., Gebregorjisi, E., Chen, D., Riggs, F., de Jong, P.,  
Crawford, A.W. and McEwan, J.C.  
Bovine BAC End Sequences from Library CHORI-240  
Unpublished (2003)  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org

## COMMENT

Clones are derived from the bovine BAC library CHORI-240  
(<http://www.chori.org/bacpac/bovine240.htm>). For BAC library  
availability, please contact Pieter de Jong ([pdjong@tigr.org](mailto:pdjong@tigr.org)).  
Clones may be purchased from BACPAC Resources  
(<http://www.chori.org/bacpac/ordering/information.htm>). This work  
was undertaken as part of the International Bovine BAC Mapping  
Consortium (IBBMC) by AgResearch Ltd., New Zealand and The  
Institute of Genomic Research (TIGR), USA.  
Plate: 293 row: M column: 13  
Seq primer: SP6  
Class: BAC ends.

FEATURES  
source  
Location/Qualifiers  
1..604  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_293M13"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pPARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 604;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 ACCCAACACTACTC 20  
|||||  
Db 456 ACCCAACACTACTC 443

RESULT 83  
CD856253 605 bp mRNA linear EST 11-JUL-2003  
LOCUS CD856253 DH0AF2652D052M1 Hadev87 Helianthus annuus cDNA clone Hadev8726505,  
DEFINITION CD856253 mRNA sequence.  
CD856253  
CD856253.1 GI:32540069  
EST.  
Helianthus annuus (common sunflower)  
Helianthus annuus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
Heliantheae; Helianthus.  
1 (bases 1 to 605)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Genoplante  
Contact: Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).

```

FEATURES
  source
    Location/Qualifiers
      1..605
        /organism="Helianthus annuus"
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        /db_xref="pasc8"
        /db_xref="taxon:4232"
        /clone="Hadev726D05"
        /tissue_type="ovary"
        /clone_id="Hadev7"

ORIGIN
  Query Match      70.0%; Score 14; DB 6; Length 605;
  Best Local Similarity 100.0%; Pred. No. 4.4e+02;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCGACCCCACTA 17
    |||||
    224 GCGACCCCACTA 237

RESULT 84
CO233457/c 620 bp mRNA linear EST 22-JUN-2004
LOCUS WS0055.B21.1.016 WS-PP-A-6 Picea glauca cDNA clone WS0055_016 3',
DEFINITION mRNA sequence.
ACCESSION CO233457
VERSION CO233457.1 GI:49055772
KEYWORDS EST.
SOURCE Picea glauca (white spruce)
ORGANISM Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
  1 (bases 1 to 620)
  Ralph,S., Kolosova,N., Cooper,D., Butterfield,Y., Kirkpatrick,R.,
  Liu,J., Palmquist,D., Scott,J., Barber,S., Yang,G., Babakaiti,R.,
  Brown-John,M., Chand,S., Featherstone,R., Masson,A., Mayo,M.,
  Moran,J., Olson,T., Wong,D., Friedmann,M.F., Rittland,C.E.,
  Siddiqui,A., Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C.,
  Rittland,K. and Bohlmann,J.
  The spruce transcriptome: Analysis of expressed sequence tags from
  multiple cDNA libraries
  Unpublished (2004)
  Contact: Joerg Bohlmann
  Genome BC forest genomics program
  University of British Columbia
  UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237,
  Vancouver, British Columbia, Canada, V6T 1Z3
  Tel: 1-604-822-0282
  Fax: 1-604-822-6097
  Email: bohlmann@interchange.ubc.ca
  Plate: WS0055 row: 0 column: 16
  High quality sequence stop: 620
  POLYVA=yes.

  Location/Qualifiers
    1..620
      /organism="Picea glauca"
      /mol_type="mRNA"
      /cultiivar="Pg-29"
      /db_xref="taxon:3330"
      /clone="WS0055_016"
      /sex="Hermaphrodite"
      /tissue_type="Early season phloem harvested June 15th, mid
        season phloem harvested July 10th and late season phloem
        harvested August 17th"
      /lab_host="E. coli DH10B cells"
      /note="Organ: Phloem from 25 year old trees harvested at
        Kalamalka Research Station in Vernon, British Columbia in
        2001; Vector: pBluescript II SK (+) XR; Site: 1: EcoRI (5'
        end of cDNA); Site: 2: XhoI (3' end of cDNA); mRNA was
        isolated from each tissue source independently and equal
        quantities of mRNA from each tissue were then pooled; cDNA
        was prepared from 5 micrograms of mRNA and directionally

```

```

  ligated into the pBluescript II SK (+) XR vector using the
  pBluescript II XR cDNA library Construction kit according
  to manufacturer's instructions with modifications
  (Stratagene). Plasmid DNA was then transformed by
  electroporation into DH10B cells (Invitrogen) for
  propagation."

ORIGIN
  Query Match      70.0%; Score 14; DB 7; Length 620;
  Best Local Similarity 100.0%; Pred. No. 4.4e+02;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCCACTACT 19
    |||||
    398 GACCCCACTACT 385

RESULT 85
CE064314/c 621 bp DNA linear GSS 24-SEP-2003
LOCUS tigr-gss-dog-17000322608251 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
ACCESSION CE064314
VERSION CE064314.1 GI:35119494
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
  Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
  1 (bases 1 to 621)
  Kirchner,E.F., Batra,V., Halpern,A.L., Levy,S., Remington,K.,
  Busch,D.B., Delcher,A.L., Pop,M., Wang,W., Frazer,C.M. and
  Venter,J.C.
  The dog genome: survey sequencing and comparative analysis
  Science 301 (5641), 1898-1903 (2003)
  22875432
  14512627
  Contact: Kirchner EF
  The Institute for Genomic Research
  Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
  Rockville, MD 20850, USA
  Tel: 301-838-0200
  Fax: 301-838-0208
  Email: ekirchner@tigr.org
  Class: shotgun.

  Location/Qualifiers
    1..621
      /organism="Canis familiaris"
      /mol_type="genomic DNA"
      /strain="Standard Poodle"
      /db_xref="taxon:9615"
      /clone_id="Dog Library"
      /note="Site 1: BclXI; Libraries were prepared from
        peripheral blood"

ORIGIN
  Query Match      70.0%; Score 14; DB 9; Length 621;
  Best Local Similarity 100.0%; Pred. No. 4.4e+02;
  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACCCAACTACTC 20
    |||||
    285 ACCCAACTACTC 272

RESULT 86
B0412273 623 bp mRNA linear EST 22-MAY-2002
LOCUS GA_B00056A10r Gossypium arboreum 7-10 dpa fiber library Gossypium
DEFINITION arborum cDNA clone GA_B00056A10r, mRNA sequence.
ACCESSION B0412273
VERSION B0412273.1 GI:21099960
KEYWORDS EST.

```



SOURCE Gossypium arboreum  
ORGANISM Gossypium arboreum  
Bakariota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
1 (bases 1 to 623)  
Wing, R.A., Friesch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.  
An integrated analysis of the genetics, development, and evolution of the cotton fiber  
Unpublished (2000)  
JOURNAL Contact: Wing RA  
COMMENT Clemson University Genomics Institute  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Total High Quality bases = 534  
Seq primer: TAATACGACTCACTATAGG  
High quality sequence start: 3  
High quality sequence stop: 615.  
Location/Qualifiers

FEATURES  
Source  
1..623  
/organism="Gossypium arboreum"  
/mol\_type="mRNA"  
/strain="AKA"  
/cultivar="8400"  
/db\_xref="taxon:29729"  
/clone="GA\_Ed005610r"  
/issue\_type="Fibers isolated from bolls harvested 7-10 dpa"  
/lab\_host="E. coli"  
/clone\_idb="Gossypium arboreum 7-10 dpa fiber library"  
/note="Vector: pBR-CMV; Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN  
Query Match 70.0%; Score 14; DB 5; Length 623;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCACACTACT 19  
|||  
Db 88 GACCCACACTACT 101  
|||

RESULT 87  
CK970699 624 bp mRNA linear EST 16-MAR-2004  
LOCUS 4086553 BARC 9BOV Bos taurus cDNA clone 9BOV31\_P02 5', mRNA  
DEFINITION sequence.  
ACCESSION CK970699  
VERSION CK970699.1 GI:45488673  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 624)  
Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gaubare, L.C.  
Production of EST from cDNA libraries derived from immunologically activated bovine gut  
Unpublished (2004)  
JOURNAL Contact: Tad S. Sonstegard  
COMMENT Bovine Functional Genomics Laboratory  
Animal and Natural Resources Institute  
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA  
Tel: 3015048416  
Fax: 3015048414  
Email: tads@anri.barc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred

0.00925 using options -trim alt - -trim fasta. Vector identified by cross\_match using options -mismatch 12 -minscore 12  
Plate: 31 row: P column: 02  
Seq primer: CCCAGTCACGACGTGTGTAACG  
High quality sequence stop: 624.  
Location/Qualifiers

FEATURES  
Source  
1..624  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/strain="Holstein"  
/db\_xref="taxon:9913"  
/clone="9BOV31\_P02"  
/sex="Male"  
/issue\_type="Pooled"  
/dev\_stage="Multiple"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_idb="BARC 9BOV"  
/note="Organ: Abomasum; Vector: pAGEN-1; Site 1: EcoRV; Site 2: NotI; Equimolar amounts of mRNA extracted from fundic and pyloric abomasums of 18 and 21 week old steers. Exposure to Oertergia oertergi was initiated at 15 weeks of age. fundic and pyloric abomasum"

ORIGIN  
Query Match 70.0%; Score 14; DB 7; Length 624;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCACACA 14  
|||  
Db 515 TTCCGACCCACACA 528  
|||

RESULT 88  
BQ412405 627 bp mRNA linear EST 22-MAY-2002  
LOCUS BQ412405  
DEFINITION BQ412405 Gossypium arboreum 7-10 dpa fiber library Gossypium  
ARBOREUM cDNA clone GA\_Ed0057F04r, mRNA sequence.  
ACCESSION BQ412405  
VERSION BQ412405.1 GI:21100092  
KEYWORDS EST.  
SOURCE Gossypium arboreum  
ORGANISM Gossypium arboreum  
Bakariota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
1 (bases 1 to 627)  
Wing, R.A., Friesch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.  
An integrated analysis of the genetics, development, and evolution of the cotton fiber  
Unpublished (2000)  
JOURNAL Contact: Wing RA  
COMMENT Clemson University Genomics Institute  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Total High Quality bases = 546  
Seq primer: TAATACGACTCACTATAGG  
High quality sequence start: 3  
High quality sequence stop: 616.  
Location/Qualifiers

FEATURES  
Source  
1..627  
/organism="Gossypium arboreum"  
/mol\_type="mRNA"  
/strain="AKA"  
/cultivar="8400"  
/db\_xref="taxon:29729"  
/clone="GA\_Ed0057F04r"  
/issue\_type="Fibers isolated from bolls harvested 7-10 dpa"

/lab host="E. coli"  
/clone\_lib="Gossypium arboreum 7-10 dpa fiber library"  
/note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

Query Match 70.0%; Score 14; DB 5; Length 627;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCACACTACT 19  
|||||  
Db 88 GACCCACACTACT 101

RESULT 89  
LOCUS CD878517/c 627 bp mRNA linear EST 11-JUL-2003  
DEFINITION AZ04.102024R011126 AZ04 Triticum aestivum cDNA clone AZ04102024,  
mRNA sequence.  
ACCESSION CD878517  
VERSION CD878517.1 GI:32562333  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 627)

REFERENCE  
AUTHORS Genoplante, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10

FEATURES  
source  
1.627  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="rectal"  
/db\_xref="taxon:4565"  
/clone="AZ04102024"  
/issue\_type="root"  
/clone\_lib="AZ04"

## ORIGIN

Query Match 70.0%; Score 14; DB 6; Length 627;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 CCGGACCCACACT 16  
|||||  
Db 183 CCGGACCCACACT 170

RESULT 90  
LOCUS B0410722 631 bp mRNA linear EST 22-MAY-2002  
DEFINITION GA\_Ed0033F04r Gossypium arboreum 7-10 dpa fiber library Gossypium  
arboreum cDNA clone GA\_Ed0033F04r, mRNA sequence.  
ACCESSION B0410722  
VERSION B0410722.1 GI:21098409  
KEYWORDS EST.  
SOURCE Gossypium arboreum  
ORGANISM Gossypium arboreum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eustosida II; Malvales; Malvaceae; Malvoideae; Gossypium.  
1 (bases 1 to 631)

AUTHORS Wing, R.A., Friesch, D., Yu, Y., Main, D., Rambo, T., Simmons, J.,  
Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.  
TITLE An integrated analysis of the genetics, development, and evolution  
of the cotton fiber  
JOURNAL Unpublished (2000)  
COMMENT Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu

FEATURES  
source  
1.631  
/organism="Gossypium arboreum"  
/mol\_type="mRNA"  
/strain="AKA"  
/cultivar="8400"  
/db\_xref="taxon:29729"  
/clone="GA\_Ed0033F04r"  
/issue\_type="Fibers isolated from bolls harvested 7-10  
dpa"  
/lab\_host="E. coli"  
/clone\_lib="Gossypium arboreum 7-10 dpa fiber library"  
/note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 631;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCACACTACT 19  
|||||  
Db 88 GACCCACACTACT 101

RESULT 91  
LOCUS CC383900 637 bp DNA linear GSS 19-MAY-2003  
DEFINITION PUH0D51TD ZM 0.6 1.0 KB Zea mays genomic clone ZM0B149506,  
genomic survey sequence.  
ACCESSION CC383900  
VERSION CC383900.1 GI:30863439  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
Clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 637)  
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and  
Bennetzen, J.  
TITLE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other\_GSSs: PUH0D51TB  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TP  
Class: sheared ends.  
FEATURES  
source  
1.637  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"

/db\_xref="taxon:4577"  
 /clone="ZM8BT495J06"  
 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 cot selected genomic DNA library"

## ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 637;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CGACCAACTACTAC 18  
 |||||  
 Db 390 CGACCAACTACTAC 403

RESULT 92  
 BQ414450 640 bp mRNA linear EST 22-MAY-2002  
 LOCUS GA\_E00086H02r Gossypium arboreum 7-10 dpa fiber library Gossypium  
 DEFINITION  
 accession BQ414450  
 VERSION BQ414450.1 GI:21102137  
 KEYWORDS EST.  
 SOURCE Gossypium arboreum  
 ORGANISM Gossypium arboreum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
 1 (bases 1 to 640)  
 Ming,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,  
 Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.  
 An integrated analysis of the genetics, development, and evolution  
 of the cotton fiber  
 Unpublished (2000)  
 Contact: Wing RA  
 Clemson University Genomics Institute  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu  
 Total High Quality bases = 496  
 Seq primer: TAAATGAGCTCAGTATAGG  
 High quality sequence start: 3  
 High quality sequence stop: 617.  
 Location/Qualifiers  
 1..640  
 /organism="Gossypium arboreum"  
 /mol\_type="mRNA"  
 /strain="AKA"  
 /cultivar="8400"  
 /db\_xref="taxon:29729"  
 /clone="GA\_E00086H02r"  
 /tissue\_type="Fibers isolated from bolls harvested 7-10  
 dpa"  
 /lab\_host="E. coli"  
 /clone\_id="Gossypium arboreum 7-10 dpa fiber library"  
 /note="Vector: pBR-CMV; Site\_1: EcoRI; Site\_2: XhoI"

## REFERENCE

## AUTHORS

TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 640;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCAACTACTACT 19  
 |||||  
 Db 89 GACCAACTACTACT 102

## RESULT 93

## LOCUS

B0646828 642 bp mRNA linear EST 07-OCT-2004

DEFINITION B0646828 Eptaretus burgeri adult Eptaretus burgeri cDNA clone  
 hg108117 5', mRNA sequence.

## ACCESSION

B0646828

B0646828.1 GI:53861689

EST.

Eptaretus burgeri (inshore hagfish)

Eptaretus burgeri

Eptaretus burgeri

Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;  
 Myxiniidae; Eptarectinidae; Eptaretus.

1 (bases 1 to 642)  
 Suzuki,T., Shin-I,T., Kohara,Y. and Kasaahara,M.  
 Transcriptome analysis of hagfish leukocytes: a framework for  
 understanding the immune system of jawless fishes  
 Dev. Comp. Immunol. 28 (10), 993-1003 (2004)  
 Contact: Tadasu Shin-I  
 Center for Genetic Resource Information  
 National Institute of Genetics  
 111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tshin@genes.nig.ac.jp.  
 Location/Qualifiers  
 1..642  
 /organism="Eptaretus burgeri"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7764"  
 /clone="hg108117"  
 /cell\_type="leukocyte-like cell"  
 /dev stage="adult"  
 /clone\_id="Eptaretus burgeri adult"  
 /note="wild caught animal"

## ORIGIN

Query Match 70.0%; Score 14; DB 4; Length 642;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CGACCAACTACTAC 18  
 |||||  
 Db 571 CGACCAACTACTAC 584

RESULT 94  
 BQ415743 642 bp mRNA linear EST 22-MAY-2002  
 LOCUS GA\_E0102F05r Gossypium arboreum 7-10 dpa fiber library Gossypium  
 DEFINITION  
 accession BQ415743  
 VERSION BQ415743.1 GI:21103430  
 KEYWORDS EST.  
 SOURCE Gossypium arboreum  
 ORGANISM Gossypium arboreum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
 1 (bases 1 to 642)  
 Ming,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,  
 Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.  
 An integrated analysis of the genetics, development, and evolution  
 of the cotton fiber  
 Unpublished (2000)  
 Contact: Wing RA  
 Clemson University Genomics Institute  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu  
 Total High Quality bases = 499  
 Seq primer: TAAATGAGCTCAGTATAGG  
 High quality sequence start: 3  
 High quality sequence stop: 633.  
 Location/Qualifiers

## REFERENCE

## AUTHORS

TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## ORIGIN

source

1. 642

/organism="Gossypium arboreum"

/mol\_type="mRNA"

/strain="AKA"

/cultivar="8400"

/db\_xref="taxon:29729"

/clone="GA\_E0102F05r"

/rissue\_type="Fibers isolated from bolls harvested 7-10 dpa"

/lab\_host="E. coli"

/clone\_lib="Gossypium arboreum 7-10 dpa fiber library"

/note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 642;

Best Local Similarity 100.0%; Pred. No. 4.4e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCACACTACT 19

Db 92 GACCCACACTACT 105

RESULT 95

BO915382 649 bp mRNA linear EST 19-AUG-2002

LOCUS OHB14G20.yg.ab1 OH ABCDI sunflower RHA801 Helianthus annuus cDNA

DEFINITION clone OHB14G20, mRNA sequence.

ACCESSION BO915382

VERSION BO915382.1 GI:22314163

KEYWORDS EST.

SOURCE Helianthus annuus (common sunflower)

ORGANISM Helianthus annuus

REFERENCE Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asterales; Asteroideae; Heliantheae; Helianthus.

AUTHORS 1 (bases 1 to 649)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.

Letuce and Sunflower ESTs from the Compositae Genome Project

http://compgenomics.ucdavis.edu/

Unpublished (2002)

COMMENT Contact: Alexander Kozik [R.W.Michelmore]

Department of Vegetable Crops, R.W.Michelmore Lab

University of California at Davis (UCD)

Asmundson Hall, UCD, Davis, CA 95616, USA

Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659

Email: akozik@ucdavis.edu [michelmoreveg@mail.ucdavis.edu]

belongs to contig OH\_CA\_Contig4100, see http://cgpdb.ucdavis.edu/ for details.

Plate: QHB14 row: G column: 20.

FEATURES

source

1. 649

/organism="Helianthus annuus"

/mol\_type="mRNA"

/cultivar="RHA801"

/db\_xref="taxon:4232"

/clone="OHB14G20"

/lab\_host="E.coli"

/clone\_lib="OH ABCDI sunflower RHA801"

/note="Vector: pBRCDNA5flab: The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/

ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 649;

Best Local Similarity 100.0%; Pred. No. 4.4e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GGCACCCACACTA 17

Db 558 GGCACCCACACTA 571

RESULT 96

AG167124 654 bp DNA linear GSS 09-JAN-2002

LOCUS Pan troglodytes DNA, clone: RP43-035B14.TU, genomic survey

DEFINITION Pan troglodytes DNA, clone: RP43-035B14.TU, genomic survey sequence.

ACCESSION AG167124

VERSION AG167124.1 GI:16696802

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

AUTHORS 1

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

BAC end sequences of library RPCT-43

Unpublished

2 (bases 1 to 654)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submision

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpansegsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the chimpanzee BAC library RPCT-43 This BAC end was generated during the Red process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: TJ

LIBRARY

Vector : pBACE3.6

R.Site 1 : EcoRI.

R.Site 2 : EcoRI.

FEATURES

source

1. 654

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

/clone="RP43-035B14.TU"

/sex="male"

/cell\_type="lymphocytes"

/clone\_lib="RPCT-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 654;

Best Local Similarity 100.0%; Pred. No. 4.4e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ACCCAACACTACTC 20

Db 367 ACCCAACACTACTC 380

RESULT 97

BX202031 658 bp DNA linear GSS 29-JAN-2003

LOCUS Danio rerio genomic clone DKEX-218C15, genomic survey sequence.

DEFINITION Danio rerio genomic clone DKEX-218C15, genomic survey sequence.

ACCESSION BX202031  
 VERSION BX202031.1 GI:28033917  
 KEYWORDS GSS.  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 658)  
 HUMPHRAY,S.V., HUCKLE,E. and DURHAM,J.L.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humphray@sanger.ac.uk Unpublished  
 COMMENT This sequence was generated from the T7 end of BAC 218C15. 218C15 is part of the Daniokey BAC library created by R. Plasterk and N.V. Keygene. Further details: [http://www.sanger.ac.uk/Projects/D\\_rerio/](http://www.sanger.ac.uk/Projects/D_rerio/).

FEATURES  
 source Location/Qualifiers  
 1..658  
 /organism="Danio rerio"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7955"  
 /clone="DKEY-218C15"  
 /tissue\_type="Testis"  
 /note="Vector pindigoBAC-536"

ORIGIN  
 Query Match 70.0%; Score 14; DB 9; Length 658;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGGACCCACACT 16  
 |||||  
 584 CGGACCCACACT 597

RESULT 98  
 LOCUS BQ407083 660 bp mRNA linear EST 22-MAY-2002  
 DEFINITION GA\_Ed0102F05f Gossypium arboreum 7-10 dpa fiber library Gossypium  
 accession BQ407083  
 VERSION BQ407083  
 KEYWORDS BQ407083.1 GI:21094770  
 EST.  
 SOURCE Gossypium arboreum  
 ORGANISM Gossypium arboreum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustoside II; Malvales; Malvaceae; Malvoideae; Gossypium.  
 1 (bases 1 to 660)  
 WING,R.A., FRIECH,D., YU,Y., MAIN,D., RAMBO,T., SIMMONS,J.,  
 HENRY,D., WOOD,T.C., LESLIE,A. and WILKINS,T.A.  
 COMMENT An integrated analysis of the genetics, development, and evolution of the cotton fiber  
 JOURNAL Unpublished (2000)  
 CONTACT: Wing RA  
 JOURNAL Clemson University Genomics Institute  
 COMMENT Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: [twing@clemson.edu](mailto:twing@clemson.edu)  
 Total High Quality bases = 478  
 Seq primer: TAATACGACTCCTATAGG  
 High quality sequence start: 16  
 High quality sequence stop: 616.

FEATURES  
 source Location/Qualifiers  
 1..660  
 /organism="Gossypium arboreum"  
 /mol\_type="mRNA"  
 /strain="AKA"  
 /cultivar="8400"

ACCESSION CR351082  
 LOCUS CR351082 662 bp mRNA linear EST 20-AUG-2003  
 DEFINITION r167b12.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
 cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN. ; mRNA  
 sequence.  
 VERSION CR351082  
 KEYWORDS CR351082.1 GI:33953769  
 EST.  
 SOURCE Meloidogyne javanica (root-knot nematode)  
 ORGANISM Meloidogyne javanica  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heterodridae; Meloidogyninae; Meloidogyne.  
 1 (bases 1 to 662)  
 MCCARTER,J., CLIFTON,S., CHAPPELL,B., PAPE,D., MARTIN,J.,  
 WYLE,T., DANTE,M., MARA,M., HILLER,L., KUCABA,T., THEISING,B.,  
 BOWERS,Y., GIBBONS,M., RITTER,E., BENNETT,J., FRANKLIN,C.,  
 TSAGAREISHVILI,R., RONKO,I., KENNEDY,S., MAGUIRE,L., BECK,C.,  
 UNDERWOOD,K., STEPHEN,M., ALLEN,M., PERSON,B., SWALLER,T.,  
 HARVEY,N., SCHURK,R., KOHN,S., SHIN,T., JACKSON,Y., CARDENAS,M.,  
 MCCANN,R., WATERSON,R. and WILSON,R.  
 COMMENT The Washington Univ. Nematode EST Project, 1999  
 JOURNAL Unpublished (1999)  
 CONTACT: McCarter JP  
 JOURNAL The Washington Univ. Nematode EST Project, 1999  
 COMMENT Washington Univ. Nematode EST Project, 1999  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
 Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (PowerScript, Clontech) and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See [www.nematode.net](http://www.nematode.net) for additional project information.

FEATURES  
 source Location/Qualifiers  
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 /tissue\_type="whole organism"  
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 /note="Vector: plasmid (ampicillin resistant); Site 1: XhoI; Site 2: NotI; Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (Dyna) and

mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5' SMART' anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information."

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 662;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACA 14  
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Db 118 TTCCGACCCCAACA 131

RESULT 100  
CF351206 662 bp mRNA linear EST 20-AUG-2003  
LOCUS r168907.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
DEFINITION cDNA 5' similar to IR:Q9VXP5 Q9VXP5 CG8959 PROTEIN.; mRNA  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CF351206  
CF351206.1 GI:33954015

REFERENCE  
AUTHORS

Meloidogyne javanica (root-knot nematode)  
Bukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
Tylenchoidea; Heterodermidae; Meloidogyninae; Meloidogyne.  
1 (bases 1 to 662).  
McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,  
Wyle, T., Dente, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,  
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,  
Taagaretshvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
McCam, R., Waterson, R. and Wilson, R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)  
Contact: McCarter, J.P.  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu

## FEATURES

source

Location/Qualifiers  
1..662  
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/db\_xref="taxon:6303"  
/issue\_type="whole organism"

Seq primer: Sps.  
www.nematode.net for additional project information.

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 662;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACA 14  
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Db 103 TTCCGACCCCAACA 116

RESULT 101  
BQ412020

LOCUS BQ412020 663 bp mRNA linear EST 22-MAY-2002  
DEFINITION GA\_Ed0053A10r Gossypium arboreum 7-10 dpa fiber library Gossypium  
ARBOREUM cDNA clone GA\_Ed0053A10r, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BQ412020  
BQ412020.1 GI:21099707

REFERENCE  
AUTHORS

Gossypium arboreum  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eustrods II; Malvales; Malvaceae; Malvoideae; Gossypium.  
1 (bases 1 to 663).  
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J.,  
Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.  
An integrated analysis of the genetics, development, and evolution  
of the cotton fiber  
Unpublished (2000)  
Contact: Wing, R.A.  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu

TOTAL High Quality bases = 457  
Seq primer: TAAATGACCTCATATGCG  
High quality sequence stop: 3  
High quality sequence stop: 601.  
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/clone\_lib="Meloidogyne javanica J2 SMART pGEM"  
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XhoI; Site 2: NotI. Cloned unidirectionally. Poly(A)+ RNA  
was concentrated and purified using Dynabeads (Dyna) and  
mRNA eluted for first strand synthesis. First strand cDNA  
was created using MMLV RT (Powerscript, Clontech) and  
primed with oligo(dT) with XhoI site and 5' SMART' anchor'  
added using chimeric DNA-RNA oligo. 12 PCR cycles were  
done using first strand and primers specific to SMART  
oligo and 3' end. Double stranded cDNA was digested using  
XhoI/NotI, fractionated on Chroma-spin 400 columns  
(Clontech) and ligated to digested pGEM-11zf(+) plasmid.  
Chemically competent DH10B cells were used as host cells.  
Library materials provided by Dr. David Bird of North  
Carolina State University. Library construction by Jeff  
Rousch. See www.nematode.net for additional project  
information."

ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 663;  
 Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCACACTACT 19  
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 Db 94 GACCCACACTACT 107

RESULT 102  
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 LOCUS r166b12.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
 DEFINITION cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN.; mRNA  
 sequence.  
 CF351008 CF351008.1 GI:33953619

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Meloidogyne javanica (root-knot nematode)  
 Meloidogyne javanica  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
 Tylenchoidea; Heterodermidae; Meloidogyninae; Meloidogyne.  
 1 (bases 1 to 665)

REFERENCE  
 AUTHORS  
 McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,  
 Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
 Bowers,Y., Gibbons,M., Rilter,E., Bennett,J., Franklin,C.,  
 Tsagarelashvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
 Underwood,K., Stepcoe,M., Allen,M., Person,B., Swaller,T.,  
 Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
 McCam,R., Materston,R. and Wilson,R.  
 The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)  
 Contact: McCarter JP  
 The Washington Univ. Nematode EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: east@watson.wustl.edu  
 Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified  
 using Dynabeads (Dyna) and mRNA eluted for first strand synthesis.  
 First strand cDNA was created using MMLV RT (Powerscript, Clontech)  
 and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added  
 using chimeric DNA-RNA oligo. 12 PCR cycles were done using first  
 strand and primers specific to SMART oligo and 3' end. Double  
 stranded cDNA was digested using XhoI/NotI, fractionated on  
 Chroma-spin 400 columns (Clontech) and ligated to digested  
 pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as  
 host cells. Library materials provided by Dr. David Bird of North  
 Carolina State University. Library construction by Jeff Rousch. See  
 www.nematode.net for additional project information.  
 Seq primer: SP6.

TITLE  
 JOURNAL  
 COMMENT

FEATURES  
 source

Location/Qualifiers

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 was concentrated and purified using Dynabeads (Dyna) and  
 mRNA eluted for first strand synthesis. First strand cDNA  
 was created using MMLV RT (Powerscript, Clontech) and  
 primed with oligo(dT) with XhoI site and 5' SMART 'anchor'  
 added using chimeric DNA-RNA oligo. 12 PCR cycles were  
 done using first strand and primers specific to SMART  
 oligo and 3' end. Double stranded cDNA was digested using  
 XhoI/NotI, fractionated on Chroma-spin 400 columns

ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 665;  
 Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCACACA 14  
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 Db 118 TTGCGACCCACACA 131

RESULT 103  
 CF350992 667 bp mRNA linear EST 20-AUG-2003  
 LOCUS r166a04.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
 DEFINITION cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN.; mRNA  
 sequence.  
 CF350992 CF350992.1 GI:33953587

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Meloidogyne javanica (root-knot nematode)  
 Meloidogyne javanica  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
 Tylenchoidea; Heterodermidae; Meloidogyninae; Meloidogyne.  
 1 (bases 1 to 667)

REFERENCE  
 AUTHORS  
 McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,  
 Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
 Bowers,Y., Gibbons,M., Rilter,E., Bennett,J., Franklin,C.,  
 Tsagarelashvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
 Underwood,K., Stepcoe,M., Allen,M., Person,B., Swaller,T.,  
 Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
 McCam,R., Materston,R. and Wilson,R.  
 The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)  
 Contact: McCarter JP  
 The Washington Univ. Nematode EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: east@watson.wustl.edu  
 Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified  
 using Dynabeads (Dyna) and mRNA eluted for first strand synthesis.  
 First strand cDNA was created using MMLV RT (Powerscript, Clontech)  
 and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added  
 using chimeric DNA-RNA oligo. 12 PCR cycles were done using first  
 strand and primers specific to SMART oligo and 3' end. Double  
 stranded cDNA was digested using XhoI/NotI, fractionated on  
 Chroma-spin 400 columns (Clontech) and ligated to digested  
 pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as  
 host cells. Library materials provided by Dr. David Bird of North  
 Carolina State University. Library construction by Jeff Rousch. See  
 www.nematode.net for additional project information.  
 Seq primer: SP6.

TITLE  
 JOURNAL  
 COMMENT

FEATURES  
 source

Location/Qualifiers

1..667  
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 /note="Vector: plasmid (ampicillin resistant); Site 1:  
 XhoI; Site 2: NotI; Cloned unidirectionally. Poly(A)+ RNA  
 was concentrated and purified using Dynabeads (Dyna) and  
 mRNA eluted for first strand synthesis. First strand cDNA

was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information."

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 667;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACA 14  
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Db 100 TTGCGACCCACACA 113

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LOCUS  
DEFINITION  
CF351019 668 bp mRNA linear EST 20-AUG-2003  
r166d01.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN.; mRNA  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
CF351019  
CF351019.1 GI:33953641  
EST.

Meloidogyne javanica (root-knot nematode)  
Meloidogyne javanica  
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
Tylenchoidea; Heterodidae; Meloidogyninae; Meloidogyne.  
1 (bases 1 to 668)

REFERENCE  
AUTHORS  
McCartter,J., Clifton,S., Chiapelli,B., Page,D., Martin,J.,  
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,  
Tsagarashvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
Underwood,K., Steploe,M., Allen,M., Person,B., Swaller,T.,  
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCamn,R., Waterston,R. and Wilson,R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)

TITLE  
JOURNAL  
COMMENT  
Contact: McCartter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
Cloned unidirectionally. Poly(A) + RNA was concentrated and purified  
using Dynabeads (Dyna) and mRNA eluted for first strand synthesis.  
First strand cDNA was created using MMLV RT (Powerscript, Clontech)  
and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added  
using chimeric DNA-RNA oligo. 12 PCR cycles were done using first  
strand and primers specific to SMART oligo and 3' end. Double  
stranded cDNA was digested using XhoI/NotI, fractionated on  
Chroma-spin 400 columns (Clontech) and ligated to digested  
pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as  
host cells. Library materials provided by Dr. David Bird of North  
Carolina State University. Library construction by Jeff Rousch. See  
www.nematode.net for additional project information.  
Seq primer: Sp6.

## FEATURES

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Location/Qualifiers  
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/mol\_type="mRNA"  
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## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 668;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACA 14  
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Db 94 TTGCGACCCACACA 107

RESULT 105  
CF351064  
LOCUS  
DEFINITION  
CF351064 668 bp mRNA linear EST 20-AUG-2003  
r166h11.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN.; mRNA  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
CF351064  
CF351064.1 GI:33953734  
EST.  
Meloidogyne javanica (root-knot nematode)  
Meloidogyne javanica  
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
Tylenchoidea; Heterodidae; Meloidogyninae; Meloidogyne.  
1 (bases 1 to 668)

REFERENCE  
AUTHORS  
McCartter,J., Clifton,S., Chiapelli,B., Page,D., Martin,J.,  
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,  
Tsagarashvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
Underwood,K., Steploe,M., Allen,M., Person,B., Swaller,T.,  
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCamn,R., Waterston,R. and Wilson,R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)

TITLE  
JOURNAL  
COMMENT  
Contact: McCartter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
Cloned unidirectionally. Poly(A) + RNA was concentrated and purified  
using Dynabeads (Dyna) and mRNA eluted for first strand synthesis.  
First strand cDNA was created using MMLV RT (Powerscript, Clontech)  
and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added  
using chimeric DNA-RNA oligo. 12 PCR cycles were done using first  
strand and primers specific to SMART oligo and 3' end. Double  
stranded cDNA was digested using XhoI/NotI, fractionated on  
Chroma-spin 400 columns (Clontech) and ligated to digested  
pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as  
host cells. Library materials provided by Dr. David Bird of North  
Carolina State University. Library construction by Jeff Rousch. See  
www.nematode.net for additional project information.  
Seq primer: Sp6.

## FEATURES

Location/Qualifiers



source

1. .668  
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/mol\_type="mRNA"  
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/tissue\_type="whole organism"  
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/clone\_id="Meloidogyne javanica J2 SMART pGEM"  
/note="Vector: plasmid (ampicillin resistant); Site 1: XhoI; Site 2: NotI; Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (Dyna1) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (PowerScript, Clontech) and primed with oligo(dT) with XhoI site and 5'SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information."

ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 668;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCACACA 14  
118 TTGGGACCCACACA 131

Db

RESULT 106  
CL715790 671 bp DNA linear GSS 26-JUL-2004  
LOCUS  
DEFINITION OR\_BBa0041P09.r OR\_BBa Oryza rufipogon genomic clone OR\_BBa0041P09  
ACCESSION CL715790  
VERSION CL715790.1 GI:50602828  
KEYWORDS GSS.  
SOURCE Oryza rufipogon  
ORGANISM Oryza rufipogon  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 671)  
Kum,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.  
ONAP Project  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: http://genome.arizona.edu  
PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Insert Length: 161 Std Error: 0.00  
Plate: 0041 row: P column: 09  
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/clone\_id="OR\_BBa"  
/note="Vector: pGIBAC1; Site\_1: HindIII; Site\_2: HindIII"

ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 671;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTGGGACCCACAC 15  
468 TTGGGACCCACAC 481

Db

RESULT 107  
CV006612/c  
LOCUS  
DEFINITION CS\_gil\_12D06\_M13Reverse Blue crab gill, normalized Callinectes sapidus cDNA clone CS\_gil\_12D06 5' similar to ref|NP\_652222.1| CG14310-P8 - Drosophila melanogaster. Score = 33.5 bits (75), Expect = 3.9, mRNA sequence.  
ACCESSION CV006612  
VERSION CV006612.1 GI:51365835  
KEYWORDS EST.  
SOURCE Callinectes sapidus (blue crab)  
ORGANISM Callinectes sapidus  
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Portunoidae; Portunidae; Callinectes.  
1 (bases 1 to 675)  
Shafer,T.H., Coblenz,P.E. and Towle,D.W.  
Expressed sequence tags from normalized cDNA libraries prepared from gill and hypodermis tissues of the blue crab, Callinectes sapidus  
Unpublished (2004)  
Contact: Thomas H. Shafer  
Department of Biological Sciences  
University of North Carolina Wilmington  
601 S. College Rd, Wilmington, NC 28403, USA  
Tel: 910-962-7275  
Fax: 910-962-4066  
Email: shafer@uncw.edu  
Plate: 12 row: D column: 06  
Seq primer: M13 Reverse  
High quality sequence stop: 487.

FEATURES  
Source  
1. .675  
/organism="Callinectes sapidus"  
/mol\_type="mRNA"  
/db\_xref="taxon:6763"  
/clone="CS\_gil\_12D06"  
/tissue\_type="Pooled anterior and posterior gills from crabs acclimated to salinities of 35 and 5 parts per thousand"  
/dev\_stage="Adult intermolt"  
/clone\_id="Blue crab gill, normalized"  
/note="Vector: PCMV Sport 6.1; Total RNA samples were prepared individually from each tissue, checked for quality, and then pooled for construction and normalization of a cDNA library by invitrogen. Plasmids were isolated and inserts sequenced from their 5'-ends by the Blue Crab Molecular Genetics Laboratory at the University of North Carolina Wilmington. Traces were trimmed, compared (BLASTx) to NCBI non-redundant protein database as of 19 July 2004, and processed for submission to dbEST by trace2dbEST software (Parkinson, Anthony and Blaxter, unpublished software)."

ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 675;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCAACTACT 19  
 |||||  
 Db 532 GACCCAACTACT 519

RESULT 108  
 LOCUS BQ405787/c  
 DEFINITION GA\_Ed0086H02f Gossypium arboreum 7-10 dpa fiber library Gossypium  
 arboreum cDNA clone GA\_Ed0086H02f, mRNA sequence.  
 ACCESSION BQ405787  
 VERSION BQ405787.1 GI:21093474  
 KEYWORDS EST.  
 SOURCE Gossypium arboreum  
 ORGANISM Gossypium arboreum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
 1 (bases 1 to 676)  
 Wing, R.A., Friebe, D., Yu, Y., Main, D., Rambo, T., Simmons, J.,  
 Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.  
 An integrated analysis of the genetics, development, and evolution  
 of the cotton fiber  
 Unpublished (2000)  
 Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu  
 Total High Quality bases = 545  
 Seq primer: TAATGACTGACTATAGG  
 High quality sequence start: 9  
 High quality sequence stop: 646.  
 Location/Qualifiers  
 1..676  
 /organism="Gossypium arboreum"  
 /mol\_type="mRNA"  
 /strain="AKA"  
 /cultivar="8400"  
 /db\_xref="taxon:29729"  
 /clone="GA\_Ed0086H02f"  
 /tissue\_type="Fibers isolated from bolls harvested 7-10  
 dpa"  
 /lab\_host="E. coli"  
 /clone\_1fb="Gossypium arboreum 7-10 dpa fiber library"  
 /note="Vector: PBK-CMV, Site\_1: EcoRI, Site\_2: XhoI"

ORIGIN  
 Query Match 70.0%; Score 14; DB 5; Length 676;  
 Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCAACTACT 19  
 |||||  
 Db 649 GACCCAACTACT 636

RESULT 109  
 LOCUS CF351188  
 DEFINITION CF351188 676 bp mRNA linear EST 20-AUG-2003  
 r168e08.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
 cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN.; mRNA  
 sequence.  
 ACCESSION CF351188  
 VERSION CF351188.1 GI:33953980  
 KEYWORDS EST.  
 SOURCE Meloidogyne javanica (root-knot nematode)  
 ORGANISM Meloidogyne javanica  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
 Tylenchoidea; Heterodridae; Meloidogyninae; Meloidogyne.

REFERENCE  
 AUTHORS  
 1 (bases 1 to 676)  
 McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,  
 Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,  
 Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,  
 Tsagaris, H., R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
 Underwood, K., Steptoe, M., Allen, M., Peterson, B., Swaller, T.,  
 Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
 McCann, R., Waterson, R. and Wilson, R.  
 The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)  
 Contact: McCarter JP  
 The Washington Univ. Nematode EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watsn.wustl.edu  
 Cloned unidirectionally. Poly(A) + RNA was concentrated and purified  
 using Dynabeads (Dyna) and mRNA eluted for first strand synthesis.  
 First strand cDNA was created using MMLV RT (Powerscript, Clontech)  
 and primed with oligo(dt) with XhoI site and 5' SMART 'anchor' added  
 using chimeric DNA-RNA oligo. 12 PCR cycles were done using first  
 strand and primers specific to SMART oligo and 3' end. Double  
 stranded cDNA was digested using XhoI/NotI, fractionated on  
 Chroma-spin 400 columns (Clontech) and ligated to digested  
 pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as  
 host cells. Library materials provided by Dr. David Bird of North  
 Carolina State University. Library construction by Jeff Rousch. See  
 www.nematode.net for additional project information.  
 Seq primer: Sp6.  
 Location/Qualifiers  
 1..676  
 /organism="Meloidogyne javanica"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6303"  
 /tissue\_type="whole organism"  
 /dev\_stage="J2"  
 /lab\_host="DH10B"  
 /clone\_1fb="Meloidogyne javanica J2 SMART pGEM"  
 /note="Vector: plasmid (ampicillin resistant); Site\_1:  
 XhoI; Site\_2: NotI; Cloned unidirectionally. Poly(A) + RNA  
 was concentrated and purified using Dynabeads (Dyna) and  
 mRNA eluted for first strand synthesis. First strand cDNA  
 was created using MMLV RT (Powerscript, Clontech) and  
 primed with oligo(dt) with XhoI site and 5' SMART 'anchor'  
 added using chimeric DNA-RNA oligo. 12 PCR cycles were  
 done using first strand and primers specific to SMART  
 oligo and 3' end. Double stranded cDNA was digested using  
 XhoI/NotI, fractionated on Chroma-spin 400 columns  
 (Clontech) and ligated to digested pGEM-11zf(+) plasmid.  
 Chemically competent DH10B cells were used as host cells.  
 Library materials provided by Dr. David Bird of North  
 Carolina State University. Library construction by Jeff  
 Rousch. See www.nematode.net for additional project  
 information."

ORIGIN  
 Query Match 70.0%; Score 14; DB 7; Length 676;  
 Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCACA 14  
 |||||  
 Db 118 TTGGGACCCACA 131

RESULT 110  
 LOCUS CF351106  
 DEFINITION CF351106 677 bp mRNA linear EST 20-AUG-2003  
 r167e08.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
 cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN.; mRNA  
 sequence.  
 ACCESSION CF351106

VERSION CF351106.1 GI:33953817  
 KEYWORDS EST.  
 SOURCE Meloidogyne javanica (root-knot nematode)  
 ORGANISM Meloidogyne javanica  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heterodermidae; Meloidogyninae; Meloidogyne.  
 REFERENCE 1 (bases 1 to 677)  
 AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Rilter,E., Bennett,J., Franklin,C., Tsagarishevili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Stepcio,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.  
 The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)  
 TITLE The Washington Univ. Nematode EST Project, 1999  
 JOURNAL Contact: McCarter JP  
 COMMENT The Washington Univ. Nematode EST Project, 1999  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information. Seq primer: SP6.

FEATURES  
 source  
 1. 677  
 /organism="Meloidogyne javanica"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6303"  
 /cissue\_type="whole organism"  
 /dev\_stage="J2"  
 /lab\_host="DH10B"  
 /clone\_id="Meloidogyne javanica J2 SMART pGEM"  
 /note="Vector: plasmid (ampicillin resistant); Site 1: XhoI; Site 2: NotI; Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information."

ORIGIN  
 Query Match 70.0%; Score 14; DB 7; Length 677;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 TTGCGAGCCACACA 14  
 ||||||||||||  
 118 TTGCGAGCCACACA 131

RESULT 111

CF351077  
 LOCUS 681 bp mRNA linear EST 20-AUG-2003  
 DEFINITION r167b05.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica cDNA 5' similar to TR:09VXP5 09VXP5 CG8959 PROTEIN. ; mRNA sequence.  
 VERSION CF351077  
 ACCESSION CF351077.1 GI:33953759  
 KEYWORDS EST.  
 SOURCE Meloidogyne javanica (root-knot nematode)  
 ORGANISM Meloidogyne javanica  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heterodermidae; Meloidogyninae; Meloidogyne.  
 REFERENCE 1 (bases 1 to 681)  
 AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Rilter,E., Bennett,J., Franklin,C., Tsagarishevili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Stepcio,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.  
 The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)  
 TITLE The Washington Univ. Nematode EST Project, 1999  
 JOURNAL Contact: McCarter JP  
 COMMENT The Washington Univ. Nematode EST Project, 1999  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information. Seq primer: SP6.

FEATURES  
 source  
 1. 681  
 /organism="Meloidogyne javanica"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6303"  
 /cissue\_type="whole organism"  
 /dev\_stage="J2"  
 /lab\_host="DH10B"  
 /clone\_id="Meloidogyne javanica J2 SMART pGEM"  
 /note="Vector: plasmid (ampicillin resistant); Site 1: XhoI; Site 2: NotI; Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information."

ORIGIN  
 Query Match 70.0%; Score 14; DB 7; Length 681;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 TTGCGAGCCACACA 14  
 ||||||||||||  
 118 TTGCGAGCCACACA 131

QY 1 TTCCGACCCACACA 14  
 |||||  
 Db 118 TTCCGACCCACACA 131

RESULT 112  
 CF350912 683 bp mRNA linear EST 20-AUG-2003  
 LOCUS r165a04.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
 DEFINITION cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN. ; mRNA  
 sequence.  
 ACCESSION CF350912  
 VERSION CF350912.1 GI:33953430  
 KEYWORDS EST.  
 SOURCE Meloidogyne javanica (root-knot nematode)  
 ORGANISM Meloidogyne javanica

REFERENCE  
 AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,  
 Wylie,T., Dente,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
 Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,  
 Tsagarisshvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
 Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,  
 Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
 McCann,R., Waterston,R. and Wilson,R.  
 The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)

TITLE  
 JOURNAL The Washington Univ. Nematode EST Project, 1999  
 COMMENT The Washington Univ. Nematode EST Project, 1999  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

Cloned unidirectionally. Poly(A) + RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with xhoi site and 5'SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information.

Seq primer: Sp6.

FEATURES  
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 1..683  
 /organism="Meloidogyne javanica"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6303"  
 /tissue\_type="whole organism"  
 /dev\_stage="J2"  
 /lab\_host="DH10B"  
 /clone\_lib="Meloidogyne javanica J2 SMART pGEM"  
 /note="Vector: plasmid (ampicillin resistant); Site 1: XhoI; Site 2: NotI; Cloned unidirectionally. Poly(A) + RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with xhoi site and 5'SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information."

ORIGIN  
 Query Match 70.0%; Score 14; DB 7; Length 683;  
 Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCACACA 14  
 |||||  
 Db 118 TTCCGACCCACACA 131

RESULT 113  
 CF350974 685 bp mRNA linear EST 20-AUG-2003  
 LOCUS r165g05.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica  
 DEFINITION cDNA 5' similar to TR:Q9VXP5 Q9VXP5 CG8959 PROTEIN. ; mRNA  
 sequence.  
 ACCESSION CF350974  
 VERSION CF350974.1 GI:33953551  
 KEYWORDS EST.  
 SOURCE Meloidogyne javanica (root-knot nematode)  
 ORGANISM Meloidogyne javanica

REFERENCE  
 AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,  
 Wylie,T., Dente,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
 Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,  
 Tsagarisshvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
 Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,  
 Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
 McCann,R., Waterston,R. and Wilson,R.  
 The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)

TITLE  
 JOURNAL The Washington Univ. Nematode EST Project, 1999  
 COMMENT The Washington Univ. Nematode EST Project, 1999  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

Cloned unidirectionally. Poly(A) + RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with xhoi site and 5'SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information.

Seq primer: Sp6.

FEATURES  
 source Location/Qualifiers  
 1..685  
 /organism="Meloidogyne javanica"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6303"  
 /tissue\_type="whole organism"  
 /dev\_stage="J2"  
 /lab\_host="DH10B"  
 /clone\_lib="Meloidogyne javanica J2 SMART pGEM"  
 /note="Vector: plasmid (ampicillin resistant); Site 1: XhoI; Site 2: NotI; Cloned unidirectionally. Poly(A) + RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with xhoi site and 5'SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns

(Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See [www.nematode.net](http://www.nematode.net) for additional project information."

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 685;  
Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCCGACCAACA 14  
Db 118 TTCCGACCAACA 131

## RESULT 114

BM026959/c 689 bp mRNA linear EST 13-OCT-2002  
LOCUS BM026959 Nori Satoh unpublished cDNA library, blood cells Ciona  
DEFINITION BM026959 Nori Satoh unpublished cDNA library, blood cells Ciona  
inestinalis cDNA clone rcibd085d12 3', mRNA sequence.

ACCESSION BM026959 GI:23942766  
VERSION BM026959  
KEYWORDS EST.  
SOURCE Ciona intestinalis  
ORGANISM Ciona intestinalis

REFERENCE Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Cionidae; Ciona.  
AUTHORS Satou Y., Satake, M., Azumi, K., Nonaka, M., Shin-i, T., Kohara, Y. and  
Satoch, N.

TITLE Expressed genes in Ciona intestinalis (2002)  
JOURNAL Unpublished (2002)  
COMMENT Contact: Nori Satoh  
Department of Zoology  
Kyoto University  
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: [satoh@ascidian.zool.kyoto-u.ac.jp](mailto:satoh@ascidian.zool.kyoto-u.ac.jp).

## FEATURES

source 1..689  
Location/Qualifiers

/organism="Ciona intestinalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:7719"  
/clone="rcibd085d12"  
/issue\_type="blood cells"  
/clone\_id="Nori Satoh unpublished cDNA library, blood  
cells"

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 689;  
Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 GCGACCAACA 17  
Db 494 GCGACCAACA 481

## RESULT 115

CL622579 689 bp DNA linear GSS 01-JUL-2004  
LOCUS CL622579 OR\_BBA0017H11.r OR\_BBA Oryza rufipogon genomic clone OR\_BBA0017H11  
DEFINITION 3' genomic survey sequence.  
ACCESSION CL622579 GI:49119745  
VERSION CL622579  
KEYWORDS GSS.

SOURCE Oryza rufipogon  
ORGANISM Oryza rufipogon

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE Ehrhartoideae; Oryzaceae; Oryza.  
AUTHORS 1 (bases 1 to 689)  
Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,  
Kudrna, D., Miller, C., Hatfield, J., Soderlund, C. and Wing, R.

## TITLE

## JOURNAL

OMP Project  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: <http://genome.arizona.edu>

PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Insert Length: 161 Std Error: 0.00  
Plate: 0017 row: H column: 11  
Seq primer: CAC TCA TTA GGC ACC CCA  
Class: BAC ends.

## FEATURES

## source

1..689  
Location/Qualifiers  
/organism="Oryza rufipogon"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4529"  
/clone="OR\_BBA0017H11"  
/issue\_type="young leaves"  
/lab\_host="DH10B-T1 phage resistant"  
/clone\_id="OR\_BBA"  
/note="Vector: pGIRAC1, Site\_1: HindIII, Site\_2: HindIII"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 689;  
Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 TTCCGACCAACAC 15  
Db 468 TTCCGACCAACAC 481

## RESULT 116

AI908584/c 696 bp mRNA linear EST 30-MAR-2000  
LOCUS AI908584 CM-B1178-220499-027 B1178 Homo sapiens cDNA, mRNA sequence.  
DEFINITION CM-B1178-220499-027 B1178 Homo sapiens cDNA, mRNA sequence.

ACCESSION AI908584  
VERSION AI908584.1 GI:6499264  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 696)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Macsukuma, A., Bata, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongenel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/seq/gethtml.pl?cl=CM&cl2=CM-BT178-027.html>  
&cl=220499&cl2=1)

Seq primer: puc 18 forward.

FEATURES  
source Location/Qualifiers

1..696

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/sex="female"

/dev\_stage="Adult"

/clone\_lib="BT178"

/note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (O.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 70.0%; Score 14; DB 1; Length 696;

Best Local Similarity 100.0%; Pred. No. 4.4e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 GACCCCAACTACT 18

Db 412 GACCCCAACTACT 399

RESULT 117

CN852507

LOCUS

DEFINITION Ha\_mx0\_01F05 Spe Lobster Multiple Tissues, Normalized Homarus

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

EST.

Homarus americanus (American lobster)

Homarus americanus

Eumalacostraca; Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;

Nephropidae; Nephropidae; Homarus.

1 (bases 1 to 704)

Towle,D.W. and Smith,C.M.

Expressed sequence tags in a normalized cDNA library prepared from

multiple tissues of adult intermolt American lobster, Homarus

americanus

Unpublished (2004)

Contact: David W. Towle

Marine DNA Sequencing and Analysis Center

Mount Desert Island Biological Laboratory

Old Bar Harbor Road, Salsbury Cove, ME 04672 USA

Tel: 207-288-9880 x474

Fax: 207-288-2130

Email: dtowle@mdibl.org

Plate: 01 row: F column: 05

Seq primer: Sp6

High quality sequence stop: 522.

Location/Qualifiers

1..704

/organism="Homarus americanus"

/mol\_type="mRNA"

/db\_xref="taxon:6706"

/clone\_lib="mx0\_01F05"

/tissue\_type="Gill, epipodite, branchiostegite, heart,

ovary, testis, antennal gland, abdominal muscle,

hepatopancreas, brain"

/dev\_stage="Adult intermolt"

/clone\_lib="Lobster Multiple Tissues, Normalized"

/note="Vector: PCMV Sport 6.1; Total RNA samples were

prepared individually from each tissue, checked for

quality, then pooled for construction and normalization

of cDNA library by Invitrogen. Plasmids were isolated and inserts end-sequenced by the Marine DNA Sequencing and Analysis Facility at Mount Desert Island Biological Laboratory. Traces were processed for submission to dbEST by trace2dbest software (Parkinson, Anthony and Blaxter, unpublished software)."

ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 704;

Best Local Similarity 100.0%; Pred. No. 4.4e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 GACCCCAACTACT 19

Db 92 GACCCCAACTACT 105

RESULT 118

B2834863/c

LOCUS

DEFINITION B2834863 706 bp DNA linear GSS 18-MAR-2003

CH240\_287D4.TV CHORI-240 Bos taurus genomic clone CH240\_287D4,

genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 706)

Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,

Shvartsbeyn,A., Gebregorgis,E., Chen,D., Riggs,F., de Jong,P.,

Crawford,A.M. and McEwan,J.C.

Bovine BAC End Sequences from Library CHORI-240

Unpublished (2003)

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@igr.org

Clones are derived from the bovine BAC library CHORI-240

(<http://www.chori.org/bacpac/bovine240.htm>). For BAC library

availability, please contact Pieter de Jong ([pdejong@mail.cho.org](mailto:pdejong@mail.cho.org)).

Clones may be purchased from BACPAC Resources

(<http://www.chori.org/bacpac/ordering/information.htm>). This work

was undertaken as part of the International Bovine BAC Mapping

Consortium (IBMC) by AgResearch Ltd., New Zealand and The

Institute of Genomic Research (TIGR), USA.

Plate: 287 row: D column: 4

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..706

/organism="Bos taurus"

/mol\_type="Genomic DNA"

/strain="bred: Hereford"

/db\_xref="taxon:9913"

/clone="CH240\_287D4"

/sex="Male"

/cell\_type="Blood"

/clone\_lib="CHORI-240"

/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;

Hereford bull 11 Domino 99375; CHORI-240 Bovine BAC

library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 706;

Best Local Similarity 100.0%; Pred. No. 4.4e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ACCGACACTACTC 20  
 |||||  
 Db 638 ACCGACACTACTC 625

RESULT 119  
 LOCUS CD939205  
 DEFINITION OV.112L23P010309 OV Triticum aestivum cDNA clone OV112L23, mRNA  
 BEQUENCE.  
 ACCESSION CD939205.1 GI:32786713  
 VERSION CD939205.1  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Pooidae; Triticeae; Triticum.  
 1 (bases 1 to 707)  
 REFERENCE Genoplane.  
 TITLE Genoplane, a major partnership french program in plant genomics  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Genoplane  
 Genoplane  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplane' (<http://www.genoplane.com>  
 and <http://genoplane-info.inbio.gen.fr>).  
 Location/Qualifiers  
 1..707  
 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /cultivar="recital"  
 /db\_xref="taxon:4565"  
 /clone="OV112L23"  
 /tissue\_type="ovary"  
 /clone\_1ib="OV"

ORIGIN  
 Query Match 70.0%; Score 14; DB 6; Length 707;  
 Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 CGGACCCCAACT 16  
 |||||  
 Db 631 CGGACCCCAACT 644

RESULT 120  
 LOCUS B2780370/c  
 DEFINITION B2780370 708 bp DNA linear GSS 14-MAR-2003  
 1139c07.g1 WGS-sbicolorf (DH5a methyl filtered) Sorghum bicolor  
 genomic clone 1139c07, genomic survey sequence.  
 ACCESSION B2780370  
 VERSION B2780370.1 GI:28957813  
 KEYWORDS GSS.  
 SOURCE Sorghum bicolor (sorghum)  
 ORGANISM Sorghum bicolor  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 708)  
 REFERENCE Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N.,  
 Katzenburger, F., King, L., Miller, B., Miller, S., Nascento, L.,  
 Zlatavern, T., Palmer, L., McCombie, W.R. and Martienssen, R.A.  
 Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)  
 Unpublished (2002)  
 JOURNAL Contact: W. Richard McCombie  
 Lita Annenberg Hazen Genome Sequencing Center  
 Cold Spring Harbor Laboratory  
 PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884  
 Fax: 516 367 8874  
 Email: [mccombie@cshl.org](mailto:mccombie@cshl.org)  
 Plate: 1139 row: c column: 07  
 Seq primer: -21M13UnivRev  
 Class: shotgun  
 High quality sequence atop: 708.  
 Location/Qualifiers  
 1..708  
 /organism="Sorghum bicolor"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:4558"  
 /clone="1139c07"  
 /lab\_host="DH5a"  
 /clone\_1ib="WGS-sbicolorf (DH5a methyl filtered)"  
 /note="Site 1: Xba I; Site 2: Xba I; The vector was  
 digested with Xba I and one nucleotide was added by fill in  
 in the recessive 3' end. The genomic DNA was nebulized,  
 end repaired, adaptor ligated and size fractionated using  
 sephadex. The resulting fragments were between 0.8 and 3  
 kb and were cloned into the vector (x/y reads in M13mp19,  
 b/g reads in pUC19). The same ligation was transformed  
 into DH5a."

ORIGIN  
 Query Match 70.0%; Score 14; DB 8; Length 708;  
 Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCACACTACT 19  
 |||||  
 Db 404 GACCCACACTACT 391

RESULT 121  
 LOCUS BM086868/c  
 DEFINITION BM086868 711 bp mRNA linear EST 22-OCT-2002  
 Intestinalis cDNA clone rc1v047d09 3', mRNA sequence.  
 ACCESSION BM086868  
 VERSION BM086868.1 GI:24262148  
 KEYWORDS EST.  
 SOURCE Clona intestinalis  
 ORGANISM Clona intestinalis  
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
 Phlebobranchia; Clonidae; Clona.  
 1 (bases 1 to 711)  
 REFERENCE Satou, Y., Shin-I, T., Kohara, Y. and Satoh, N.  
 TITLE Expressed genes in Clona intestinalis (2002c)  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Nori Satoh  
 Department of Zoology  
 Kyoto University  
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
 Tel: 81-75-753-4081  
 Fax: 81-75-705-1113  
 Email: [satoh@acidian.zool.kyoto-u.ac.jp](mailto:satoh@acidian.zool.kyoto-u.ac.jp).  
 Location/Qualifiers  
 1..711  
 /organism="Clona intestinalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7719"  
 /clone="rc1v047d09"  
 /tissue\_type="whole animal"  
 /dev\_stage="larva"  
 /clone\_1ib="Nori Satoh unpublished cDNA library, larva"

ORIGIN  
 Query Match 70.0%; Score 14; DB 5; Length 711;  
 Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GCGACCCCAACTA 17

Db 495 GCGACCCCACTACT 482

# RESULT 122

CF473928  
LOCUS

## DEFINITION

CF473928 712 bp mRNA linear EST 05-SEP-2003  
RTMW2\_19 B10\_g1\_A021 Well-watered loblolly pine roots WM2 Pinus taeda cDNA clone RTMW2\_19\_B10\_A021 5', mRNA sequence.

## ACCESSION

CF473928 GI:34491300

## KEYWORDS

pinus taeda (loblolly pine)

## SOURCE

pinus taeda

## REFERENCE

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 712)  
Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and Neale, D.  
An EST database from well-watered loblolly pine (Pinus taeda) roots

## TITLE

Unpublished (2003)

## COMMENT

Other ESTs: RTMW2\_19\_B10\_b1\_A021  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpirata@uga.edu

RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.  
Seq primer: JENREV (CAGGAACAGCTATGACC).

## FEATURES

source

1..712  
Location/Qualifiers

/organism="Pinus taeda"

/mol\_type="mRNA"

/strain="CLONES"

/db\_xref="taxon:3352"

/clone="RTMW2\_19\_B10\_A021"

/lab\_host="DH10B-T1 phage-resistant E. coli"

/clone\_lib="Well-watered loblolly pine roots WM2"

/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

## ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 4.4e+02; Length 712;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCCACTACT 19

Db 640 GACCCCACTACT 653

## RESULT 123

CG197500  
LOCUS

## DEFINITION

CG197500 713 bp DNA linear GSS 21-AUG-2003  
PU1FF58TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMB1a056920,

## ACCESSION

CG197500

## VERSION

CG197500.1 GI:34088575

## KEYWORDS

GSS.

## SOURCE

ORGANISM

Zea mays

Ze mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 713)

Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennett, J.

Maize Genomics Consortium

Unpublished (2003)

Other GSSs: PU1FF58TB

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TP

Class: sheared ends.

Location/Qualifiers

1..713

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone\_lib="ZMMB1a056920"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high cot selected genomic DNA library"

## ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 4.4e+02; Length 713;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCACTACT 14

Db 376 TTGCGACCCCACTACT 389

## RESULT 124

CC700610/c  
LOCUS

## DEFINITION

CC700610 716 bp DNA linear GSS 19-JUN-2003  
OGU1M02TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMB1a0477A03,

## ACCESSION

CC700610

## VERSION

CC700610.1 GI:32105386

## KEYWORDS

GSS.

## SOURCE

Zea mays

## ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 716)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunez, G.A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: OGU1M02TV

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TP

Class: sheared ends.

Location/Qualifiers

1..716

/organism="Zea mays"

/mol\_type="genomic DNA"



/strain="873"  
/db\_xref="taxon:4577"  
/clone="ZMMBM0471A03"  
/clone\_lib="ZM\_0.7\_1.5\_KB"  
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 716;  
Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 TTCCGACCCCAACA 14  
Db 634 TTCCGACCCCAACA 621

RESULT 125  
CE147261 716 bp DNA linear GSS 25-SEP-2003  
LOCUS tigr-g98-dog-17000371298782 Dog Library Canis familiaris genomic,  
DEFINITION genomic survey sequence.  
ACCESSION CE147261  
VERSION CE147261.1 GI:35263354  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 716)  
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
Venter, J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)  
JOURNAL MEDLINE  
PUBMED 14512627

## COMMENT

Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org  
Class: shotgun.

## FEATURES

Source Location/Qualifiers  
1..716  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BstXI; Libraries were prepared from  
peripheral blood"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 716;  
Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 7 ACCCACTACTC 20  
Db 38 ACCCACTACTC 51

RESULT 126  
CC154782 718 bp DNA linear GSS 25-APR-2003  
LOCUS CSU-K34.124F11.T7 CSU-K34 Aedes aegypti genomic clone  
DEFINITION CSU-K34.124F11, genomic survey sequence.  
ACCESSION CC154782  
VERSION CC154782.1 GI:30108078  
KEYWORDS GSS.

SOURCE Aedes aegypti (yellow fever mosquito)  
ORGANISM Aedes aegypti  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes;  
Stegomyia.

REFERENCE 1 (bases 1 to 718)  
Loftus, B., Shetty, J., Knudson, D. and Severson, D.  
BAC end sequencing of Aedes aegypti  
Unpublished (2003)  
Other GSSs: CSU-K34.124F11.SP6  
Contact: Brendan Loftus  
Department of Eukaryotic Genomics  
TIGR

## AUTHORS

Loftus, B., Shetty, J., Knudson, D. and Severson, D.

## JOURNAL

Unpublished (2003)

## COMMENT

Other GSSs: CSU-K34.124F11.SP6  
Contact: Brendan Loftus  
Department of Eukaryotic Genomics  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-3543  
Fax: 301-838-0208  
Email: entae@tigr.org  
Library was provided by Susan Brown and Dennis Knudson at Colorado  
State University.  
Seq primer: T7  
Class: BAC ends.

## FEATURES

Source Location/Qualifiers  
1..718  
/organism="Aedes aegypti"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7159"  
/clone="CSU-K34.124F11"  
/clone\_lib="CSU-K34"  
/note="Vector: pBACe3.6; Site 1: EcoRI; Source DNA: Aedes  
aegypti; strain unknown (derived from freshly hatched  
larvae at the Vitis Research Centre, Poona, India.  
Reference: SINGH, K. R. P., 1967 Cell cultures derived  
from larvae of Aedes albopictus (Skuse) and Aedes aegypti  
(L.). Current Science 36: 506-508; ATC-10 cell line ATCC  
CCL-125"

## ORIGIN

Query Match 70.0%; Score 14; DB 8; Length 718;  
Best Local Similarity 100.0%; Pred. No. 4,4e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 TTCCGACCCCAACA 14  
Db 184 TTCCGACCCCAACA 197

## RESULT 127

BQ971958 721 bp mRNA linear EST 21-AUG-2002  
LOCUS QHB9D19.yg.ab1 QH ABCDI sunflower RH801 Helianthus annuus cDNA  
DEFINITION QHB9D19.yg.ab1 QH ABCDI sunflower RH801 Helianthus annuus cDNA  
ACCESSION BQ971958  
VERSION BQ971958.1 GI:22389479  
KEYWORDS EST.

## SOURCE

Helianthus annuus (common sunflower)

## ORGANISM

Helianthus annuus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
Heliantheae; Helianthus.

## REFERENCE

1 (bases 1 to 721)

## AUTHORS

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,  
Lin, H., Van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,  
Ellison, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,  
Lai, Z., Church, S., Jackson, L. and Bradford, K.  
Lettuce and Sunflower ESTs from the Compositae Genome Project  
http://compogenomics.ucdavis.edu/  
Unpublished (2002)

## JOURNAL

Unpublished (2002)

## COMMENT

Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Amondson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659  
 Email: akozk@atgc.org [michelmore@vegmail.ucdavis.edu]  
 belongs to contig OH\_Ca\_Contig4100, see <http://cspdb.ucdavis.edu/>  
 for details.  
 Plate: QHB9 row: D column: 19.  
 Location/Qualifiers  
 1..721  
 /organism="Helianthus annuus"  
 /mol\_type="mRNA"  
 /cultivar="RHA801"  
 /db\_xref="taxon:4232"  
 /clone="QHB9D19"  
 /lab\_host="E.coli"  
 /clone\_lib="OH ABCDI sunflower RHA801"  
 /note="Vector: pBRCDNA5fiab: The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cspdb.ucdavis.edu/>  
 TAG\_LIB=OH ABCDI sunflower RHA801  
 TAG\_SEQ=TTGAGCCGGC"

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 721;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCGACCCACACCTA 17  
 |||||  
 Db 556 GCGACCCACACCTA 569

RESULT 128 728 bp DNA linear GSS 03-JUN-2004  
 AG407958  
 LOCUS  
 DEFINITION Mus musculus molossinus DNA, clone:MSM901-267C14.T7, genomic survey  
 sequence.

ACCESSION AG407958 GI:48050644  
 VERSION AG407958.1  
 KEYWORDS Mus musculus molossinus  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
 TITLE BAC end Sequences of Library MSM901  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 728)  
 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
 Direct Submision  
 Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9111, Fax: 81-45-503-9170  
 E-mail: hattori@psc.riken.jp, URL: <http://hgp.gsc.riken.go.jp/>  
 Clones are derived from the mouse BAC library MSM901. For BAC library availability, please contact Kunya Abe (abe@rtc.riken.jp).  
 Teukuba Institute, Bio Resource Center.  
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
 Koyada, Teukuba, 305-0074 Japan  
 phone: 81-298-36-9189, fax: 81-298-36-9199  
 e-mail: abe@rtc.riken.jp  
 PRIMERS  
 Sequencing : T7  
 LIBRARY  
 Vector : pBAC3.6  
 R.Site 1 : EORI

## COMMENT

COMMENT

R.Site 2 : EORI.  
 Location/Qualifiers  
 1..728  
 /organism="Mus musculus molossinus"  
 /mol\_type="genomic DNA"  
 /sub\_species="molossinus"  
 /db\_xref="taxon:57486"  
 /clone="MSM901-267C14.T7"  
 /sex="male"  
 /tissue\_type="mixture of kidney and spleen"  
 /clone\_lib="MSM901 Mouse Male BAC Library"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 728;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TCGCACCCACAC 15  
 |||||  
 Db 487 TCGCACCCACAC 500

RESULT 129 730 bp mRNA linear EST 29-SRP-2004  
 CV434255/c  
 LOCUS  
 DEFINITION CS\_hyp\_33b05\_M13Reverse Blue crab hypodermis, normalized  
 Callinectes sapidus cDNA clone CS\_hyp\_33b05.5, similar to  
 ref|NP\_652222.1| CG14310-P8 - Drosophila melanogaster. Score = 33.9  
 bits (76), Expect = 3.5, mRNA sequence.

ACCESSION CV434255 GI:52843545  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS Shafer, T.H., Coblenz, F.E. and Towle, D.W.  
 TITLE Expressed sequence tags from normalized cDNA libraries prepared from gill and hypodermis tissues of the blue crab, Callinectes sapidus  
 JOURNAL Unpublished (2004)  
 CONTACT: Thomas H. Shafer  
 Department of Biological Sciences  
 University of North Carolina Wilmington  
 601 S. College Rd, Wilmington, NC 28403, USA  
 Tel: 910-962-7275  
 Fax: 910-962-4066  
 Email: shafer@uncw.edu  
 Plate: 33 row: b column: 05  
 Seq primer: M13 Reverse  
 High quality sequence stop: 494.  
 Location/Qualifiers  
 1..730  
 /organism="Callinectes sapidus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6763"  
 /clone="CS\_hyp\_33b05"  
 /tissue\_type="Pooled hypodermal epithelium from the mid-dorsal region and arthrodial membrane of pre-molt (stage D2) and 3-hour postmolt crabs"  
 /dev\_stage="adult"  
 /clone\_lib="Blue crab hypodermis, normalized"  
 /note="Vector: PCMV Sport 6.1; Total RNA samples were prepared individually from each tissue, checked for quality, and then pooled for construction and normalization of a cDNA library by Invitrogen. Plasmids were isolated and inserts sequenced from their 5'-ends by the Blue Crab Molecular Genetics Laboratory at the University of North Carolina Wilmington. Tissues were trimmed, compared (BLASTx) to NCBI non-redundant protein database as of 19 July 2004, and processed for submission

## FEATURES

source



**AUTHORS** Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J., and Benneken, J.

**TITLE** Maize Genomics Consortium

**JOURNAL** Unpublished (2003)

**COMMENT** Other GSSs: PUAH367B  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TP  
Class: sheared ends.

**FEATURES** Location/Qualifiers  
1..746  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMB7A0537F24"  
/clone\_id="ZM\_0\_6\_1.0\_KB"  
/note="Vector: PCR4-TOPD; Site 1: EcoRI; 0.6-1.0 kb high cor selected genomic DNA library"

**ORIGIN**

Query Match 70.0%; Score 14; DB 9; Length 746;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 4 GCGACCCACACTA 17  
642 GCGACCCACACTA 655  
|||||  
|||||

**RESULT 133**  
BF864639/c  
LOCUS 747 bp mRNA linear EST 19-JAN-2001  
DEFINITION BF864639 963053E05 y1 C. reinhardtii CC-1690, Stress condition I, normalized, lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.  
BF864639.1 GI:12254783  
EST.  
Chlamydomonas reinhardtii  
Chlamydomonas reinhardtii  
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.  
1 (bases 1 to 747)  
Grossman, A., Davies, J., Federspiel, N., Harris, E., Hauser, C., Lefebvre, P., McDermott, J. P., Shrager, J., Silflow, C. and Stern, D. Analyses of the Chlamydomonas reinhardtii Genome: A Model Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants, Project phase 3 Unpublished (2000)  
Contact: Charles Hauser  
DCMB Box 91000  
Duke University  
Durham, NC 27708-1000  
Tel: 919 613 8159  
Fax: 919 613 8177  
Email: chauser@duke.edu.

**FEATURES** Location/Qualifiers  
1..747  
/organism="Chlamydomonas reinhardtii"  
/mol\_type="mRNA"  
/strain="CC-1690 wild type mt+ 21gr"  
/db\_xref="taxon:3055"  
/clone\_id="C. reinhardtii CC-1690, Stress condition I, normalized, lambda Zap II"  
/note="Vector: Bluescript II SK-; Site 1: EcoRI, Site 2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to

**ORIGIN**

Query Match 70.0%; Score 14; DB 2; Length 747;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 2 TCGGACCCACAC 15  
711 TCGGACCCACAC 698  
|||||  
|||||

**RESULT 134**  
AG575296  
LOCUS 749 bp DNA linear GSS 05-JUN-2004  
DEFINITION Mus musculus molossinus DNA, clone:MSWg01-499C06.TU, genomic survey sequence.  
AG575296  
AG575296.1 GI:48336126  
GSS.  
KEYWORDS Mus musculus molossinus  
ORGANISM Mus musculus molossinus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

**REFERENCE**  
1 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y. BAC end Sequences of Library MSWg01 Unpublished  
2 (bases 1 to 749)  
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y. Direct Submision  
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
Clones are derived from the mouse BAC library MSWg01. For BAC library availability, please contact Kumiya Abe (abe@rtc.riken.jp).  
Tsukuba Institute, Bio Resource Center,  
The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@rtc.riken.jp  
PRIMERS  
Sequencing : TU  
LIBRARY : PBACe3.6  
Vector : EcoRI  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI.

**FEATURES** Location/Qualifiers  
1..749  
/organism="Mus musculus molossinus"  
/mol\_type="genomic DNA"  
/sub\_species="molossinus"  
/db\_xref="taxon:57486"  
/clone="MSWg01-499C06.TU"  
/sex="male"  
/tissue\_type="mixture of kidney and spleen"  
/clone\_id="MSWg01 Mouse Male BAC Library"

**ORIGIN**

Query Match 70.0%; Score 14; DB 9; Length 749;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 ACCGACACTACTC 20  
 Db 519 ACCGACACTACTC 532

RESULT 135  
 CC889635/c  
 LOCUS  
 DEFINITION CC889635 753 bp DNA linear GSS 31-JUL-2003  
 ZMMBRC0504N21f ZMMBRC Zea mays genomic clone ZMMBRC0504N21 5',  
 genomic survey sequence.  
 ACCESSION CC889635  
 VERSION CC889635.1 GI:33367503  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoidae; Andropogoneae; Zea.  
 1 (bases 1 to 753)  
 Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,  
 Ronzard,K., Fuks,G., Yu,Y., Wang,R. and Messing,J.  
 Sequencing of the maize genome at PGIR (2003b)  
 Unpublished (2003)  
 CONTACT: Bharti, A.K.  
 Dr. Joachim Messing's lab  
 The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
 University  
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
 Tel: 732 445 3801  
 Fax: 732 445 5735  
 Email: bharti@waksman.rutgers.edu  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence start: 118.  
 Location/Qualifiers  
 1..753  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /cultiivar="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBRC0504N21"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="ZMMBRC"  
 /note="Vector: pTRABAC1.3; Site\_1: BamHI; Site\_2: BamHI"

ORIGIN  
 Query Match 70.0%; Score 14; DB 9; Length 753;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 GCGACCCACACTA 17  
 Db 718 GCGACCCACACTA 705

RESULT 136  
 BW407445/c  
 LOCUS  
 DEFINITION BW407445 Yutaka Satou unpublished cDNA library, embryo whole animal  
 Ciona intestinalis cDNA clone ciem854g11 3', mRNA sequence.  
 ACCESSION BW407445  
 VERSION BW407445.1 GI:47823273  
 KEYWORDS EST.  
 SOURCE Ciona intestinalis  
 ORGANISM Ciona intestinalis  
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
 Phlebobranchia; Clonidae; Ciona.  
 1 (bases 1 to 754)  
 Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.  
 Expressed genes in Ciona intestinalis (2004)  
 Unpublished (2004)  
 Contact: Yutaka Satou

Department of Zoology  
 Kyoto University  
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
 Tel: 81-75-753-4095  
 Fax: 81-75-705-1113  
 Email: yutaka@ascidian.zool.kyoto-u.ac.jp.

FEATURES  
 source  
 1..754  
 /organism="Ciona intestinalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7719"  
 /clone="ciem854g11"  
 /issue\_type="whole animal"  
 /dev\_stage="embryo"  
 /clone\_lib="Yutaka Satou unpublished cDNA library, embryo  
 whole animal"

ORIGIN  
 Query Match 70.0%; Score 14; DB 5; Length 754;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 GCGACCCACACTA 17  
 Db 496 GCGACCCACACTA 483

RESULT 137  
 BQ968763  
 LOCUS  
 DEFINITION BQ968763 760 bp mRNA linear EST 21-AUG-2002  
 OHB35B10.YG.ab1 OH ABCD1 sunflower RHA801 Helianthus annuus cDNA  
 clone OHB35B10, mRNA sequence.  
 ACCESSION BQ968763  
 VERSION BQ968763.1 GI:22386284  
 KEYWORDS EST.  
 SOURCE Helianthus annuus (common sunflower)  
 ORGANISM Helianthus annuus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;  
 asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
 Heliantheae; Helianthus.  
 1 (bases 1 to 760)  
 Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,  
 Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,  
 Ellison,P., Kolman,J., Staben,M.S., Livingston,K., Zhou,Y.,  
 Lai,Z., Church,S., Jackson,L. and Bradford,K.  
 Lettuce and Sunflower ESTs from the Compositae Genome Project  
 http://compgenome.ucdavis.edu/  
 Unpublished (2002)  
 Contact: Alexander Kozik [R.W.Michelmore]  
 Department of Vegetable Crops, R.W.Michelmore Lab  
 University of California at Davis (UCD)  
 Asmudson Hall, UCD, Davis, CA 95616, USA  
 Tel: 1-(530)-742-1742  
 Fax: 1-(530)-752-9659  
 Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]  
 belongs to contig OH\_Ca.Contig4100, see http://cgdb.ucdavis.edu/  
 for details.  
 Plate: OHB35 row: B column: 10.  
 Location/Qualifiers  
 1..760  
 /organism="Helianthus annuus"  
 /mol\_type="mRNA"  
 /cultiivar="RHA801"  
 /db\_xref="taxon:4232"  
 /clone="OHB35B10"  
 /clone\_lib="OH ABCD1 sunflower RHA801"  
 /lab\_host="E. coli"  
 /note="Vector: pBRCDNA5flab; The library was constructed  
 from 11 different sources of RNA from a single genotype.  
 Separate cDNAs were generated using primers that  
 incorporated unique 5' and 3' tags to distinguish each  
 source of RNA. cDNAs were then pooled, size-fractionated,

directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at [http://cgpsdb.ucdavis.edu/TAG\\_TISSUE=chemical\\_induction](http://cgpsdb.ucdavis.edu/TAG_TISSUE=chemical_induction)  
TAG\_LIB=OH ABCDI sunflower RHAB01  
TAG\_SEQ=GTGAGCCGGG

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 760;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GCGACCACTACTC 17  
|||||  
Db 556 GCGACCACTACTC 569

## RESULT 138

LOCUS BX172443 765 bp DNA linear GSS 28-JAN-2003  
DEFINITION Danio rerio genomic clone DKER-145G10, genomic survey sequence.  
ACCESSION BX172443  
VERSION BX172443.1 GI:28004148  
KEYWORDS GSS.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio

REFERENCE 1 (bases 1 to 765)  
AUTHORS Humphray, S.J., Huckle, E. and Durham, J.L.  
TITLE Direct Submission  
JOURNAL Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humphray@sanger.ac.uk Unpublished  
This sequence was generated from the SP6 end of BAC 145G10. 145G10 is part of the Daniokey BAC library created by R. Plasterk and N.V. Keygene. Further details: [http://www.sanger.ac.uk/projects/D\\_rerio/](http://www.sanger.ac.uk/projects/D_rerio/)

## COMMENT

FEATURES  
source  
Location/Qualifiers  
1..765  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKER-145G10"  
/tissue\_type="Testis"  
/note="vector pindigobAC-536"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 765;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ACCCAACTACTC 20  
|||||  
Db 569 ACCCAACTACTC 582

RESULT 139  
LOCUS BF631334 768 bp mRNA linear EST 22-OCT-2001  
DEFINITION HVSMB0015K06f Hordeum vulgare seedling shoot EST library  
clone HVSMB0015K06f, mRNA sequence.

ACCESSION BF631334  
VERSION BF631334.2 GI:13092041  
KEYWORDS EST.  
SOURCE Hordeum vulgare subsp. vulgare  
ORGANISM Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.

## REFERENCE

1 (bases 1 to 768)  
AUTHORS Wing, R., Close, T.J., Kleinof, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, R.D., Oates, R. and Main, D.  
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex drought-stressed seedling shoot cDNA library  
JOURNAL Unpublished (2001)

## COMMENT

On Dec 19, 2000 this sequence version replaced gi:11895492.  
Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Total hg bases = 329  
Seq primer: AATTACCTCTACTAAGCG  
High quality sequence stop: 431.  
Location/Qualifiers  
1..768  
/organism="Hordeum vulgare subsp. vulgare"  
/mol\_type="mRNA"  
/cultivar="Morex"  
/sub\_species="vulgare"  
/db\_xref="taxon:112509"  
/clone="HVSMB0015K06f"  
/tissue\_type="Seedling shoot"  
/lab\_host="NUC121"  
/clone\_lib="Hordeum vulgare seedling shoot EST library  
HVCDA0002 (Dehydration stress)"  
/note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;  
Seeds were surface sterilized then germinated under aseptic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedlings were incubated at 90% RH for 24 hr. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, 600000 pfu were in vivo excised to give plasmid SK(-) cDNA phagemids. These steps were performed in the TU Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinof A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30 (<http://wheat.pw.usda.gov/99pages/bgn/31/cover.html>)"

## FEATURES

source  
Location/Qualifiers  
1..768  
/organism="Hordeum vulgare subsp. vulgare"  
/mol\_type="mRNA"  
/cultivar="Morex"  
/sub\_species="vulgare"  
/db\_xref="taxon:112509"  
/clone="HVSMB0015K06f"  
/tissue\_type="Seedling shoot"  
/lab\_host="NUC121"  
/clone\_lib="Hordeum vulgare seedling shoot EST library  
HVCDA0002 (Dehydration stress)"  
/note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;  
Seeds were surface sterilized then germinated under aseptic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedlings were incubated at 90% RH for 24 hr. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, 600000 pfu were in vivo excised to give plasmid SK(-) cDNA phagemids. These steps were performed in the TU Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinof A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30 (<http://wheat.pw.usda.gov/99pages/bgn/31/cover.html>)"

## ORIGIN

Query Match 70.0%; Score 14; DB 2; Length 768;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ACCCAACTACTC 20  
|||||  
Db 757 ACCCAACTACTC 744

RESULT 140  
LOCUS CB350437 769 bp mRNA linear EST 17-MAY-2003  
DEFINITION P2A06 Cotton fiber subtracted cDNA library Gossypium hirsutum cDNA, mRNA sequence.

ACCESSION CB350437  
 VERSION GI:30841117  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Gossypium hirsutum (upland cotton)  
 EST  
 Gossypium hirsutum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
 1 (bases 1 to 769)  
 J1.S.J., Lu,Y.C., Feng,J.X., Wei,G., Li,J., Shi,Y.H., Fu,Q., Liu,D., Luo,Y.C. and Zhu,Y.X.  
 Isolation and analyses of genes preferentially expressed during early cotton fiber development by subtractive PCR and cDNA array  
 Nucleic Acids Res. 31 (10), 2534-2543 (2003)  
 JOURNAL 25622070  
 MEDLINE 12736302  
 PUBMED  
 COMMENT  
 Contact: Zhu, Y.  
 National Laboratory of Protein Engineering and Plant Genetic Engineering  
 College of Life Sciences, Peking University  
 Beijing 100871, China  
 Tel: 86 10 6275 1193  
 Fax: 86 10 6275 4427  
 Email: zhuyx@water.pku.edu.cn.  
 Location/Qualifiers  
 1..769  
 /organism="Gossypium hirsutum"  
 /mol\_type="mRNA"  
 /cultivar="Xu-142"  
 /db\_xref="taxon:3635"  
 /tissue\_type="fiber"  
 /dev\_stage="10 days post anthesis (dpa)"  
 /clone\_lib="Cotton fiber subtracted cDNA library"  
 /note="The library was constructed using PCR-select cDNA subtraction method with 10 dpa cotton fiber as tester and fiberless mutant as driver"

ORIGIN  
 Query Match 70.0%; Score 14; DB 6; Length 769;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GACCCACACTACT 19  
 |||||  
 Db 659 GACCCACACTACT 646

RESULT 141  
 BH422873 771 bp DNA linear GSS 12-DEC-2001  
 LOCUS BOHFW02TF BOHF Brassica oleracea genomic clone BOHFW02, genomic survey sequence.  
 ACCESSION BH422873  
 VERSION BH422873.1 GI:17608601  
 KEYWORDS GSS.  
 SOURCE  
 ORGANISM  
 Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 771)  
 Town,C.D., Van Aken,S., Utechtack,T., Koo,H. and Fraser,C.M.  
 Whole genome shotgun sequencing of Brassica oleracea  
 Unpublished (2001)  
 Other GSSs: BOHFW02TF  
 Contact: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TF

Class: sheared ends.  
 Location/Qualifiers  
 1..771  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /strain="T01000DH3"  
 /db\_xref="taxon:3712"  
 /clone="BOHFW02"  
 /clone\_lib="BOHF"  
 /note="Vector: pHOS1; Site\_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"

ORIGIN  
 Query Match 70.0%; Score 14; DB 8; Length 771;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCACACA 14  
 |||||  
 Db 258 TTCCGACCCACACA 271

RESULT 142  
 AZ187767 779 bp DNA linear GSS 30-AUG-2000  
 LOCUS SP\_1009\_B2\_H12\_SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1009 Col=24 Row=P, genomic survey sequence.  
 ACCESSION AZ187767  
 VERSION AZ187767.1 GI:8370946  
 KEYWORDS GSS.  
 SOURCE  
 ORGANISM  
 Strongylocentrotus purpuratus  
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae; Strongylocentrotus.  
 1 (bases 1 to 779)  
 Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Pousetka,A.J., Livingston,B.T., Wray,G.A., Etlensohn,C.A., Iehrach,H., Britten,R.J., Davidson,E.H. and Hood,L.  
 A sea urchin genome project: Sequence scan, virtual map, and additional resources  
 Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)  
 20402566  
 JOURNAL 10920195  
 MEDLINE  
 PUBMED  
 COMMENT  
 Contact: Cameron, RA, Davidson, EH, Hood, L  
 Division of Biology 156-29  
 Pasadena California 91125, USA  
 Tel: (626) 395-8421  
 Fax: (626) 793-3047  
 Email: acameron@caltech.edu  
 Plate: 1009 row: P column: 24  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 779.  
 Location/Qualifiers  
 1..779  
 /organism="Strongylocentrotus purpuratus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7668"  
 /clone="Plate=1009 Col=24 Row=P"  
 /clone\_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"  
 /note="Organ: sperm, Vector: BACs3.6; BAC Clones in E-Coli DH10B"

ORIGIN  
 Query Match 70.0%; Score 14; DB 8; Length 779;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCACTACTAC 18  
 Db 15 CGACCACTACTAC 28

RESULT 143  
 BZ822648  
 LOCUS 779 bp DNA linear GSS 18-MAR-2003  
 DEFINITION PUBB95STD ZM\_0.6\_1.0\_KB Zea mays genomic clone ZMMBTA317P22,  
 genomic survey sequence.  
 ACCESSION BZ822648  
 VERSION BZ822648  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 779)  
 Whitejaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
 Resnick,A., Frazer,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Benneken,J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Other GSSs: PUBB95TB  
 Contact: Cathy Whitejaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitejaw@tigr.org  
 Seq primer: TF  
 Class: sheared ends.

FEATURES  
 source  
 1..779  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBTA317P22"  
 /clone\_1db="ZM\_0.6\_1.0\_KB"  
 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 Cot selected genomic DNA library"

ORIGIN  
 Query Match 70.0%; Score 14; DB 8; Length 779;  
 Best Local Similarity 100.0%; Pred.No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCACTACTCTC 20  
 Db 518 ACCCACTACTCTC 531

RESULT 144  
 AG581296  
 LOCUS 783 bp DNA linear GSS 05-JUN-2004  
 DEFINITION Mus musculus molossinus DNA, clone:MSMg01-507A20.T7, genomic survey  
 sequence.  
 ACCESSION AG581296  
 VERSION AG581296.1 GI:48342126  
 KEYWORDS GSS.  
 SOURCE Mus musculus molossinus  
 Mus musculus molossinus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.  
 BAC end Sequences of Library MSMg01  
 2 (bases 1 to 783)  
 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.  
 Direct Submission

JOURNAL  
 Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 1-7-22 Suenho-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/  
 Tel:81-45-503-9111, Fax:81-45-503-9170)  
 Clones are derived from the mouse BAC library MSMg01. For BAC  
 library availability, please contact Kunya Abe (abe@rtc.riken.jp).  
 Tsukuba Institute, Bio Resource Center,  
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
 Koyadai, Tsukuba, 305-0074 Japan  
 phone: 81-298-36-9189, fax: 81-298-36-9139  
 e-mail: abe@rtc.riken.jp

COMMENT  
 PRIMERS  
 Sequencing : T7  
 LIBRARY  
 Vector : pBAC3.6  
 R.Site 1 : EcoRI  
 R.Site 2 : EcoRI.

FEATURES  
 source  
 Location/Qualifiers  
 1..783  
 /organism="Mus musculus molossinus"  
 /mol\_type="genomic DNA"  
 /sub\_species="molossinus"  
 /db\_xref="taxon:57486"  
 /clone="MSMg01-507A20.T7"  
 /sex="male"  
 /tissue\_type="mixture of kidney and spleen"  
 /clone\_1db="MSMg01 Mouse Male BAC Library"

ORIGIN  
 Query Match 70.0%; Score 14; DB 9; Length 783;  
 Best Local Similarity 100.0%; Pred.No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCACTACTCTC 20  
 Db 521 ACCCACTACTCTC 534

RESULT 145  
 BZ468932  
 LOCUS 785 bp DNA linear GSS 13-DEC-2002  
 DEFINITION BONPQ48TR BO\_1.6\_2\_KB tot Brassica oleracea genomic clone BONPQ48,  
 genomic survey sequence.  
 ACCESSION BZ468932  
 VERSION BZ468932.1 GI:26764413  
 KEYWORDS GSS.  
 SOURCE Brassica oleracea  
 ORGANISM Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 785)  
 Town,C.D., Van Aken,S., Uterback,T., Koo,H. and Frazer,C.M.  
 Whole genome shotgun sequencing of Brassica oleracea  
 Unpublished (2001)  
 Other GSSs: BONPQ48TF  
 Contact: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TR  
 Class: sheared ends.

FEATURES  
 source  
 Location/Qualifiers  
 1..785  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /strain="TO1000DH3"  
 /db\_xref="taxon:3712"  
 /clone="BONPQ48"



```

/clone.lib="BO_1.6.2_KB.tot"
/notes="vector: pHD51_Site_1: BstXI, 1.6-2 kb sheared
total DNA inserted into pHD51 using BstXI linkers"
ORIGIN
Query Match      70.0%; Score 14; DB 8; Length 785;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTCCGACCCACACA 14
      |||||
      302 TTCCGACCCACACA 315

RESULT 146
B2477400      791 bp      DNA      linear      GSS 13-DEC-2002
LOCUS      BOND31TR.B0.1.6.2_KB.tot Brassica oleracea genomic clone BOND31,
DEFINITION      genomic survey sequence.
ACCESSION      B2477400.1 GI:26779798
VERSION      B2477400.1 GI:26779798
KEYWORDS      GSS.
SOURCE      Brassica oleracea
ORGANISM      Brassica oleracea
REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE      rosids; eurosid II; Brassicales; Brassicaceae; Brassica.
JOURNAL      1 (bases 1 to 791)
OTHERS      Town,C.D., Van Aken,S., Uteback,T., Koo,H. and Fraser,C.M.
COMMENT      Whole genome shotgun sequencing of Brassica oleracea
      Unpublished (2001)
      Other_GSSs: BOND31TF
      Contact: Chris Town
      TIGR
      9712 Medical Center Drive, Rockville, MD 20850, USA.
      Tel: 301-838-3523
      Fax: 301-838-0208
      Email: cdtown@tigr.org
      DNA is from a doubled haploid provided by Tom Osborn.
      Seq primer: TR
      Class: sheared ends.
FEATURES
      source      location/qualifiers
      1..791
      /organism="Brassica oleracea"
      /mol_type="genomic DNA"
      /strain="TO1000DH3"
      /db_xref="taxon:3712"
      /clone="BOND31"
      /clone.lib="BO_1.6.2_KB.tot"
      /notes="vector: pHD51_Site_1: BstXI, 1.6-2 kb sheared
      total DNA inserted into pHD51 using BstXI linkers"
ORIGIN
Query Match      70.0%; Score 14; DB 8; Length 791;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TTCCGACCCACACA 14
      |||||
      445 TTCCGACCCACACA 458

RESULT 147
B0852379      793 bp      mRNA      linear      EST 16-OCT-2002
LOCUS      AGENCOURT.10402281.NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6617916
DEFINITION      5', mRNA sequence.
ACCESSION      B0852379
VERSION      B0852379.1 GI:24037342
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 793)
AUTHORS      NIH-MGC http://mgs.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
      Email: cgaps-remail.nih.gov
      Tissue Procurement: CLONTECH
      cDNA Library Preparation: CLONTECH Laboratories, Inc.
      cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
      DNA Sequencing by: Agencourt Bioscience Corporation
      Clone distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LNL at:
      http://image.llnl.gov
      Plate: LUCM2863 row: p column: 12
      High quality sequence stop: 659.
FEATURES
      source      location/qualifiers
      1..793
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="IMAGE:6617916"
      /lab_host="DH10B (T1 phage-resistant)"
      /clone.lib="NIH_MGC_82"
      /notes="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
      SfiI (ggcgctcgcc); Site_2: SfiI (ggcattatggcc); 5' and
      3' adaptors were used in cloning as follows: 5' adaptor
      sequence: 5'-CACGGCCATTATGGC-3' and 3' adaptor sequence:
      5'-ATTCTAGAGCGCGCGCGCAGATG-dt(30)BN-3' (where B = A,
      C, or G and N = A, C, G, or T). Average insert size
      1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
      inserts by PCR. This library was enriched for full-length
      clones and was constructed by Clontech Laboratories (Palo
      Alto, CA)."
ORIGIN
Query Match      70.0%; Score 14; DB 5; Length 793;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      7 ACCCAACACTACTC 20
      |||||
      312 ACCCAACACTACTC 325

RESULT 148
CF449870      793 bp      mRNA      linear      EST 04-SEP-2003
LOCUS      EST686215 normalized cDNA library of onion Allium cepa cDNA clone
DEFINITION      ACCT90, mRNA sequence.
ACCESSION      CF449870
VERSION      CF449870.1 GI:34472572
KEYWORDS      EST.
SOURCE      Allium cepa (onion)
ORGANISM      Allium cepa
REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS      Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
TITLE      Allium.
JOURNAL      1 (bases 1 to 793)
OTHERS      Havey,M.J., Cheung,F., Van Aken,S., Uteback,T. and Town,C.D.
COMMENT      Expressed Sequence Tags from a normalized library of mixed onion
      tissues (Allium cepa)
      Unpublished (2003)
      Contact: Havey MJ
      Department of Horticulture
      USDA-ARS and University of Wisconsin
      1575 Linden Drive, Madison, WI 53706, USA
      Tel: 608-262-1830
      Fax: 608-262-4743
      Email: mjhavey@facstaff.wisc.edu
      TIGR sequence name ACCT90TR. For more information:
      http://haveylab.hort.wisc.edu
      Seq primer: CAG GAA ACA GCT ATG ACC.

```

FEATURES  
source

Location/Qualifiers  
1. 793  
/organism="Allium cepa"  
/mol\_type="rRNA"  
/culturvar="Red Creole (bulbs), unknown (callus), Ebano & Texas Legend (roots)"  
/db\_xref="taxon:4679"  
/clone="ACACT90"  
/tissue\_type="Callus, roots, and young bulbs"  
/clone\_lib="normalized cDNA library of onion"  
/note="Vector: pCMVSPORT6.1-cdb (Invitrogen); Site 1: EcoRV (5'); Site 2: NotI (3'); Equal molar amounts of mRNA from callus, roots, and young bulbs were combined to synthesize the library. Normalization to enrich for low-copy transcripts was performed by proprietary techniques of Invitrogen."

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 793;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACTACTCTC 20  
|||||  
Db 97 ACCCAACTACTCTC 110

## RESULT 149

LOCUS CC860424 800 bp DNA linear GSS 24-JUN-2003  
DEFINITION NDL.118M17.77 Notre Dame Liverpool Aedes aegypti genomic clone  
ACCESSION CC860424  
VERSION CC860424.1 GI:33220434  
KEYWORDS GSS.  
SOURCE Aedes aegypti (yellow fever mosquito)  
ORGANISM Aedes aegypti  
Eukaryote; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes; Stegomyia.

REFERENCE 1 (bases 1 to 800)  
AUTHORS Loftus,B., Shetty,J., Knudson,D. and Severson,D.  
TITLE BAC end sequencing of Aedes aegypti  
JOURNAL Unpublished (2003)  
COMMENT Other GSSs: NDL.118M17.SP6  
Contact: Brendan Loftus  
Department of Eukaryotic Genomics  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-3543  
Fax: 301-838-0208  
Email: enta@tigr.org  
Library was provided by David Severson  
Seq primer: T7  
Class: BAC ends.

## FEATURES

source

Location/Qualifiers  
1. 800  
/organism="Aedes aegypti"  
/mol\_type="genomic DNA"  
/strain="Liverpool"  
/db\_xref="taxon:7159"  
/clone="Notre Dame Liverpool-118M17"  
/clone\_lib="Notre Dame Liverpool"  
/note="Vector: pECBAC1; Site 1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 800;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACTACTCTC 20  
|||||  
Db 140 ACCCAACTACTCTC 153

## RESULT 150

LOCUS CK860367/c 801 bp mRNA linear EST 09-MAR-2004  
DEFINITION 31304 in vitro Root Solanum tuberosum cDNA, mRNA sequence.  
ACCESSION CK860367  
VERSION CK860367.1 GI:45290024  
KEYWORDS EST.  
SOURCE Solanum tuberosum (potato)  
ORGANISM Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE 1 (bases 1 to 801)  
AUTHORS Flinn,B., Rothwell,C., Sardana,R., Griffiths,R., Lague,M., De Koeijer,D., Audy,P., Goyer,C., Li,X.-Q., Wang-Pruski,G. and Regan,S.  
TITLE Generation of ESTs from in vitro root tissues of potato  
JOURNAL Unpublished (2004)  
COMMENT Contact: Barry Flinn  
The Canadian Potato Genome Project - BioAtlantech  
921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA  
Email: bflinn@biatlantech.nb.ca  
Seq primer: T3.

## FEATURES

source

Location/Qualifiers  
1. 801  
/organism="Solanum tuberosum"  
/mol\_type="rRNA"  
/cultivar="Shepody"  
/db\_xref="taxon:4113"  
/tissue\_type="Root"  
/lab\_host="XL10-Gold"  
/clone\_lib="In vitro Root"  
/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI; Site 2: XhoI; supplier: Developmental series. Sterile stem sections from pathogen-free Solanum tuberosum var. Shepody, clone 1756, nuclear stock were cultured in Magenta boxes containing 1/10 strength MS medium, solidified with 0.8% (w/v) Phytagar. Roots of all sizes, originating from the stem bottoms were collected from these cultures, washed to remove residual Phytagar, and used in RNA isolations and library construction."

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 801;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCAACTACTCT 19  
|||||  
Db 727 GACCCAACTACTCT 714

## RESULT 151

LOCUS CC631959 802 bp DNA linear GSS 19-JUN-2003  
DEFINITION OGDUQ89TH ZM 0.7.1.5 KB Zea mays genomic clone ZMMBMA0423009,  
ACCESSION CC631959  
VERSION CC631959.1 GI:32006725  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 802)  
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uutterback,T., Resnick,A., Fraser,C.M., Buddiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.

TITLE Consortium for Maize Genomics  
JOURNAL Unpublished (2002)  
COMMENT Other GSSs: OGU089TV  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TR  
Class: sheared ends.  
Location/Qualifiers  
1. 802  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_id="ZMMBMA0423009"  
/note="Vector: pBCKS; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

ORIGIN  
Query Match 70.0%; Score 14; DB 9; Length 802;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CGACCAACTACTAC 18  
|||||  
99 CGACCAACTACTAC 112

Db 99 CGACCAACTACTAC 112

RESULT 152  
CG155334 806 bp DNA linear GSS 21-AUG-2003  
LOCUS PUIKRS9TB.ZM.0.6.1.0 KB Zea mays genomic clone ZMMBTA0605122,  
DEFINITION genomic survey sequence.  
ACCESSION CG155334  
VERSION CG155334.1 GI:34046135  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 806)  
White, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,  
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and  
Bennetzen, J.  
Maize Genomics Consortium  
Unpublished (2003)  
Other GSSs: PUIKRS9TDT  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TR  
Class: sheared ends.  
Location/Qualifiers  
1. 806  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_id="ZMMBTA0605122"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high  
COT selected genomic DNA library"

ORIGIN  
Query Match 70.0%; Score 14; DB 9; Length 806;

Best Local Similarity 100.0%; Pred. No. 4.3e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ACCCAACTACTC 20  
|||||  
195 ACCCAACTACTC 208

Db 195 ACCCAACTACTC 208

RESULT 153  
BF666995 809 bp mRNA linear EST 22-DEC-2000  
LOCUS 602130174F1.NIH\_MGC\_56 Homo sapiens cDNA clone IMAGE:4286922 5',  
DEFINITION mRNA sequence.  
ACCESSION BF666995  
VERSION BF666995.1 GI:11982403  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 809)  
NIH-MGC http://mgs.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNCM124 row: c column: 19  
High quality sequence stop: 619.  
Location/Qualifiers  
1. 809  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_id="IMAGE:4286922"  
/tissue\_type="primitive neuroectoderm"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_id="NIH\_MGC\_56"  
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site 1:  
SfiI (ggcgccgcgcgc); Site 2: SfiI (ggccatgatggc);  
Double-stranded cDNA was prepared from cell line RNA. 5'  
and 3' adaptors were used in cloning as follows: 5'  
adaptor sequence: 5'-CAGCGCCATTTGACC-3' and 3' adaptor  
sequence: 5'-ATTCTAGAGCGGAGCGGCGCACATG-dT(30)BN-3'  
(where B = A, C, or G and N = A, C, G, or T). Average  
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies  
contained inserts by PCR. This library was enriched for  
full-length clones and was constructed by Clontech  
Laboratories (Palo Alto, CA)."

ORIGIN  
Query Match 70.0%; Score 14; DB 2; Length 809;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ACCCAACTACTC 20  
|||||  
435 ACCCAACTACTC 422

Db 435 ACCCAACTACTC 422

RESULT 154  
BF666387 811 bp mRNA linear EST 21-DEC-2000  
LOCUS 602123719F1.NIH\_MGC\_56 Homo sapiens cDNA clone IMAGE:4280812 5',  
DEFINITION mRNA sequence.  
ACCESSION BF666387  
VERSION BF666387.1 GI:11940282

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE 1 (bases 1 to 811)  
JOURNAL NIH-MGC <http://mgc.nci.nih.gov/>.  
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LCM108 row: e column: 05  
High quality sequence stop: 625.  
Location/Qualifiers  
1. 811  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4280812"  
/tissue\_type="primitive neuroectoderm"  
/lab\_host="DH10B (TI phage-resistant)"  
/clone\_lib="NIH\_MGC\_56"  
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site: 1;  
SfiI (ggccatctggcc); Site 2: SfiI (ggccatctggcc);  
Double-stranded cDNA was prepared from cell line RNA. 5'  
and 3' adaptors were used in cloning as follows: 5'  
adaptor sequence: 5'-CACGCCATTTCGCC-3' and 3' adaptor  
sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dT(30)BN-3'  
(where B = A, C, or G and N = A, C, G, or T). Average  
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies  
contained inserts by PCR. This library was enriched for  
full-length clones and was constructed by Clontech  
Laboratories (Palo Alto, CA)."

ORIGIN  
Query Match 70.0%; Score 14; DB 2; Length 811;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACTACTCTC 20  
|||||  
Db 431 ACCCAACTACTCTC 418

RESULT 155  
CNS0100/c 811 bp DNA linear GSS 14-JUN-2001  
LOCUS Anopheles gambiae GSS SP6 end of clone 26113 of NotreDamel library  
DEFINITION from strain PEST of Anopheles gambiae (African malaria mosquito),  
genomic survey sequence.  
ACCESSION AL153606  
VERSION AL153606.1 GI:7014525  
KEYWORDS GSS.  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
Anophelinae.  
1 (bases 1 to 811)  
Genoscope.  
Direct Submission  
Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr)  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr))  
2 (bases 1 to 811)  
Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.

TITLE Direct Submission  
JOURNAL Submitted (16-FEB-2000) BIMI, Institut Pasteur, 25, rue du Dr.  
Roux, Paris 75015, France  
COMMENT This clone is from an A. gambiae BAC library provided by F.H.  
Collins and sequenced by Genoscope in collaboration with the  
Laboratory of Biochem. and Biol. Molec. of Insects, Institut  
Pasteur.  
FEATURES  
source  
1. 811  
/organism="Anopheles gambiae"  
/mol\_type="genomic DNA"  
/strain="PEST"  
/db\_xref="taxon:7165"  
/clone\_lib="26113"  
/clone\_lib="NotreDamel"  
/note="end : SP6"

ORIGIN  
Query Match 70.0%; Score 14; DB 9; Length 811;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCAACTACT 19  
|||||  
Db 704 GACCCAACTACT 691

RESULT 156  
BX143045 812 bp DNA linear GSS 28-JAN-2003  
LOCUS Danio rerio genomic clone DKEY-108C18, genomic survey sequence.  
DEFINITION BX143045  
ACCESSION BX143045  
VERSION BX143045.1 GI:27974382  
KEYWORDS GSS.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 812)  
Humphrey,S.J., Huckle,E. and Durham,J.L.  
Direct Submission  
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome  
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
[humphrey@sanger.ac.uk](mailto:humphrey@sanger.ac.uk) Unpublished  
This sequence was generated from the T7 end of BAC 108C18. 108C18  
is part of the Daniokey BAC Library created by R. Plasterk and N.V.  
Keygene. Further details:  
[http://www.sanger.ac.uk/Projects/D\\_rerio/](http://www.sanger.ac.uk/Projects/D_rerio/).  
Location/Qualifiers  
1. 812  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKEY-108C18"  
/tissue\_type="Testis"  
/note="Vector pIndigobac-536"

ORIGIN  
Query Match 70.0%; Score 14; DB 9; Length 812;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACTACTCTC 20  
|||||  
Db 668 ACCCAACTACTCTC 655

RESULT 157  
BZ822645 815 bp DNA linear GSS 18-MAR-2003  
LOCUS PUFH957B ZM 0.6.1.0 KB Zea mays genomic clone ZMBRta317p22,  
DEFINITION genomic survey sequence.

ACCESSION B2822645  
 VERSION B2822645.1 GI:29038301  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 815)  
 WhiteJaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Frazer,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennerzen,J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Other\_GSSs: PUFH95TD  
 Contact: Cathy WhiteJaw

TITLE JOURNAL  
 COMMENT

FEATURES  
 source  
 1. 815  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBTA317P2"  
 /clone\_1lb="ZM\_0.6.1.0 KB"  
 /note="Vector: pCR4-TORO; Site\_1: EcoRI; 0.6-1.0 kb high  
 Cor selected genomic DNA library"

ORIGIN  
 Query Match 70.0%; Score 14; DB 8; Length 815;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACTACTCTC 20  
 |||||  
 664 ACCCAACTACTCTC 651

Db

RESULT 158  
 LOCUS CG459141  
 DEFINITION CG459141 827 bp DNA linear GSS 17-SEP-2003  
 genomic survey sequence.  
 ACCESSION CG459141  
 VERSION CG459141.1 GI:3484141  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 827)  
 WhiteJaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Frazer,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennerzen,J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Contact: Cathy WhiteJaw

TITLE JOURNAL  
 COMMENT

FEATURES  
 source  
 1. 827  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBTA060M21"  
 /clone\_1lb="ZM\_0.6.1.0 KB"  
 /note="Vector: pCR4-TORO; Site\_1: EcoRI; 0.6-1.0 kb high  
 Cor selected genomic DNA library"

ORIGIN  
 Query Match 70.0%; Score 14; DB 9; Length 827;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCAACTACTAC 18  
 |||||  
 Db 174 CGACCAACTACTAC 187

RESULT 159  
 LOCUS CG112064  
 DEFINITION PUFN188TD ZM\_0.6.1.0 KB Zea mays genomic clone ZMMBTA0689P07,  
 genomic survey sequence.  
 ACCESSION CG112064  
 VERSION CG112064.1 GI:33995501  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 829)  
 WhiteJaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Frazer,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennerzen,J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Other\_GSSs: PUFN188TB  
 Contact: Cathy WhiteJaw

TITLE JOURNAL  
 COMMENT

FEATURES  
 source  
 1. 829  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBTA0689P07"  
 /clone\_1lb="ZM\_0.6.1.0 KB"  
 /note="Vector: pCR4-TORO; Site\_1: EcoRI; 0.6-1.0 kb high  
 Cor selected genomic DNA library"

ORIGIN  
 Query Match 70.0%; Score 14; DB 9; Length 829;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCAACTACTAC 18  
 |||||  
 Db 174 CGACCAACTACTAC 187

RESULT 160  
 LOCUS CG086099/c  
 DEFINITION PUFK169TD ZM\_0.6.1.0 KB Zea mays genomic clone ZMMBTA0670L18,  
 genomic survey sequence.  
 genomic survey sequence.

ACCESSION CG086099 GI:33968393  
 VERSION CG086099.1  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 846)  
 WhiteLAW,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Resnick,A., Frazer,C.M., Yuan,Y., San Miguel,P., Ma,J. and Benneker,J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Other GSSs: PUFRL69TB  
 Contact: Cathy WhiteLAW  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteLAW@tigr.org  
 Seq primer: TF  
 Class: sheared ends.

FEATURES  
 source  
 1..846  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="873"  
 /db\_xref="taxon:4577"  
 /clone="ZMBR0670118"  
 /clone\_1lb="2M 0.6-1.0 KB"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high Cor selected genomic DNA library"

ORIGIN  
 Query Match 70.0%; Score 14; DB 9; Length 846;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCACACTACT 19  
 |||||  
 Db 518 GACCCACACTACT 505

RESULT 161  
 CO368423 856 bp mRNA linear EST 29-JUN-2004  
 LOCUS RTK1\_40\_C05\_g1\_A029 Roots minus potassium Pinus taeda cDNA clone  
 DEFINITION RTK1\_40\_C05\_A029 5', mRNA sequence.  
 ACCESSION CO368423  
 VERSION CO368423.1 GI:49449740  
 KEYWORDS EST.  
 SOURCE Pinus taeda (loblolly pine)  
 ORGANISM Pinus taeda  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pinus.  
 1 (bases 1 to 856)  
 Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Zimmermann,C. and Dean,J.F.D.  
 An EST database from potassium-deficient loblolly pine (Pinus taeda) roots  
 Unpublished (2004)  
 Other ESTs: RTK1\_40\_C05\_b1\_A029  
 Contact: Cordonnier-Pratt MM  
 Laboratory for Genomics and Bioinformatics  
 The University of Georgia, Department of Plant Biology  
 Plant Sciences Building, Rm. 2302, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 583 0210  
 Email: mmpat@uga.edu  
 RNA prepared and library constructed by W. Walter Lorenz (School of Forest Resources, University of Georgia); plant material prepared by Craig Zimmermann (School of Forest Resources, University of

Georgia) using rooted cuttings provided by the Forest Biology Research Cooperative (FBRC) and the CLONES project at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.  
 Seq primer: JENREV (GAGGAACGCTATGAC).  
 Location/Qualifiers  
 1..856  
 /organism="Pinus taeda"  
 /mol\_type="mRNA"  
 /strain="3 CLONES"  
 /db\_xref="taxon:3352"  
 /clone="RTK1\_40\_C05\_A029"  
 /lab\_host="DH10B-T1 phage-resistant E. coli"  
 /clone\_1lb="Roots minus potassium"  
 /note="Organ: Root; Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from the roots of 1-year-old loblolly pine (Pinus taeda) cuttings that were rooted and then planted in washed sand. The rooted cuttings were maintained for 117 days (July 2003 harvest) under ambient conditions in a local greenhouse. They were kept on a weekly regimen of 0.5x nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain a 15% soil moisture content. For twenty-eight days (28 d) prior to harvesting roots for mRNA preparation, the trees received Hoagland's solution lacking potassium (K) to induce a potassium-deficiency. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts can be excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN  
 Query Match 70.0%; Score 14; DB 7; Length 856;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGCACCAACTA 17  
 |||||  
 Db 38 GGCACCAACTA 51

RESULT 162  
 CM007611/c 861 bp DNA linear GSS 23-SEP-2004  
 LOCUS ZMMLA0009F06.f ZMMLA Zea mays genomic clone ZMMLA0009F06 5',  
 DEFINITION genomic survey sequence.  
 ACCESSION CM007611  
 VERSION CM007611.1 GI:52588449  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 861)  
 Wing,R., Luo,M., Soderlund,C. and Haller,K.  
 ZMML sequences  
 Unpublished (2004)  
 Contact: Rod A. Wing  
 Arizona Genomics Institute  
 University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9395  
 Fax: 520 621 1259  
 Email: http://genome.arizona.edu  
 Plate: 0009 row: F column: 06  
 Class: BAC ends.

FEATURES  
 source  
 1..861  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"

[illegible]

RESULT	164
LOCUS	CS504784
DEFINITION	SAIL_742_G03.v1 SAIL Collection Arabidopsis thaliana genomic clone
ACCESSION	SAIL_742_G03.v1, genomic survey sequence.
VERSION	CLS04784
KEYWORDS	CLS04784..1 GI:46002104
SOURCE	GSS.
ORGANISM	Arabidopsis thaliana (thale cress)
AUTHORS	Arabidopsis thaliana Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 877)
REFERENCE	Dietrich,B., Hu,P., Bawaen,J., Ko,C., Clarke,J.D., Cotton,D., Bullis,D., Snell,J., Miguel,T., Hutcheson,D., Kimmerly,B., Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A. A high-throughput Arabidopsis reverse genetics system Plant Cell 14 (12), 2985-2994 (2002) 22356987
JOURNAL	PUBMED
COMMENT	Contact: Sessions A Applied Trait Genetics Syngenta Biotechnology Inc. 3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA Email: allen.sessions@syngenta.com ABRC Stock Number CS831179; T-DNA left border flanking sequences of Syngenta Arabidopsis insertion library (SAIL) lines are available through the Arabidopsis Biological Resource Center (ABRC). Sequences represent a pool of amplified genomic regions and not single contiguous sequences. Class: TDNA tagged. Location/Qualifiers 1..877 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /ecotype="Columbia" /db_xref="taxon:3702" /clone="SAIL_742_G03.v1" /clone_lib="SAIL_Collection" /note="T-DNA left border sequences were isolated using a modified Tail-PCR strategy"
FEATURES	
Source	
Query Match	70.0%; Score 14;. DB 9; Length 877;
Best Local Similarity	100.0%; Pred. No. 4.3e+02;
Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	4 GCGACCAACTA 17       
Db	84 GCGACCAACTA 97
RESULT	165
LOCUS	CG226100
DEFINITION	OGSDM80TC_ZM_0_7_1.5_KB Zea mays genomic clone ZMWBM8083BN15,
ACCESSION	CG226100
VERSION	CG226100.1 GI:34125988
KEYWORDS	GSS.
SOURCE	Zea mays Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 883) whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Remick,A., Frazer,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Numborg,A., Robbins,D. and Lakey,N.
REFERENCE	
AUTHORS	

TITLE Consortium for Maize Genomics  
JOURNAL Unpublished (2002)  
COMMENT Contact: Cathy WhiteIaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteIaw@tigr.org  
Seq primer: TP  
Class: sheared ends.  
Location/Qualifiers  
1. .883  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_1ib="ZMMBMA0838N15"  
/note="Vector: pBCK-; Site\_1: HindIII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

ORIGIN  
Query Match 70.0%; Score 14; DB 9; Length 883;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCCAACTACTAC 18  
|||||  
Db 93 CGACCCAACTACTAC 106

RESULT 166  
CG956406 888 bp DNA linear GSS 15-DEC-2003  
LOCUS MBEIR68TF\_mch2 Medicago truncatula genomic clone 64K16, genomic  
DEFINITION survey sequence.  
ACCESSION CG956406  
VERSION CG956406.1 GI:39872964  
KEYWORDS GSS:  
SOURCE Medicago truncatula (barrel medic)  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
Medicago.  
1 (bases 1 to 888)  
TOWN,C.D., Shetty,J., Koo,H. and Feldblum,T.F.  
AUTHORS Sequencing of BAC ends from Medicago truncatula  
JOURNAL Unpublished (2003)  
COMMENT Other\_GSSs: MBEIR68TR  
Contact: Chris Town  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
Seq primer: TGTAAACGACGCGCCACT  
Class: BAC ends.  
Location/Qualifiers  
1. .888  
/organism="Medicago truncatula"  
/mol\_type="genomic DNA"  
/cultivar="genotype A17"  
/db\_xref="taxon:3880"  
/clone\_1ib="64K16"  
/note="Vector: pBelBAC11; Site\_1: HindIII; Site\_2:  
HindIII; Cook, D.R. and Kim, D.U, unpublished"

ORIGIN  
Query Match 70.0%; Score 14; DB 9; Length 888;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCAACTACT 19  
|||||  
Db 642 GACCCAACTACT 655

RESULT 167  
BZ817219 893 bp DNA linear GSS 18-MAR-2003  
LOCUS PUFDS06TB\_ZM\_0.6.1.0\_KB\_Zea mays genomic clone ZMMBTA296A11,  
DEFINITION genomic survey sequence.  
ACCESSION BZ817219  
VERSION BZ817219.1 GI:29032041  
KEYWORDS GSS:  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 893)  
WhiteIaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
Bennetzen,J.  
REFERENCE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other\_GSSs: PUFDS06TD  
Contact: Cathy WhiteIaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteIaw@tigr.org  
Seq primer: TR  
Class: sheared ends.  
Location/Qualifiers  
1. .893  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_1ib="ZMMBTA296A11"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
cot selected genomic DNA library"

ORIGIN  
Query Match 70.0%; Score 14; DB 8; Length 893;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCCAACTACTAC 18  
|||||  
Db 164 CGACCCAACTACTAC 177

RESULT 168  
CO921238 906 bp mRNA linear EST 16-AUG-2004  
LOCUS AGENCOURT\_30432439 NIH\_ZGC\_14 Danio rerio cDNA clone IMAGE:7408909  
DEFINITION 5', mRNA sequence.  
ACCESSION CO921238  
VERSION CO921238.1 GI:51271451  
KEYWORDS EST:  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.



Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cga@db-remail.nih.gov

Tissue Procurement: John Ngai, Nancy Freeman, NIDCD  
CDNA Library Preparation: Dr. Sumio Sugano  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt BioScience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov

Plate: LLM15612 row: j column: 11  
High quality sequence start: 9  
High quality sequence stop: 695.

## FEATURES

## Source

Location/Qualifiers

1..906  
/organism="Danio rerio"

/mol\_type="mRNA"

/db\_xref="taxon:7955"

/clone="IMAGE:7408909"

/rissue\_type="olfactory epithelium"

/lab\_host="DH10B Tona"

/clone\_1lb="NTB ZGC\_14"

/note="Organ: olfactory epithelium; Vector: pME18S-FL3;  
Site 1: DraIII; Site 2: DraIII; 1st strand cDNA was primed  
with an oligo(dT) primer

[GGCGTGAAGACGCGCTATGCGCTTTTCTTTTCTTTT];  
double-stranded cDNA was ligated to a DraIII adaptor  
[GGCCUACUGG], digested and directionally cloned into  
distinct DraIII sites of the pME18S-FL3. Library was size  
selected for 1.0 kb, with a average insert size of ~1.2kb.

Library constructed by Yutaka Suzuki (University of Tokyo  
Institute of Medical Science). Custom primers recommended  
for sequencing: 5' end primer 5'-GGATGTCCTTCTCTCTA-3'  
and 3' end primer 5'-CGACCTGACCTCGACACA-3'. Note: This  
is a Zebrafish Gene Collection (ZGC) library"

## ORIGIN

## Query Match

Best Local Similarity 100.0%; Score 14; DB 7; Length 906;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## Qy

2 TCGCCACCCACAC 15

## Db

876 TCGCGACCCACAC 889

## RESULT 169

CG126612 916 bp DNA linear GSS 20-AUG-2003

LOCUS PUF5N84TD 2M\_0.6\_1.0\_KB Zea mays genomic clone ZMMB7A0723M24,  
DEFINITION genomic survey sequence.

## ACCESSION

CG126612

## VERSION

CG126612.1 GI:34010049

## KEYWORDS

GSS.

## SOURCE

Zea mays

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.

## REFERENCE

White, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,  
Bennett, A., Frazer, C.M., Yuan, Y., San Miguel, P., Ma, J., and

## AUTHORS

Bennett, J.

## TITLE

Maize Genomics Consortium

## JOURNAL

Unpublished (2003)

## COMMENT

Other GSSs: PUF5N84TB  
Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org

Seq primer: TF  
Class: sheared ends.  
Location/Qualifiers

## FEATURES

## Source

1..916

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone="ZMMB7A0723M24"

/clone\_1lb="2M\_0.6\_1.0\_KB"

/note="Vector: pCR4-TOP0; Site 1: EcoRI; 0.6-1.0 kb high  
cor selected genomic DNA library"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 916;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## Qy

7 ACCCACTACTCTC 20

## Db

785 ACCCACTACTCTC 772

## RESULT 170

CG388749 929 bp DNA linear GSS 27-AUG-2003

LOCUS ZMMB0569P17f ZMMB0C Zea mays genomic clone ZMMB0C0569P17 5',  
DEFINITION genomic survey sequence.

## ACCESSION

CG388749

## VERSION

CG388749.1 GI:34307901

## KEYWORDS

GSS.

## SOURCE

Zea mays

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.

## REFERENCE

1 (bases 1 to 929)  
Bharti, A.K., Young, S., Kavchok, S., Keiser, G., Bronzino, A.C.,  
Rouzaud, K., Fu, G., Yu, Y., Wing, R., and Messing, J.  
Sequencing of the maize genome at PGR (2003b)

## AUTHORS

Contact: Bharti, A.K.

## JOURNAL

Unpublished (2003)

## COMMENT

Dr. Joachim Messing's lab  
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
University  
190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
Tel: 732 445 3801  
Fax: 732 445 5735  
Email: bharti@waksman.rutgers.edu

## Seq primer: T7

Class: BAC ends  
High quality sequence start: 51.

## Location/Qualifiers

1..929

## /organism="Zea mays"

/mol\_type="genomic DNA"

## /cultivar="B73"

/db\_xref="taxon:4577"

## /clone="ZMMB0C0569P17"

/lab\_host="E. coli DH10B"

## /note="Vector: pTARBAC1.3; Site\_1: BamHI; Site\_2: BamHI"

## ORIGIN

## Query Match

70.0%; Score 14; DB 9; Length 929;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## Qy

4 GCGACCCACACTA 17

## Db

824 GCGACCCACACTA 811

```

RESULT 171
BU961968          930 bp      mRNA      linear      EST 21-OCT-2002
LOCUS              AGENCOURT 10617415 NIH MGC 169 Mus musculus cDNA clone
DEFINITION         IMAGE:6742628 5', mRNA sequence.
ACCESSION          BU961968
VERSION            BU961968.1 GI:24191540
KEYWORDS            EST.
SOURCE             Mus musculus (house mouse)
ORGANISM            Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 930)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Jonathan Kuo, NIMH
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LICM3080 row: P column: 19
High quality sequence, stop: 134.
Location/Qualifiers
1..930
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6742628"
/lab_host="DH10B (TI-phage-resistant)"
/clone_lib="NIH_MGC_169"
/note="Organ: Testicles; Vector: pDNR-LIB; Site 1: SfiI
(ggcatatggcc); Site 2: SfiI (ggcggcggcggc); cDNA made
by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTCGTCATCACCCAGAGTCGTCATTCAGCCCGG-3' and
5'-ATTCTAGAGGCCGAGGCGCCGACATG-dt(30)NM-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in the laboratory of M.
Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."

ORIGIN
Query Match          70.0%; Score 14; DB 5; Length 930;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
7 ACCCAACACTAC 20
|||||
826 ACCCAACACTAC 839

RESULT 172
BZ817225          937 bp      DNA      linear      GSS 18-MAR-2003
LOCUS              BZ817225/c
DEFINITION         genomic survey sequence.
ACCESSION          BZ817225
VERSION            BZ817225.1 GI:29032047
KEYWORDS            GSS.
SOURCE             Zee mays
ORGANISM            Zee mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
1 (bases 1 to 937)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.

```

```

TITLE             Maize Genomics Consortium
JOURNAL            Unpublished (2003)
COMMENT            Other GSSs: PUFDS06TB
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: sheared ends.
Location/Qualifiers
1..937
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM061000"
/clone_lib="ZM061000"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

ORIGIN
Query Match          70.0%; Score 14; DB 8; Length 937;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
5 CGACCACACTAC 18
|||||
886 CGACCACACTAC 873

RESULT 173
AG602080          944 bp      DNA      linear      GSS 05-JUN-2004
LOCUS              AG602080/c
DEFINITION         Mus musculus molossinus DNA, clone:MSMG01-534G02.TU, genomic survey
sequence.
ACCESSION          AG602080
VERSION            AG602080.1 GI:48362910
KEYWORDS            GSS.
SOURCE             Mus musculus molossinus
ORGANISM            Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
BAC end Sequences of Library MSMG01
Unpublished
2 (bases 1 to 944)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
Submitted (17-NOV-2003) Maabira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsukuba, Ibaraki, Japan
(E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the mouse BAC library MSMG01. For BAC
library availability, please contact Kunita Aoe (abe@tc.riken.jp).
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@tc.riken.jp
PRIMERS
Sequencing : TU
LIBRARY
Vector : PBAC3.6
R Site 1 : EcoRI
R Site 2 : EcoRI.
Location/Qualifiers
1..944
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"

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/sub\_species="molossinus"  
/db\_xref="taxon:57486"  
/clone="MSMg01-534602.TJ"  
/sex="male"  
/tissue\_type="mixture of kidney and spleen"  
/clone\_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 944;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 ACCCACTACTCTC 20  
|||||  
669 ACCCACTACTCTC 656

RESULT 174  
CG056404 948 bp DNA linear GSS 19-AUG-2003  
LOCUS PUFV68TD ZM\_0.6.1.0\_KB Zea mays genomic clone ZMMB7a0742L16,  
DEFINITION genomic survey sequence.  
ACCESSION CG056404  
VERSION CG056404.1 GI:33928584  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 948)  
Whiteaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
Reinick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
Benneken,J.  
Maize Genomics Consortium  
Unpublished (2003)  
Other GSSs: PUFV68TB  
Contact: Cathy Whiteaw  
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteaw@tigr.org  
Seq primer: TP  
Class: sheared ends.  
Location/Qualifiers  
1..948  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4577"  
/clone="ZMMB7a0742L16"  
/clone\_lib="ZM\_0.6.1.0\_KB"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high  
cor selected genomic DNA library"

ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 948;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 ACCCACTACTCTC 20  
|||||  
911 ACCCACTACTCTC 924

RESULT 175  
BE957748 952 bp mRNA linear EST 14-DEC-2000  
LOCUS BE957748  
DEFINITION 601655861R2 NIH\_MGC\_55 Homo sapiens cDNA clone IMAGE:3838934 3',  
mRNA sequence.  
ACCESSION BE957748  
VERSION BE957748.2 GI:11774319

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 952)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
On Oct 3, 2000 this sequence version replaced gi:10568453.  
Contact: Robert Strauberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
plate: LICM526 row: 1 column: 15  
High quality sequence stop: 4.  
Location/Qualifiers  
1..952  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3838934"  
/tissue\_type="from acute myelogenous leukemia"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH MGC 55"  
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);  
Site 1: SfiI (ggccgctggc); Site 2: SfiI  
(ggccatcggc); Double-stranded cDNA was prepared from  
cell line RNA. 5' and 3' adaptors were used in cloning as  
follows: 5' adaptor sequence: 5'-CACGCCATTATGGC-3' and  
3' adaptor sequence:  
5'-ATTAGAGCGCGCGCGCATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T) Average insert size  
1.65 kb (range 0.9-4.0 kb). 14/15 clones contained  
inserts by PCR. This library was enriched for full-length  
clones and was constructed by Clontech Laboratories (Palo  
Alto, CA)."

ORIGIN

Query Match 70.0%; Score 14; DB 2; Length 952;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGCGACCGACCA 14  
|||||  
918 TTGGCGACCGACCA 931

RESULT 176  
CG218509 955 bp DNA linear GSS 22-AUG-2003  
LOCUS OGMKR46TV ZM\_0.7.1.5\_KB Zea mays genomic clone ZMMB7a0610G20,  
genomic survey sequence.  
ACCESSION CG218509  
VERSION CG218509.1 GI:34118397  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 955)  
Whiteaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,  
Reinick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,  
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other GSSs: OGMKR46TH

Contact: Cathy Whitelaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitelaw@tigr.org  
 Seq primer: TR  
 Class: sheared ends.  
 Location/Qualifiers  
 source  
 1..955  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone\_1lb="ZM 0.7-1.5 KB"  
 /note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb  
 methylation filtered genomic DNA library"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 955;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACACTACTC 20  
 |||||  
 Db 253 ACCCAACACTACTC 240

RESULT 177  
 LOCUS CG126611 965 bp DNA linear GSS 20-AUG-2003  
 DEFINITION genomic survey sequence.  
 CG126611  
 CG126611 GI:34010048  
 GSS.  
 SOURCE  
 ORGANISM  
 Zea mays  
 Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 1 (bases 1 to 965)  
 WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,  
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Bennetzen,J.  
 Maize Genomics Consortium  
 Unpublished (2003)  
 Other GSSs: PUF5N84TD  
 Contact: Cathy Whitelaw  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitelaw@tigr.org  
 Seq primer: TR  
 Class: sheared ends.  
 Location/Qualifiers  
 source  
 1..965  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone\_1lb="ZM 0.6-1.0 KB"  
 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
 cot selected genomic DNA library"

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

FEATURES  
 source

ORIGIN  
 Query Match 70.0%; Score 14; DB 9; Length 965;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACACTACTC 20  
 |||||  
 Db 471 ACCCAACACTACTC 484

RESULT 178  
 LOCUS BZ463975/c 974 bp DNA linear GSS 13-DEC-2002  
 DEFINITION BONGK66TR BO 1.6-2 KB lot Brassica oleracea genomic clone BONGK66,  
 genomic survey sequence.  
 BZ463975  
 BZ463975 GI:26750364  
 GSS.  
 SOURCE  
 ORGANISM  
 Brassica oleracea  
 Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 974)  
 Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.  
 Whole genome shotgun sequencing of Brassica oleracea  
 Unpublished (2001)  
 Other GSSs: BONGK66TF  
 Contact: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TR  
 Class: sheared ends.  
 Location/Qualifiers  
 source  
 1..974  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /strain="TO1000DH3"  
 /db\_xref="taxon:3712"  
 /clone\_1lb="BO 1.6-2 KB lot"  
 /note="Vector: pHO51; Site 1: BclXI; 1.6-2 kb sheared  
 total DNA inserted into pHO51 using BclXI linkers"

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Query Match 70.0%; Score 14; DB 8; Length 974;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCACACA 14  
 |||||  
 Db 479 TTCCGACCCACACA 466

RESULT 179  
 LOCUS BY1717843/c 975 bp mRNA linear EST 17-DEC-2002  
 DEFINITION BY1717843 RIKEN full-length enriched, adult male thymus Mus musculus  
 CDNA clone 5830427D03 5', mRNA sequence.  
 BY1717843  
 BY1717843 GI:27130960  
 EST.  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 975)  
 Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,  
 Nikaido,I., Oseko,N., Saito,R., Suzuki,H., Yamanka,I.,  
 Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,  
 Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,  
 Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,  
 Batalov,S., Beisel,K.W., Blake,J.A., Bradic,D., Brusic,V.,  
 Chochia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Giasi, C., Godzik, A., Gough, J., Grimmond, S., Gusticich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kanaaj, H., Kawasawa, Y., Kedzierzki, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglot, D.R., Matsuda, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numa, K., Okido, T., Pavan, W.J., Perera, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wanstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Zimin, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Waki, J., Aizawa, K., Aizawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shindawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)

22354683  
 12466851

**TITLE**  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Shuhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216

**JOURNAL MEDLINE PUBMED**  
 22354683  
 12466851

**COMMENT**  
 Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/  
 Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carrincci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watanabe, K., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

# FEATURES

**source**  
 1. 975  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="5830427D03"  
 /sex="male"  
 /tissue\_type="thymus"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_1ib="RIKEN full-length enriched, adult male thymus"  
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia"

# FEATURES

**source**

**ORIGIN**  
 Query Match 70.0%; Score 14; DB 6; Length 975;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Db**  
 7 ACCGACACTACTC 20  
 863 ACCGACACTACTC 850

**RESULT 180**  
 CK272536 976 bp mRNA linear EST 03-AUG-2004  
 EST718614 potato abiotic stress cDNA library Solanum tuberosum cDNA  
 clone POAD580 5' end, mRNA sequence.

**DEFINITION**  
 CK272536  
 CK272536.1 GI:39829514

**ACCESSION**  
 CK272536  
 CK272536.1 GI:39829514

**VERSION**  
 EST

**KEYWORDS**  
 Solanum tuberosum (potato)  
 Solanum tuberosum  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.

**SOURCE**  
 Solanum tuberosum (potato)  
 EST

**ORGANISM**  
 Solanum tuberosum (potato)  
 EST

**REFERENCE**  
 1 (bases 1 to 976)  
 Buell, C.R., Hart, A., Zismann, V., Karanicheva, S.A. and Baker, B.  
 Generation of ESTs from abiotic stressed potato tissue  
 Unpublished (2003)  
 Other ESTs: EST18615

**AUTHORS**  
 Contact: Robin Buell  
 The Institute for Genomic Research  
 9712 Medical Center Dr. Rockville, MD 20850, USA  
 Email: potato-array@tigr.org  
 Clones can be requested from the University of Arizona Genomics Institute via http://genome.arizona.edu/orders/  
 Seq primer: ATT TAG GTG ACA CTA TAG.

**TITLE**  
 Other ESTs: EST18615

**JOURNAL**  
 Unpublished (2003)

**COMMENT**  
 Location/Qualifiers  
 1. 976  
 /organism="Solanum tuberosum"  
 /mol\_type="mRNA"  
 /cultivar="Kennebec"  
 /db\_xref="taxon:4113"  
 /clone="POAD580"  
 /tissue\_type="abiotic stress treated leaf and root tissue"  
 /lab\_host="DH10B-Tona"  
 /clone\_1ib="potato abiotic stress cDNA library"  
 /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: Solanum tuberosum var. Kennebec plants were grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at 6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d. Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after

cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 976;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCAACTACT 19  
Db 68 GACCCAACTACT 55

## RESULT 181

CG086097 976 bp DNA linear GSS 20-AUG-2003  
LOCUS PUPK1697B\_ZM\_0.6\_1.0\_KB\_Zea\_mays\_genomic\_clone\_ZMBH0670L18,  
DEFINITION genomic survey sequence.

ACCESSION CG086097  
VERSION CG086097.1 GI:33968391  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD 1 (bases 1 to 976)

AUTHORS White, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennett, J.

TITLE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other GSSs: PUPK1697D  
Contact: Cathy Whitelaw

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TR  
Class: sheared ends.

FEATURES  
source location/Qualifiers  
1..976

/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMBH0670L18"  
/clone\_1b="ZM\_0.6\_1.0\_KB"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; 0.6-1.0 kb high  
Cot selected genomic DNA library"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 976;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCAACTACT 19  
Db 811 GACCCAACTACT 824

## RESULT 182

CK406129 980 bp mRNA linear EST 05-JAN-2004  
LOCUS CK406129  
DEFINITION AUF Ifsbn 236 g1l Ictalurus furcatus spleen cDNA library Ictalurus furcatus cDNA 5', mRNA sequence.

ACCESSION CK406129  
VERSION CK406129.1 GI:40565632  
KEYWORDS EST.  
SOURCE Ictalurus furcatus  
ORGANISM Ictalurus furcatus

REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes; Ictaluridae; Ictalurus.  
1 (bases 1 to 980)

AUTHORS Liu, Z., Li, P., Liu, L., He, C., Kucuktas, H., Feng, J., Chen, L., Peatman, E., Baoprasertkul, P., Simmons, M., Muir, W., Grizzle, J., Dunham, R. and Brady, Y.  
30,000 new catfish ESTs: new resources for functional analysis of genes involved in aquaculture performance traits  
Unpublished (2004)  
Contact: Liu ZD

JOURNAL The Fish Molecular Genetics and Biotechnology Laboratory, Department of Fisheries and Allied Aquacultures and Program of Cell and Molecular Biosciences  
Auburn University  
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA  
Tel: 334 844 4054  
Fax: 334 844 9208  
Email: zliu@acesag.auburn.edu  
Seq primer: T7.

FEATURES  
source location/Qualifiers  
1..980

/organism="Ictalurus furcatus"  
/mol\_type="mRNA"  
/db\_xref="taxon:66913"  
/clone\_1b="Ictalurus furcatus spleen cDNA library"  
/note="Organ: Spleen; Vector: pSport1; Site\_1: NotI; Site\_2: SalI"

## ORIGIN

Query Match 70.0%; Score 14; DB 7; Length 980;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GACCCAACTACT 19  
Db 258 GACCCAACTACT 271

RESULT 183 998 bp DNA linear GSS 23-SEP-2004  
LOCUS CL986792/C  
DEFINITION ZMBH0003d24.f ZMBH Zea mays genomic clone ZMBH0003d24 5', genomic survey sequence.

ACCESSION CL986792  
VERSION CL986792.1 GI:52554870  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD 1 (bases 1 to 998)

AUTHORS Ma, J., SanMiguel, P., Liu, R., Haller, K., Soderlund, C. and Bennett, J.  
ZMBH sequences  
Unpublished (2004)  
Contact: Jeff Bennett  
Bennetzen Lab  
The University of Georgia  
Department of Genetics, C426a Life Sciences Building, Athens, GA 30602, USA  
Tel: 706-542-3698  
Fax: 706-583-0972

Email: maize@uga.edu  
 Plate: 0003 row: d column: 24  
 Class: BAC ends.

## FEATURES

## SOURCE

Location/Qualifiers  
 1. .998  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBHe0003d24"  
 /issue\_type="Immature ear"  
 /dev\_stage="6-8 weeks"  
 /lab\_host="DH10B"  
 /clone\_lib="ZMMBHe"  
 /note="Vector: TOPOpcr4; Site\_1: EcoRI; Site\_2: EcoRI"

## ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 998;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTGCGACCCACACA 14  
 Db 88 TTCCGACCCACACA 75

RESULT 184  
 BG116258 1020 bp mRNA linear EST 30-JAN-2001  
 LOCUS 602318508P1 NIH\_MGC\_88 Homo sapiens cDNA clone IMAGE:4418929 5',  
 DEFINITION mRNA sequence.

ACCESSION BG116258  
 VERSION BG116258.1 GI:12609764  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1020)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LLM10153 row: P column: 02  
 High quality sequence start: 22  
 High quality sequence stop: 257.

## FEATURES

## SOURCE

Location/Qualifiers  
 1. .1020  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4418929"  
 /issue\_type="duodenal adenocarcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_88"  
 /note="Organ: small intestine; Vector: PCMV-SPORT6;  
 Site 1: NotI; Site 2: SalI; Cloned unidirectionally;  
 oligo-dT primed. Average insert size 1.767 kb. Library  
 enriched for full-length clones and constructed by Life  
 Technologies. Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 70.0%; Score 14; DB 4; Length 1020;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCCCACTAC 18  
 Db 677 CGACCCCACTAC 690

RESULT 185  
 BQ719721 1024 bp mRNA linear EST 16-JUL-2002  
 LOCUS AGENCOURT\_8304560 lupsk1\_sym pathetic\_trunk Homo sapiens cDNA clone  
 DEFINITION IMAGE:6193778 5', mRNA sequence.  
 BQ719721  
 ACCESSION BQ719721.1 GI:21858618  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1024)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: Dr. James R. Lupski  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LLM13597 row: P column: 03  
 High quality sequence stop: 386.

## FEATURES

## SOURCE

Location/Qualifiers  
 1. .1024  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6193778"  
 /sex="male"  
 /issue\_type="sympathetic trunk"  
 /dev\_stage="adult, 16 yr"  
 /lab\_host="DH10B"  
 /clone\_lib="lupski\_sym pathetic\_trunk"  
 /note="Vector: PCMV-SPORT6 (Life Technologies); Site\_1:  
 NotI; Site 2: SalI; cDNA made by oligo-dT priming.  
 Directionally cloned using the following adaptors:  
 5'-TCGACCCGCGTCGCG-3' and  
 5'-GACTAGTCTAGATCGGACGGCCGCT(15)-3'. Size selected >  
 1 kb for average insert length 1.9 kb. This is a primary  
 library, non-amplified. Library constructed by Life  
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
 College of Medicine); available through Life  
 Technologies."

## ORIGIN

Query Match 70.0%; Score 14; DB 5; Length 1024;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCCCACTAC 18  
 Db 978 CGACCCCACTAC 991

RESULT 186  
 BZ603974 1029 bp DNA linear GSS 08-JUN-2003  
 LOCUS WHAD967r Human MCF7 breast cancer cell line library (MCF7\_1) Homo  
 DEFINITION sapiens genomic clone MCF7\_1-23023, genomic survey sequence.  
 ACCESSION BZ603974  
 VERSION BZ603974.1 GI:31512436  
 KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1029)  
Volik, S., Zhao, S., Chin, K., Brebner, J. H., Herndon, D. R., Tao, Q., Kowbel, D., Huang, G., Lapuk, A., Xue, W.-L., Magrane, G., de Jong, P., Gray, J. W., and Collins, C. Sequence-based analysis of aberrant genomes  
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)

TITLE End-sequence profiling: Sequence-based analysis of aberrant genomes

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)

MEDLINE 22709111

PUBMED 12788976

COMMENT Contact: Volik SV  
Collin Collins, lab  
UCSF Comprehensive Cancer Center  
UCSF Box 0808, San Francisco, CA 94143-0808, USA  
Tel: 415 502 7066  
Fax: 415 502 5665  
Email: svolik@cc.ucsf.edu  
This clone is available from Amplicon Express  
http://www.genomex.com  
Class: BAC ends.

FEATURES  
Location/Qualifiers  
1..1029  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="MCF7\_1-23023"  
/sex="female"  
/clone\_1id="Human MCF7 breast cancer cell line library (MCF7\_1)"  
/note="Vector: pECBAC1, Site 1: HindIII. This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."

ORIGIN  
Query Match 70.0%; Score 14; DB 8; Length 1029;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCGACACTACTC 20  
|||||  
520 ACCGACACTACTC 507

Db

RESULT 187  
CL992091/c 1032 bp DNA linear GSS 23-SEP-2004  
ZMMBHf0003f23.f ZMMBHf Zea mays genomic clone ZMMBHf0003f23 5',  
genomic survey sequence.

DEFINITION CL992091  
CL992091 Zea mays genomic clone ZMMBHf0003f23 5',  
GSS.

ACCESSION CL992091.1 GI:52560169

VERSION GSS.

KEYWORDS

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 1032)  
Ma, J., SanMiguel, P., Liu, R., Haller, K., Soderlund, C. and Bennettzen, J.  
ZMMBH sequences  
Unpublished (2004)  
Contact: Jeff Bennettzen  
Bennetzen lab  
The University of Georgia  
Department of Genetics, C426a Life Sciences Building, Athens, GA 30602, USA  
Tel: 706-542-3698  
Fax: 706-583-0972  
Email: maize@uga.edu  
Plate: 0003 row: f column: 23

TITLE Zea mays

JOURNAL

COMMENT

Class: BAC ends.

FEATURES  
Location/Qualifiers  
1..1032  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBHf0003f23"  
/tissue\_type="immature ear"  
/dev stage="6-8 weeks"  
/lab\_host="DH10B"  
/clone\_1id="ZMMBHf"  
/note="Vector: TOPopcr4, Site\_1: EcoRI, Site\_2: EcoRI"

ORIGIN  
Query Match 70.0%; Score 14; DB 9; Length 1032;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCACACA 14  
|||||  
88 TTGGGACCCACACA 75

Db

RESULT 188  
BG177123 1047 bp mRNA linear EST 06-FEB-2001  
602313372f1 NIH\_MGC\_85 Homo sapiens CDNA clone IMAGE:4419329 5',  
mRNA sequence.

DEFINITION BG177123  
BG177123 1 GI:12683826  
EST.

ACCESSION BG177123

VERSION BG177123

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 1047)  
NIH-MGC http://mgc.ncl.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: Louis Staudt, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM10154 row: p column: 18  
High quality sequence start: 4  
High quality sequence stop: 326.  
Location/Qualifiers  
1..1047  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4419329"  
/tissue\_type="lymphoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1id="NIH MGC 85"  
/note="Organ: lymph. Vector: PCMV-SPORT6, Site 1: NotI, Site 2: SalI. Cloned unidirectionally; oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC library."

ORIGIN  
Query Match 70.0%; Score 14; DB 4; Length 1047;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TCGGACCCACAC 15



```

Db          994 TCGCGACCCACAC 1007
|||||
RESULT 189
CM509808/c 1049 bp DNA linear GSS 06-OCT-2004
LOCUS ZMMBHC0001124.r ZMMBHC Zea mays genomic clone ZMMBHC0001124.3'
DEFINITION genomic survey sequence.
ACCESSION CM509808
VERSION CM509808.1 GI:53839314
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1049)
AUTHORS Ma,J., Sam Miguel,P., Liu,R., Haller,K., Soderlund,C. and
Bennetzen,J.
TITLE ZMMBHC sequences
JOURNAL Unpublished (2004)
COMMENT Contact: Jeff Bennetzen
Bennetzen Lab
The University of Georgia
Department of Genetics, C426a Life Sciences Building, Athens, GA
30602, USA
Tel: 706-542-3698
Fax: 706-583-0972
Email: maizeuga.edu
Plate: 0001 row: 1 column: 24
Class: BAC ends
FEATURES
Source
Location/Qualifiers
1..1049
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBHC0001124"
/tissue_type="Immature ear"
/dev_stage="6-8 weeks"
/lab_host="DH10B"
/clone_lib="ZMMBHC"
/notes="Vector: TOPopcr4, Site_1: EcoRI, Site_2: EcoRI"
ORIGIN
Query Match 70.0%; Score 14; DB 9; Length 1049;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTGCGACCCACACA 14
|||||
Db 88 TTGCGACCCACACA 75
|||||
RESULT 190
BE791977/c 1072 bp mRNA linear EST 20-SEP-2000
LOCUS BE791977.1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940364 5',
DEFINITION mRNA sequence.
ACCESSION BE791977
VERSION BE791977.1 GI:10213175
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1072)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov

```

```

Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: LICM790 row: k column: 21
High quality sequence stop: 737.
FEATURES
Source
Location/Qualifiers
1..1072
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3940364"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B.(phage-resistant)"
/notes="Organ: lung; Vector: pOT87; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN
Query Match 70.0%; Score 14; DB 2; Length 1072;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 ACCCAGACTACTC 20
|||||
Db 1065 ACCCAGACTACTC 1052
|||||
RESULT 191
AG071244/c 1102 bp DNA linear GSS 03-NOV-2001
LOCUS AG071244
DEFINITION Pan troglodytes DNA, clone: PTB-062G02.R, genomic survey sequence.
ACCESSION AG071244
VERSION AG071244.1 GI:16623046
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1
AUTHORS Fujiiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1102)
AUTHORS Fujiiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submision
JOURNAL Submitted (02-AUG-2001) Ageo Fujiiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Sueniyo-chou, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel:81-45-503-9111, Fax:81-45-503-9170
URL:http://hgp.gsc.riken.go.jp/
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the Rad process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY Vector : pKS145
R.site 1 : SacI
R.site 2 : SacI.
Location/Qualifiers
1..1102
FEATURES
Source

```

```

/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-062G02.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match          70.0%; Score 14; DB 9; Length 1102;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACACTACTC 20
    |||||
Db 513 ACCCAACACTACTC 500

RESULT 192
LOCUS B08792 1115 bp DNA linear GSS 14-MAY-1997
DEFINITION F3E6-T7 IGF Arabidopsis thaliana genomic clone F3E6, genomic survey
sequence.
ACCESSION B08792
VERSION B08792.1 GI:2089911
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1115)
PENG, J., DEWAR, K., BUEHLER, E., KIM, C., LI, Y., SHINN, P., SUN, H. and
ECKER, J.
BAC End Sequences at ATGC
Unpublished (1997)
Other GSSs: F3E6-5p6
Contact: Ecker J.
Arabidopsis Thaliana Genome Center
University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia, PA
19104
Tel: 215-898-9384
Fax: 215-898-8780
Email: jecker@atgenom.bio.upenn.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 78
High quality sequence stop: 973.
Location/Qualifiers
1. 1115
/mol_type="genomic DNA"
/organism="Arabidopsis thaliana"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="F3E6"
/sex="hermaphrodite"
/clone_lib="IGF"
/notes="Vector: BelobACII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"

ORIGIN
Query Match          70.0%; Score 14; DB 8; Length 1115;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCCAACACTACTC 20
    |||||
Db 547 ACCCAACACTACTC 560

RESULT 193
LOCUS CL494700 1125 bp DNA linear GSS 01-APR-2004
DEFINITION SAIL_599_G08.V1 SAIL Collection Arabidopsis thaliana genomic clone
SAIL_599_G08.V1, genomic survey sequence.
ACCESSION CL494700
VERSION CL494700.1 GI:45984532
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1125)
Sessions, A., Burke, E., Presting, G., Aux, G., McEliver, J., Paton, D.,
Dietrich, B., Ho, P., Bacwaden, J., Ko, C., Clarke, J. D., Cotton, D.,
Bullis, D., Snell, J., Miguel, T., Hutchinson, D., Kimmery, B.,
Mitxel, T., Katagiri, F., Glazebrook, J., Law, M. and Goff, S. A.
A high-throughput Arabidopsis reverse genetics system
Plant Cell 14 (12), 2985-2994 (2002)
22356987
MEDLINE
PUBMED 12468722
Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwalis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syngenta.com
ABRC Stock Number C8825573; T-DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
Class: TDNA tagged.
Location/Qualifiers
1. 1125
/mol_type="genomic DNA"
/organism="Arabidopsis thaliana"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="SAIL_599_G08.V1"
/clone_lib="SAIL_Collection"
/notes="T-DNA left border sequences were isolated using a
modified TAIL-PCR strategy"

ORIGIN
Query Match          70.0%; Score 14; DB 9; Length 1125;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCACACTACT 19
    |||||
Db 819 GACCCACACTACT 806

RESULT 194
LOCUS BU504326 1126 bp mRNA linear EST 12-SEP-2002
DEFINITION AGENCOURT 8968993 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6492135
5', mRNA sequence.
ACCESSION BU504326
VERSION BU504326.1 GI:22810559
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1126)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)

```

DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
 Plate: LNL4044 row: k column: 16  
 High quality sequence start: 106  
 High quality sequence stop: 216.

## FEATURES

## source

Location/Qualifiers

1. 1126

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGR:6492135"

/tissue\_type="retina"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_94"

/note="Organ: eye; Vector: PCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 3.3 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH\_MGC Library."

## ORIGIN

## Query Match

70.0%; Score 14; DB 5; Length 1126;

Best Local Similarity 100.0%; Pred. No. 4.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 TC6GACCCAAAC 15

408 TC6GACCCAAAC 421

## RESULT 195

## AG078906

1132 bp DNA linear GSS 03-NOV-2001

AG078906 Pan troglodytes DNA, clone: PTB-074F17.R, genomic survey sequence.

## ACCESSION

AG078906.1 GI:16630708

## VERSION

## KEYWORDS

GSS.

Pan troglodytes (chimpanzee)

## SOURCE

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

## REFERENCE

## AUTHORS

1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

BAC end sequences of library PTB

Unpublished

2 (bases 1 to 1132)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (02-ANG-2001) Ageo Fujiyama, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail: shimpbes@sc.riken.go.jp; URL: <http://hgp.gsc.riken.go.jp/>,

Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end

was generated during the R&D process and may have higher chance of

clone cracking errors.

## PRIMERS

Sequencing: M13Rev

LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI

Location/Qualifiers

1. 1132

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

/clone="PTB-074F17.R"

/sex="male"

## FEATURES

## source

/cell\_type="Tymphoblast"  
 /clone\_lib="PTB Chimpanzee Male BAC Library"

## ORIGIN

## Query Match

70.0%; Score 14; DB 9; Length 1132;

Best Local Similarity 100.0%; Pred. No. 4.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 TC6GACCCAAAC 15

873 TC6GACCCAAAC 886

## RESULT 196

## BU466931

1161 bp mRNA linear EST 30-NOV-2002

60337833F1 CSEORBN20 Gallus gallus cdna clone CHEST282a10 5', mRNA

sequence.

BU466931

BU466931.1 GI:25960508

## KEYWORDS

## SOURCE

Gallus gallus (chicken)

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 1161)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken CDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)

22335634

12445392

Contact: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1OD, UK

Tel: 01612008930

Fax: 01612360409

Email: [Simon.Hubbard@umist.ac.uk](mailto:Simon.Hubbard@umist.ac.uk).

Location/Qualifiers

1. 1161

/organism="Gallus gallus"

/mol\_type="mRNA"

/strain="layer and broiler"

/db\_xref="taxon:9031"

/clone="CHEST282a10"

/sex="Male and female"

/tissue\_type="Chondrocytes isolated from growth plate

cartilage"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="CSEORBN20"

/note="Vector: pBluescript II KS(+); Site 1: EcoRI;

Site 2: NotI. This normalized library was constructed from

1 million independent clones. cDNA synthesis was initiated

using an oligo(dT) primer, using methylated C in the first

strand synthesis reaction. Following this first strand

reaction, double-stranded cDNA was blunted, ligated to

NotI adapters, digested with EcoRI, size-selected, and

cloned into the NotI and EcoRI compatible sites of a

custom modified MCS of the pBluescript (KS+) vector. The

library was normalized in 2 rounds using conditions

adapted from Soares et al., PNAS (1994) 91: 9228-9232 and

Bonaldo et al., Genome Research 6 (1996): 791, except that

a significantly longer reannealing hybridization was

used."

## ORIGIN

## Query Match

70.0%; Score 14; DB 5; Length 1161;

Best Local Similarity 100.0%; Pred. No. 4.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCCCACTAC 18  
 DB 497 CGACCCCACTAC 510

RESULT 197  
 B2573835 1187 bp DNA linear GSS 17-DEC-2002  
 B2573835  
 LOCUS  
 DEFINITION msh2\_3383.x1 msh Pseudomonas aeruginosa genomic clone msh2\_3383,  
 genomic survey sequence.  
 ACCESSION B2573835  
 VERSION B2573835.1 GI:27208896  
 KEYWORDS GSS.  
 SOURCE Pseudomonas aeruginosa  
 ORGANISM Pseudomonas aeruginosa  
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 Pseudomonadaceae; Pseudomonas.

REFERENCE  
 1 (bases 1 to 1187)  
 Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,  
 Burns,J.L., Kaul,R. and Olsen,M.V. Whole-Genome-Sequence variation among multiple isolates of  
 Pseudomonas aeruginosa library  
 J. Bacteriol. (2002) in press  
 CONTACT: Chris K. Raymond  
 Genome Center  
 University of Washington  
 Box 352145, Seattle, WA 98105-2145, USA  
 Tel: 2062216954  
 Fax: 2066857244  
 Email: craymond@u.washington.edu  
 Class: shotgun.

FEATURES  
 source  
 1..1187  
 /organism="Pseudomonas aeruginosa"  
 /mol\_type="genomic DNA"  
 /strain="M5H"  
 /db\_xref="taxon:287"  
 /clone="msh2\_3383"  
 /clone\_1b="msh"  
 /note="Environmental isolate. Whole genomic shotgun  
 library."

ORIGIN  
 Query Match 70.0%; Score 14; DB 8; Length 1187;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACCCCACTAC 18  
 DB 1062 CGACCCCACTAC 1075

RESULT 198  
 B2571441 1260 bp mRNA linear EST 12-MAR-2002  
 B2571441  
 LOCUS  
 DEFINITION AGENCOURT 6626371 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5752888  
 5', mRNA Sequence.  
 ACCESSION B2571441  
 VERSION B2571441.1 GI:19371820  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE  
 1 (bases 1 to 1260)  
 NIH-MGC http://mgc.ncl.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgabbs@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.

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 male lung, age 27; and 1 male testis, age 69. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.8 kb,  
 insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics tracking code  
 021. Note: this is a NIH\_MGC Library."

ORIGIN  
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 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 842 TCGCGACCCACAC 855

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 CC210351  
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 DEFINITION CH261-18512\_RML.1 CH261 Gallus gallus genomic clone CH261-18512,  
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 ACCESSION CC210351  
 VERSION CC210351.1 GI:30529019  
 KEYWORDS GSS.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.

REFERENCE  
 1 (bases 1 to 1262)  
 Kremetzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,  
 Warren,W., Graves,T., Mardis,E. and Wilson,R.  
 Gallus gallus BAC End Reads  
 Unpublished (2003)  
 CONTACT: Richard K. Wilson  
 Genome Sequencing Center  
 Washington University School of Medicine  
 Email: submissions@watson.wustl.edu  
 Insert Length: 182000 Std Error: 0.00  
 Seq primer: RML TACGACTCCTATAGGGAGA  
 Class: BAC ends  
 High quality sequence start: 165  
 High quality sequence stop: 504.

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 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 998 GCGACCCGACACTA 1011

## RESULT 200

CL106095

LOCUS ISB1-46D17\_Sp6.1 ISB1 Xenopus tropicalis genomic clone ISB1-46D17, 1277 bp DNA linear GSS 05-JAN-2004

DEFINITION ISB1-46D17\_Sp6.1 ISB1 Xenopus tropicalis genomic clone ISB1-46D17, genomic survey sequence.

ACCESSION CL106095

VERSION CL106095.1 GI:40599730

KEYWORDS GSS.

SOURCE Xenopus tropicalis (western clawed frog)

ORGANISM Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 1277)  
 Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,  
 Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome

Unpublished (2003)

Contact: Richard K Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@watson.wustl.edu

Insert Length: 75000 Std Error: 0.00

Seq primer: Sp6 ATTAGGTGACACTAATAG

Class: BAC ends

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High quality sequence stop: 427.

Location/Qualifiers

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## ORIGIN

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1135 ACCCAACTACTC 1148

Search completed: April 25, 2005, 14:49:26  
 Job time : 1995.68 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: April 25, 2005, 13:09:45 ; Search time 76.3158 Seconds  
(without alignments)  
428.817 Million cell updates/sec

Title: US-08-887-505B-28

Perfect score: 20

Sequence: 1 TTCCGGACCCCACTACTC 20

Scoring table: OLIGO\_NUC

Searched: 1202784 seqs, 818138359 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database: Issued Patents NA:\*

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- 2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq:\*
- 4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq:\*
- 5: /cgn2\_6/prodata/1/ina/PCBUS\_COMB.seq:\*
- 6: /cgn2\_6/prodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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11	20 100.0	33 3	US-08-441-970-126	Sequence 126, App
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16	20 100.0	46 1	US-08-164-388-10	Sequence 10, Appl
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C 154	20	100.0	252	3	US-08-441-970-34	Sequence 34, Appl	C 227	20	100.0	289	3	US-09-677-192-20	Sequence 20, Appl
C 155	20	100.0	252	3	US-08-441-970-35	Sequence 35, Appl	C 228	20	100.0	289	3	US-09-677-192-23	Sequence 23, Appl
C 156	20	100.0	252	3	US-08-441-970-36	Sequence 36, Appl	C 229	20	100.0	289	4	US-09-402-618B-20	Sequence 20, Appl
C 157	20	100.0	252	3	US-08-441-970-37	Sequence 37, Appl	C 230	20	100.0	289	4	US-09-402-618B-23	Sequence 23, Appl
C 158	20	100.0	252	3	US-08-441-970-38	Sequence 38, Appl	C 231	20	100.0	289	4	US-09-825-574-20	Sequence 20, Appl
C 159	20	100.0	252	3	US-08-441-970-39	Sequence 39, Appl	C 232	20	100.0	289	4	US-09-825-574-23	Sequence 23, Appl
C 160	20	100.0	252	3	US-08-441-970-40	Sequence 40, Appl	C 233	20	100.0	289	4	US-09-676-768-20	Sequence 20, Appl
C 161	20	100.0	252	3	US-08-441-970-41	Sequence 41, Appl	C 234	20	100.0	289	4	US-09-676-768-23	Sequence 23, Appl
C 162	20	100.0	252	3	US-08-441-970-42	Sequence 42, Appl	C 235	20	100.0	305	1	US-08-332-616A-1	Sequence 1, Appl
C 163	20	100.0	252	3	US-08-441-970-43	Sequence 43, Appl	C 236	20	100.0	305	1	US-08-332-616A-1	Sequence 1, Appl
C 164	20	100.0	252	3	US-08-441-970-44	Sequence 44, Appl	C 237	20	100.0	308	3	US-08-444-818-108	Sequence 108, Appl
C 165	20	100.0	252	3	US-08-441-970-45	Sequence 45, Appl	C 238	20	100.0	308	3	US-08-444-818-110	Sequence 110, Appl
C 166	20	100.0	252	3	US-08-441-970-48	Sequence 48, Appl	C 239	20	100.0	308	3	US-08-444-818-110	Sequence 110, Appl
C 167	20	100.0	252	3	US-08-441-970-49	Sequence 49, Appl	C 240	20	100.0	308	3	US-08-444-818-112	Sequence 112, Appl
C 168	20	100.0	256	2	US-08-483-695-1	Sequence 1, Appl	C 241	20	100.0	308	3	US-08-444-818-114	Sequence 114, Appl
C 169	20	100.0	256	2	US-08-483-695-24	Sequence 24, Appl	C 242	20	100.0	308	3	US-08-444-818-116	Sequence 116, Appl
C 170	20	100.0	256	2	US-08-483-695-25	Sequence 25, Appl	C 243	20	100.0	308	3	US-08-444-818-118	Sequence 118, Appl
C 171	20	100.0	256	2	US-08-483-695-26	Sequence 26, Appl	C 244	20	100.0	324	2	US-08-470-426B-1	Sequence 1, Appl
C 172	20	100.0	256	2	US-07-965-285-1	Sequence 1, Appl	C 245	20	100.0	324	2	US-08-470-426B-15	Sequence 15, Appl
C 173	20	100.0	256	2	US-07-965-285-24	Sequence 24, Appl	C 246	20	100.0	337	2	US-08-756-386-56	Sequence 56, Appl









C 685	12	60.0	4115	US-09-912-161-7	Sequence 7, Appl1	C 758	12	60.0	254964	4	US-09-949-016-12583	Sequence 12583, A
C 686	12	60.0	4576	US-08-832-883-49	Sequence 49, Appl1	C 759	12	60.0	254964	4	US-09-949-016-17392	Sequence 17392, A
C 687	12	60.0	4576	US-08-832-877-49	Sequence 49, Appl1	C 760	12	60.0	265038	4	US-09-949-016-15779	Sequence 15779, A
C 688	12	60.0	4700	US-09-150-4608-9	Sequence 9, Appl1	C 761	12	60.0	321022	4	US-09-949-016-11852	Sequence 11852, A
C 689	12	60.0	4898	US-09-636-499-17	Sequence 17, Appl1	C 762	12	60.0	321022	4	US-09-949-016-14166	Sequence 14166, A
C 690	12	60.0	5438	US-08-456-2008-5	Sequence 5, Appl1	C 763	12	60.0	340380	4	US-09-949-016-15479	Sequence 15479, A
C 691	12	60.0	5521	US-08-956-1715E-408	Sequence 408, App	C 764	12	60.0	450395	4	US-09-949-016-15173	Sequence 15173, A
C 692	12	60.0	5521	US-08-781-586A-408	Sequence 408, App	C 765	12	60.0	462589	4	US-09-949-016-12900	Sequence 12900, A
C 693	12	60.0	10082	US-09-949-016-15359	Sequence 15359, A	C 766	12	60.0	476064	4	US-09-949-016-12412	Sequence 12412, A
C 694	12	60.0	11947	US-09-949-016-13414	Sequence 13414, A	C 767	12	60.0	536165	4	US-09-949-016-12412	Sequence 12412, A
C 695	12	60.0	12847	US-09-949-016-13866	Sequence 13866, A	C 768	12	60.0	1230025	4	US-09-438-1852A-1	Sequence 1, Appl1
C 696	12	60.0	135595	US-09-949-016-12529	Sequence 12529, A	C 769	12	60.0	1230230	3	US-09-103-8400A-2	Sequence 2, Appl1
C 697	12	60.0	13970	US-09-949-016-12529	Sequence 12529, A	C 770	12	60.0	4403765	3	US-09-103-8400A-2	Sequence 2, Appl1
C 698	12	60.0	20951	US-09-949-016-16690	Sequence 16690, A	C 771	12	60.0	4403765	3	US-09-103-8400A-2	Sequence 2, Appl1
C 699	12	60.0	22547	US-09-805-455-3	Sequence 3, Appl1	C 772	12	60.0	4411529	3	US-09-103-8400A-1	Sequence 1, Appl1
C 700	12	60.0	23218	US-09-949-016-13679	Sequence 13679, A	C 773	12	60.0	4411529	3	US-09-103-8400A-1	Sequence 1, Appl1
C 701	12	60.0	23218	US-09-949-016-11367	Sequence 11367, A	C 774	12	60.0	4411529	3	US-09-103-8400A-1	Sequence 1, Appl1
C 702	12	60.0	23319	US-09-949-016-13366	Sequence 13366, A	C 775	11	55.0	11	3	US-09-034-205-17	Sequence 17, Appl1
C 703	12	60.0	23417	US-09-949-016-14047	Sequence 14047, A	C 776	11	55.0	11	3	US-08-534-097A-17	Sequence 17, Appl1
C 704	12	60.0	24221	US-09-949-016-14964	Sequence 14964, A	C 777	11	55.0	11	3	US-08-651-588-17	Sequence 17, Appl1
C 705	12	60.0	24979	US-08-147-777-3	Sequence 3, Appl1	C 778	11	55.0	11	3	US-09-677-218B-17	Sequence 17, Appl1
C 706	12	60.0	24979	US-08-452-872-3	Sequence 3, Appl1	C 779	11	55.0	11	4	US-09-677-192-17	Sequence 17, Appl1
C 707	12	60.0	24979	PCT-US93-03985-3	Sequence 3, Appl1	C 780	11	55.0	11	4	US-09-625-574-17	Sequence 17, Appl1
C 708	12	60.0	26502	US-09-949-016-14585	Sequence 14585, A	C 781	11	55.0	11	4	US-09-676-768-17	Sequence 17, Appl1
C 709	12	60.0	28030	US-09-949-016-12305	Sequence 12305, A	C 782	11	55.0	12	1	US-08-685-116A-36	Sequence 36, Appl1
C 710	12	60.0	28030	US-09-949-016-16948	Sequence 16948, A	C 783	11	55.0	12	1	US-08-685-484-36	Sequence 36, Appl1
C 711	12	60.0	32068	US-09-949-016-12970	Sequence 12970, A	C 784	11	55.0	12	1	US-08-847-108-36	Sequence 36, Appl1
C 712	12	60.0	32068	US-09-949-016-12971	Sequence 12971, A	C 785	11	55.0				



c 977 11 55.0 601 4 US-09-949-016-142848 Sequence 142848,  
c 978 11 55.0 601 4 US-09-949-016-146893 Sequence 146893,  
c 979 11 55.0 601 4 US-09-949-016-146894 Sequence 146894,  
c 980 11 55.0 601 4 US-09-949-016-148707 Sequence 148707,  
c 981 11 55.0 601 4 US-09-949-016-150286 Sequence 150286,  
c 982 11 55.0 601 4 US-09-949-016-150287 Sequence 150287,  
c 983 11 55.0 601 4 US-09-949-016-151641 Sequence 151641,  
c 984 11 55.0 601 4 US-09-949-016-151642 Sequence 151642,  
c 985 11 55.0 601 4 US-09-949-016-152838 Sequence 152838,  
c 986 11 55.0 601 4 US-09-949-016-152882 Sequence 152882,  
c 987 11 55.0 601 4 US-09-949-016-159966 Sequence 159966,  
c 988 11 55.0 601 4 US-09-949-016-159974 Sequence 159974,  
c 989 11 55.0 601 4 US-09-949-016-161602 Sequence 161602,  
c 990 11 55.0 601 4 US-09-949-016-165862 Sequence 165862,  
c 991 11 55.0 601 4 US-09-949-016-167050 Sequence 167050,  
c 992 11 55.0 601 4 US-09-949-016-169379 Sequence 169379,  
c 993 11 55.0 601 4 US-09-949-016-169380 Sequence 169380,  
c 994 11 55.0 601 4 US-09-949-016-176033 Sequence 176033,  
c 995 11 55.0 601 4 US-09-949-016-176565 Sequence 176565,  
c 996 11 55.0 601 4 US-09-949-016-179675 Sequence 179675,  
c 997 11 55.0 601 4 US-09-949-016-179676 Sequence 179676,  
c 998 11 55.0 601 4 US-09-949-016-180761 Sequence 180761,  
c 999 11 55.0 601 4 US-09-949-016-180762 Sequence 180762,  
c1000 11 55.0 601 4 US-09-949-001-812 Sequence 812, App

## ALIGNMENTS

RESULT 1  
US-09-493-353-13

Sequence 13, Application US/09493353  
Patent No. 6638714  
GENERAL INFORMATION:  
APPLICANT: Johnson & Johnson  
APPLICANT: Linmen, J.M.  
APPLICANT: Gorman, K.M.  
TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS FOR EFFICIENT  
DETECTION OF HEPATITIS C VIRUS (HCV) AND METHODS OF USE  
TITLE OF INVENTION: THEROP  
FILE REFERENCE: 2094/1E286-US1  
CURRENT APPLICATION NUMBER: US/09/493,353  
CURRENT FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/118,497  
PRIOR FILING DATE: 1999-02-03  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 13  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide primer  
US-09-493-353-13

Query Match 100.0%; Score 20; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCAACTACTC 20  
Db 2 TTGGGACCCCAACTACTC 21

RESULT 2  
US-08-648-272-21/c  
Sequence 21, Application US/08648272  
Patent No. 6107028  
GENERAL INFORMATION:  
APPLICANT: Kay, Mark A.  
APPLICANT: Lieber, Andre  
TITLE OF INVENTION: Ribozymes for Treating Hepatitis C  
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/648,272  
FILING DATE: 15-MAY-1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/534,220  
FILING DATE: 11-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/476,257  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/357,508  
FILING DATE: 14-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-WR 2106  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-648-272-21

Query Match 100.0%; Score 20; DB 3; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCAACTACTC 20  
Db 24 TTGGGACCCCAACTACTC 5

RESULT 3  
US-09-494-332A-12  
Sequence 12, Application US/09494332A  
Patent No. 6623919  
GENERAL INFORMATION:  
APPLICANT: GORMAN, Kevin  
APPLICANT: PATTERSON, David  
APPLICANT: LINMEN, Jeffrey  
APPLICANT: SONG, Kening  
TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS FOR EFFICIENT MULTIPLEX DETECTION OF HEP  
FILE REFERENCE: 2049/1E285-US1  
CURRENT APPLICATION NUMBER: US/09/494,332A  
CURRENT FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: US 60/118,498  
PRIOR FILING DATE: 1999-02-03  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Version 3.0  
SEQ ID NO 12  
LENGTH: 27  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide primer

US-09-494-332A-12

Query Match 100.0%; Score 20; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCACTACTC 20  
Db 4 TTGGGACCCCACTACTC 23

RESULT 4

US-09-493-353-12

Sequence 12, Application US/09493353  
Patent No. 6638714  
GENERAL INFORMATION:  
APPLICANT: Johnson & Johnson  
APPLICANT: Limmen, J.M.  
APPLICANT: Gorman, K.M.  
TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS FOR EFFICIENT  
DETECTION OF HEPATITIS C VIRUS (HCV) AND METHODS OF USE  
FILE REFERENCE: 2094/1E286-US1  
CURRENT APPLICATION NUMBER: US/09/493,353  
PRIORITY FILING DATE: 2000-01-28  
PRIORITY APPLICATION NUMBER: 60/118,497  
PRIORITY FILING DATE: 1999-02-03  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 12  
LENGTH: 27  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide primer  
US-09-493-353-12

Query Match 100.0%; Score 20; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCACTACTC 20  
Db 4 TTGGGACCCCACTACTC 23

RESULT 5

US-08-438-639-50

Sequence 50, Application US/08438639  
Patent No. 5712383  
GENERAL INFORMATION:  
APPLICANT: Sheridan, Patrick  
APPLICANT: Chang, Chu-An  
APPLICANT: Running, Joyce  
APPLICANT: Urdea, Michael S.  
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING NUCLEIC ACID  
TITLE OF INVENTION: PROBES ON POLYSTYRENE SURFACES  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION - R440  
STREET: P.O. Box 8097  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438,639  
FILING DATE: 10-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/813,338  
FILING DATE: 23-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Kenneth, M.  
REGISTRATION NUMBER: 34,174  
REFERENCE/DOCKET NUMBER: 0232.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2719  
TELEFAX: (510) 655-3542  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-438-639-50

Query Match 100.0%; Score 20; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCACTACTC 20  
Db 10 TTGGGACCCCACTACTC 29

RESULT 6

US-07-813-338A-50

Sequence 50, Application US/07813338A  
Patent No. 5747244  
GENERAL INFORMATION:  
APPLICANT: Sheridan, Patrick  
APPLICANT: Chang, Chu-An  
APPLICANT: Running, Joyce  
APPLICANT: Urdea, Michael S.  
TITLE OF INVENTION: PROCESS FOR IMMOBILIZING NUCLEIC ACID  
TITLE OF INVENTION: PROBES ON POLYSTYRENE SURFACES  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION - R440  
STREET: P.O. Box 8097  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/813,338A  
FILING DATE: 23-DEC-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Kenneth, M.  
REGISTRATION NUMBER: 34,174  
REFERENCE/DOCKET NUMBER: 0232.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2719  
TELEFAX: (510) 655-3542  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-813-338A-50



Query Match 100.0%; Score 20; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACTACTC 20  
10 TTGCGAGCCCAACTACTC 29

Db

RESULT 7  
US-08-470-124-60

Sequence 60, Application US/08470124  
Patent No. 5849481

GENERAL INFORMATION:

APPLICANT: Urdea, Michael S.

APPLICANT: Horn, Thomas

APPLICANT: Chang, Chu-An

APPLICANT: Warner, Brian

APPLICANT: Fultz, Timothy J.

TITLE OF INVENTION: LARGE COM-TYPE BRANCHED

TITLE OF INVENTION: POLYNUCLEOTIDES

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Morrison & Foerster

STREET: 545 Middlefield Road, Suite 200

CITY: Menlo Park

STATE: California

COUNTRY: USA

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470.124

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/813,588

FILING DATE: 23 December 1991

ATTORNEY/AGENT INFORMATION:

NAME: Ciotli, Thomas E.

REGISTRATION NUMBER: 21,013

REFERENCE/DOCKET NUMBER: 22300-20104.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-813-5600

TELEFAX: 415-327-2951

TELEX: 706141

INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-470-124-60

Query Match 100.0%; Score 20; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACTACTC 20  
10 TTGCGAGCCCAACTACTC 29

Db

RESULT 8  
US-08-441-971-126

Sequence 126, Application US/08441971  
Patent No. 6071693

GENERAL INFORMATION:

APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS Version 3.3

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,971

FILING DATE: 16-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/221,653

FILING DATE:

APPLICATION NUMBER: US/07/881,528

FILING DATE:

APPLICATION NUMBER: 07/697,326

FILING DATE: 8 May 1991

ATTORNEY/AGENT INFORMATION:

NAME: Janluk, Anthony J.

REGISTRATION NUMBER: 29,809

REFERENCE/DOCKET NUMBER: C0772/7000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 720-3500

TELEFAX: (617) 720-2441

TELEX: EZEKIEL

INFORMATION FOR SEQ ID NO: 126:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-441-971-126

Query Match 100.0%; Score 20; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACTACTC 20  
10 TTGCGAGCCCAACTACTC 29

Db

RESULT 9  
US-08-221-653-126

Sequence 126, Application US/08221653  
Patent No. 6190864

GENERAL INFORMATION:

APPLICANT: Tai-An Cha

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS Version 3.3

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:



APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 126:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-221-653-126

Query Match 100.0%; Score 20; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
DB 10 TTGCGACCCCAACTACTC 29

RESULT 10  
US-08-442-144A-126  
Sequence 126, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439

TELEX:  
INFORMATION FOR SEQ ID NO: 126:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
US-08-442-144A-126

Query Match 100.0%; Score 20; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
DB 10 TTGCGACCCCAACTACTC 29

RESULT 11  
US-08-441-970-126  
Sequence 126, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 126:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-441-970-126

Query Match 100.0%; Score 20; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCAACTACTC 20  
DB 10 TTGCGACCCCAACTACTC 29

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RESULT 12
US-09-358-972-181/C
; Sequence 181, Application US/09358972
; Patent No. 6235480
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lieppe, Donna
; APPLICANT: Mandrekas, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: Pro-103 6868/75528
; CURRENT APPLICATION NUMBER: US/09/358, 972
; CURRENT FILING DATE: 1999-07-22
; EARLIER APPLICATION NUMBER: 09/252, 436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042, 287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 181
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; OTHER INFORMATION: probe for Hepatitis C
US-09-358-972-181

Query Match          100.0%; Score 20; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTGGGACCCCAACTACTC 20
Db      29 TTGGGACCCCAACTACTC 10

RESULT 13
US-09-406-147-43/C
; Sequence 43, Application US/09406147
; Patent No. 6270974
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K
; APPLICANT: Lieppe, Donna
; APPLICANT: Mandrekas, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B
; APPLICANT: Andrews, Christine A
; APPLICANT: Hartnett, James R
; APPLICANT: Gu, Trent
; APPLICANT: Wood, Keith V
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: EXOGENOUS NUCLEIC ACID DETECTION
; FILE REFERENCE: EXOGENOUS NUCLEIC ACID DETECTION
; CURRENT APPLICATION NUMBER: US/09/406, 147
; CURRENT FILING DATE: 1999-09-27
; EARLIER APPLICATION NUMBER: 09/352, 436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042, 287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
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; LENGTH: 40
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-406-147-43

Query Match          100.0%; Score 20; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTGGGACCCCAACTACTC 20
Db      29 TTGGGACCCCAACTACTC 10

RESULT 14
US-09-790-417-181/C
; Sequence 181, Application US/09790417
; Patent No. 6730479
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lieppe, Donna
; APPLICANT: Mandrekas, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: Pro-103 6868/75528
; CURRENT APPLICATION NUMBER: US/09/790, 417
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/358, 972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/042, 287
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 181
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; OTHER INFORMATION: probe for Hepatitis C
US-09-790-417-181

Query Match          100.0%; Score 20; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTGGGACCCCAACTACTC 20
Db      29 TTGGGACCCCAACTACTC 10

RESULT 15
US-08-429-181-10
; Sequence 10, Application US/08429181
; Patent No. 5635352
; GENERAL INFORMATION:
; APPLICANT: URDEA, MICHAEL S.
; APPLICANT: FULTZ, TIMOTHY
; APPLICANT: WARNER, BRIAN D.
; APPLICANT: COLLINS, MARK
; TITLE OF INVENTION: SOLUTION PHASE NUCLEIC ACID SANDWICH
; TITLE OF INVENTION: ASSAYS HAVING REDUCED BACKGROUND NOISE
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION - INTELLECTUAL PROPERTY
; ADDRESS: R440
```

STREET: 4560 HORTON STREET  
CITY: EMERYVILLE  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/429,181  
FILING DATE: 26-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/164,388  
FILING DATE: 08-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: GOLDMAN, KENNETH M.  
REGISTRATION NUMBER: 34,174  
REFERENCE/DOCKET NUMBER: 0300.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2719  
TELEFAX: (510) 655-3542  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-429-181-10

Query Match 100.0%; Score 20; DB 1; Length 46;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
Db 10 TTCCGACCCCACTACTC 29

RESULT 16  
US-08-164-388-10  
Sequence 10, Application US/08164388  
Patent No. 5681697  
GENERAL INFORMATION:  
APPLICANT: URDEA, MICHAEL S.  
APPLICANT: FILITZ, TIMOTHY  
APPLICANT: WARNER, BRIAN D.  
APPLICANT: COLLINS, MARK  
TITLE OF INVENTION: SOLUTION PHASE NUCLEIC ACID SANDWICH  
TITLE OF INVENTION: ASSAYS HAVING REDUCED BACKGROUND NOISE  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CHIRON CORPORATION - INTELLECTUAL PROPERTY  
ADDRESS: R440  
STREET: 4560 HORTON STREET  
CITY: EMERYVILLE  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/164,388  
FILING DATE: 08-DEC-1993  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:

NAME: GOLDMAN, KENNETH M.  
REGISTRATION NUMBER: 34,174  
REFERENCE/DOCKET NUMBER: 0300.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2719  
TELEFAX: (510) 655-3542  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 46 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-164-388-10

Query Match 100.0%; Score 20; DB 1; Length 46;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
Db 10 TTCCGACCCCACTACTC 29

RESULT 17  
US-09-798-641-31  
Sequence 31, Application US/09798641  
Patent No. RE38442  
GENERAL INFORMATION:  
APPLICANT: Zhang, David Y., Brandwein, Margaret  
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:  
HYBRIDIZATION SIGNAL AMPLIFICATION METHOD (HSAM)  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10112-0228  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASEQ Version #1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/798,641  
FILING DATE: 02-Mar-2001  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/690,495  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacLeod, Janet M.  
REGISTRATION NUMBER: 35,263  
REFERENCE/DOCKET NUMBER: 29545-A-PCT/USA-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-408-2597  
TELEFAX: 212-765-2519  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1..108  
SEQUENCE DESCRIPTION: SEQ ID NO: 31;  
US-09-798-641-31

Query Match 100.0%; Score 20; DB 1; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 4 TTGGGACCCCAACTACTC 23

## RESULT 18

US-08-690-495-31  
; Sequence 31, Application US/08690495  
; Patent No. 5876924

GENERAL INFORMATION:  
APPLICANT: Zhang, David Y., Brandwein, Margaret  
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:  
TITLE OF INVENTION: HYBRIDIZATION SIGNAL AMPLIFICATION METHOD (HSAM)  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Brumbaugh, Graves, Donohue & Raymond  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10112-0228

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASSEQ Version #1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/690,495  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Macleod, Janet M.  
REGISTRATION NUMBER: 35,263  
REFERENCE/DOCKET NUMBER: 29545-A-PCT/USA-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-408-2597  
TELEFAX: 212-765-2519  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..108  
US-08-690-495-31

Query Match 100.0%; Score 20; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 4 TTGGGACCCCAACTACTC 23

RESULT 19  
US-08-690-494-31  
; Sequence 31, Application US/08690494  
; Patent No. 5942391

GENERAL INFORMATION:  
APPLICANT: Zhang, David Y., Brandwein, Margaret  
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:  
TITLE OF INVENTION: HYBRIDIZATION SIGNAL AMPLIFICATION METHOD (HSAM)  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Brumbaugh, Graves, Donohue & Raymond

STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10112-0228

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASSEQ Version #1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/690,494  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Macleod, Janet M.  
REGISTRATION NUMBER: 35,263  
REFERENCE/DOCKET NUMBER: 29545-A-PCT/USA-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-408-2597  
TELEFAX: 212-765-2519  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..108  
US-08-690-494-31

Query Match 100.0%; Score 20; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 4 TTGGGACCCCAACTACTC 23

## RESULT 20

US-09-299-217-31  
; Sequence 31, Application US/09299217  
; Patent No. 6569647

GENERAL INFORMATION:  
APPLICANT: Zhang, David Y., Brandwein, Margaret  
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:  
TITLE OF INVENTION: HYBRIDIZATION SIGNAL AMPLIFICATION METHOD (HSAM)  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Brumbaugh, Graves, Donohue & Raymond  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10112-0228

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASSEQ Version #1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/299,217  
FILING DATE: 23-Apr-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/690,494  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Macleod, Janet M.  
REGISTRATION NUMBER: 35,263

REFERENCE/DOCKET NUMBER: 29545-A-PCT/USA-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-408-2597  
TELEFAX: 212-765-2519  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..108  
US-09-299-217-31  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
Query Match 100.0%; Score 20; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGGACCCCAACTACTC 20  
DB 4 TTGGGACCCCAACTACTC 23  
RESULT 21  
US-09-728-265-31  
Sequence 31, Application US/09728265  
Patent No. 6593086  
GENERAL INFORMATION:  
APPLICANT: Zhang, David Y.  
TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD.  
TITLE OF INVENTION: RAMIFICATION-EXTENSION AMPLIFICATION METHOD (RAM)  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Stroock & Stroock & Lavan  
STREET: 180 Maiden Lane  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10038  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PCDOS/MSDOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/728,265  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pokocilow, Steven B  
REGISTRATION NUMBER: 26,405  
REFERENCE/DOCKET NUMBER: Old 29545A/PCT/USA-B // New 251305/0018  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212806-6663  
TELEFAX: 2128066006  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..108  
US-09-728-265-31  
Query Match 100.0%; Score 20; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 4 TTGGGACCCCAACTACTC 23  
RESULT 22  
PCT-US95-07671-31  
Sequence 31, Application PC/TUS9507671  
GENERAL INFORMATION:  
APPLICANT: Zhang, David Y.  
TITLE OF INVENTION: LIGATION-DEPENDENT AMPLIFICATION FOR THE  
TITLE OF INVENTION: DETECTION OF INFECTIOUS PATHOGENS AND ABNORMAL GENES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10112-0228  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/07671  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Seide, Rochelle K  
REGISTRATION NUMBER: 32,300  
REFERENCE/DOCKET NUMBER: 29545-A-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-408-2626  
TELEFAX: 212-765-2519  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..108  
PCT-US95-07671-31  
Query Match 100.0%; Score 20; DB 5; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGGACCCCAACTACTC 20  
DB 4 TTGGGACCCCAACTACTC 23  
RESULT 23  
US-08-244-116B-12/C  
Sequence 12, Application US/08244116B  
Patent No. 5763159  
GENERAL INFORMATION:  
APPLICANT: Simmonds, Peter  
APPLICANT: Chan, Shiu-Wan  
APPLICANT: Yap, Peng L.  
TITLE OF INVENTION: Hepatitis-C Virus Testing  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Bell, Seltzer, Park & Gibson, P.A.  
STREET: 1211 East Morehead Street  
CITY: Charlotte  
STATE: No. 5763159th Carolina

COUNTRY: United States  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/244,116B  
FILING DATE: 15-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/02143  
FILING DATE: 20-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Stbley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 1749-125  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 704-377-1561  
TELEFAX: 704-334-2014  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 194 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Hepatitis-C virus  
US-08-244-116B-12

Query Match 100.0%; Score 20; DB 1; Length 194;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACTACTC 20  
DB 189 TTGCGACCCACACTACTC 170

RESULT 24  
US-09-034-205-37/c  
Sequence 37, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neiri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-37

Query Match 100.0%; Score 20; DB 3; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACTACTC 20  
DB 199 TTGCGACCCACACTACTC 180

RESULT 25  
US-08-934-097A-37/c  
Sequence 37, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neiri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
STRUCTURE PROBING WITH STRUCTURE-BRIDGING  
OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-37

Query Match 100.0%; Score 20; DB 3; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
DB 199 TTGGGACCCCACTACTC 180

## RESULT 26

US-08-851-588-37/C  
Sequence 37, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION/DOCKET NUMBER: 40,027  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-37

Query Match 100.0%; Score 20; DB 3; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
DB 199 TTGGGACCCCACTACTC 180

## RESULT 27

US-09-677-218B-37/C  
Sequence 37, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION/DOCKET NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-09-677-218B-37

Query Match 100.0%; Score 20; DB 3; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
DB 199 TTGGGACCCCACTACTC 180

## RESULT 28

US-09-677-192-37/C  
Sequence 37, Application US/09677192  
Patent No. 6358691  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
FILE REFERENCE: FORS-04708  
CURRENT APPLICATION NUMBER: US/09/677,192  
CURRENT FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 09/034,205  
PRIOR FILING DATE: 1998-03-03  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 37  
LENGTH: 232  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-677-192-37

Query Match 100.0%; Score 20; DB 3; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCACTACTC 20  
Db 199 TTCCGACCCCACTACTC 180

RESULT 29  
US-09-402-618B-37/C  
Sequence 37, Application US/09402618B  
Patent No. 6709815  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance  
APPLICANT: Neil, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/09/402,618B  
CURRENT FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 37  
LENGTH: 232  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-402-618B-37

Query Match  
Best Local Similarity 100.0%; Score 20; DB 4; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCACTACTC 20  
Db 199 TTCCGACCCCACTACTC 180

RESULT 30  
US-09-825-574-37/C  
Sequence 37, Application US/09825574  
Patent No. 6709819  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neil, Bruce  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097

FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Karmin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-09-825-574-37

Query Match  
Best Local Similarity 100.0%; Score 20; DB 4; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCACTACTC 20  
Db 199 TTCCGACCCCACTACTC 180

RESULT 31  
US-09-676-768-37/C  
Sequence 37, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear



MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-09-676-768-37

Query Match 100.0%; Score 20; DB 4; Length 232;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 199 TTGCGACCCCAACTACTC 180

RESULT 32  
US-09-034-205-32/c  
Sequence 32, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-32  
Query Match 100.0%; Score 20; DB 3; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 206 TTGCGACCCCAACTACTC 187

RESULT 33  
US-09-034-205-36/c  
Sequence 36, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-36  
Query Match 100.0%; Score 20; DB 3; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 206 TTGCGACCCCAACTACTC 187

RESULT 34  
US-08-934-097A-32/c  
Sequence 32, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
STRUCTURE PROBING WITH STRUCTURE-BRIDGING  
OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-32

Query Match 100.0%; Score 20; DB 3; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 206 TTGGGACCCCAACTACTC 187

RESULT 35  
US-08-934-097A-36/C  
Sequence 36, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-36

Query Match 100.0%; Score 20; DB 3; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 206 TTGGGACCCCAACTACTC 187

RESULT 36  
US-08-851-588-32/C  
Sequence 32, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-32

Query Match 100.0%; Score 20; DB 3; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 206 TTGGGACCCCAACTACTC 187

RESULT 37  
US-08-851-588-36/C  
Sequence 36, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:

APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-36

Query Match 100.0%; Score 20; DB 3; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 206 TTGGGACCCCAACTACTC 187

RESULT 38  
US-09-677-218B-32/c  
Sequence 32, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

US-09-677-218B-32

Query Match 100.0%; Score 20; DB 3; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 206 TTGGGACCCCAACTACTC 187

RESULT 39  
US-09-677-218B-36/c  
Sequence 36, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

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; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 239 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: other nucleic acid
;   DESCRIPTION: /desc = "DNA"
;
; US-09-677-218B-36
;
Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 239;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 206 TTGGGACCCCAACTACTC 187

RESULT 40
US-09-677-192-32/c
; Sequence 32, Application US/09677192
; Patent No. 6358691
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
; FILE REFERENCE: FORS-04708
; CURRENT APPLICATION NUMBER: US/09/677,192
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/034,205
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 239
; TYPE: DNA
; ORGANISM: Hepatitis C virus
;
US-09-677-192-32
;
Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 239;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 206 TTGGGACCCCAACTACTC 187

RESULT 41
US-09-677-192-36/c
; Sequence 36, Application US/09677192
; Patent No. 6358691
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
; FILE REFERENCE: FORS-04708
; CURRENT APPLICATION NUMBER: US/09/677,192
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/034,205
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 239
; TYPE: DNA
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; TYPE: DNA
; ORGANISM: Hepatitis C virus
;
US-09-677-192-36
;
Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 239;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 206 TTGGGACCCCAACTACTC 187

RESULT 42
US-09-402-618B-32/c
; Sequence 32, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 239
; TYPE: DNA
; ORGANISM: Hepatitis C virus
;
US-09-402-618B-32
;
Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 239;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 206 TTGGGACCCCAACTACTC 187

RESULT 43
US-09-402-618B-36/c
; Sequence 36, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 239
; TYPE: DNA
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ORGANISM: Hepatitis C virus  
US-09-402-618B-36

Query Match 100.0%; Score 20; DB 4; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
DB 206 TTGGGACCCCAACTACTC 187

## RESULT 44

US-09-825-574-32/c  
Sequence 32, Application US/09825574  
Patent No. 6709819  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Fors, Lance  
Neti, Bruce P.  
Brow, Mary Ann D.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-825-574-32

Query Match 100.0%; Score 20; DB 4; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
DB 206 TTGGGACCCCAACTACTC 187

RESULT 45  
US-09-825-574-36/c

Sequence 36, Application US/09825574  
Patent No. 6709819  
GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neti, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 239 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-09-825-574-36

Query Match 100.0%; Score 20; DB 4; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
DB 206 TTGGGACCCCAACTACTC 187

## RESULT 46

US-09-676-768-32/c  
Sequence 32, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Pang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance  
Neti, Bruce P.  
Brow, Mary Ann D.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-676-768-32  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
Query Match 100.0%; Score 20; DB 4; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGGACCCCAACTACTC 20  
DB 206 TTGGGACCCCAACTACTC 187  
RESULT 47  
US-09-676-768-36/c  
Sequence 36, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-676-768-36  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
Query Match 100.0%; Score 20; DB 4; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGGACCCCAACTACTC 20  
DB 206 TTGGGACCCCAACTACTC 187  
RESULT 48  
US-09-034-205-33/c  
Sequence 33, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-33

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
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Db 207 TTGGGACCCCAACTACTC 188

## RESULT 49

US-09-034-205-35/c  
; Sequence 35, Application US/09034205  
; Patent No. 6194149  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Nerl, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
; TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/034,205  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: FORS-03268  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 240 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
US-09-034-205-35

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 207 TTGGGACCCCAACTACTC 188

## RESULT 50

US-09-034-205-38/c  
; Sequence 38, Application US/09034205  
; Patent No. 6194149  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Nerl, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
; TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/034,205  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: FORS-03268  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 240 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
US-09-034-205-38

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 208 TTGGGACCCCAACTACTC 189

## RESULT 51

US-08-934-097A-33/c  
; Sequence 33, Application US/08934097A  
; Patent No. 6210880  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Nerl, Bruce P.  
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
; TITLE OF INVENTION: Structure Probing With Structure-Bridging  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/934,097A  
; FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-33

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
Db 207 TTCCGACCCCACTACTC 188

RESULT 52  
US-08-934-097A-35/C  
Sequence 35, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-35

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
Db 207 TTCCGACCCCACTACTC 188

RESULT 53  
US-08-934-097A-38/C  
Sequence 38, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-38

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
Db 208 TTCCGACCCCACTACTC 189

RESULT 54  
US-08-934-097A-33/C  
Sequence 33, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-33



APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-33

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
DB 207 TTGGGACCCCACTACTC 188

RESULT 55  
US-08-851-588-35/C  
Sequence 35, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588

FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-35

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
DB 207 TTGGGACCCCACTACTC 188

RESULT 56  
US-08-851-588-38/C  
Sequence 38, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-38

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20  
|||||  
Db 208 TTCCGACCCCACTACTC 189

RESULT 57  
US-09-677-218B-33/c  
; Sequence 33, Application US/09677218B  
; Patent No. 6355437  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; Fors, Lance  
; Brow, Mary Ann D.  
; Neil, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
; STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/677,218B  
; FILING DATE: 02-Oct-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/034,205  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: FORS-03268  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 240 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-677-218B-33

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20  
|||||  
Db 207 TTCCGACCCCACTACTC 188

RESULT 58  
US-09-677-218B-35/c  
; Sequence 35, Application US/09677218B  
; Patent No. 6355437  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; Fors, Lance  
; Brow, Mary Ann D.  
; Neil, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
; STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:

APPLICANT: Lyamichev, Victor I.  
; Fors, Lance  
; Brow, Mary Ann D.  
; Neil, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
; STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/677,218B  
; FILING DATE: 02-Oct-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/034,205  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: FORS-03268  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 240 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
US-09-677-218B-35

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20  
|||||  
Db 207 TTCCGACCCCACTACTC 188

RESULT 59  
US-09-677-218B-38/c  
; Sequence 38, Application US/09677218B  
; Patent No. 6355437  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; Fors, Lance  
; Brow, Mary Ann D.  
; Neil, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
; STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELEPHONE: (415) 397-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-677-218B-38

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 208 TTGGGACCCCAACTACTC 189

RESULT 60  
US-09-677-192-33/c  
Sequence 33, Application US/09677192  
Patent No. 6358691  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neil, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
FILE REFERENCE: FORS-04708  
CURRENT APPLICATION NUMBER: US/09/677,192  
CURRENT FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 09/034,205  
PRIOR FILING DATE: 1998-03-03  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 33  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-677-192-33

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 207 TTGGGACCCCAACTACTC 188

RESULT 61  
US-09-677-192-35/c

Sequence 35, Application US/09677192  
Patent No. 6358691  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neil, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
FILE REFERENCE: FORS-04708  
CURRENT APPLICATION NUMBER: US/09/677,192  
CURRENT FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 09/034,205  
PRIOR FILING DATE: 1998-03-03  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 35  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-677-192-35

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 207 TTGGGACCCCAACTACTC 188

RESULT 62  
US-09-677-192-38/c  
Sequence 38, Application US/09677192  
Patent No. 6358691  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neil, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
FILE REFERENCE: FORS-04708  
CURRENT APPLICATION NUMBER: US/09/677,192  
CURRENT FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 09/034,205  
PRIOR FILING DATE: 1998-03-03  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 38  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-677-192-38

Query Match 100.0%; Score 20; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 208 TTGGGACCCCAACTACTC 189

RESULT 63  
US-09-402-618B-33/c  
Sequence 33, Application US/09402618B  
Patent No. 6709815  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance

APPLICANT: Neri, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/09/402,618B  
CURRENT FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 33  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-402-618B-33

Query Match 100.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
Db 207 TTCCGACCCCAACTACTC 188

RESULT 64  
US-09-402-618B-35/c  
Sequence 35, Application US/09402618B  
Patent No. 6709815  
GENERAL INFORMATION:

APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/09/402,618B  
CURRENT FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 35  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-402-618B-35

Query Match 100.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
Db 207 TTCCGACCCCAACTACTC 188

RESULT 65  
US-09-402-618B-38/c  
Sequence 38, Application US/09402618B  
Patent No. 6709815  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce

APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/09/402,618B  
CURRENT FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 38  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-402-618B-38

Query Match 100.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
Db 208 TTCCGACCCCAACTACTC 189

RESULT 66  
US-09-825-574-33/c  
Sequence 33, Application US/09825574  
Patent No. 6709819  
GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid Structure Probing With Structure-Bridging Oligonucleotides.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-825-574-33

Query Match 100.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 207 TTGGGACCCCAACTACTC 188

## RESULT 67

US-09-825-574-35/c  
Sequence 35, Application US/09825574  
Patent No. 6709819

GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Fors, Lance  
Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
US-09-825-574-35

Query Match 100.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 207 TTGGGACCCCAACTACTC 188

RESULT 68  
US-09-825-574-38/c

Sequence 38, Application US/09825574  
Patent No. 6709819

GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-825-574-38

Query Match 100.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 208 TTGGGACCCCAACTACTC 189

RESULT 69  
US-09-676-768-33/c  
Sequence 33, Application US/09676768  
Patent No. 6780565

GENERAL INFORMATION:

APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-676-768-33

Query Match 100.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 207 TTGGGACCCCACTACTC 188

RESULT 70  
US-09-676-768-35/c  
Sequence 35, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamlichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
US-09-676-768-35

Query Match 100.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 207 TTGGGACCCCACTACTC 188

RESULT 71  
US-09-676-768-38/c  
Sequence 38, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamlichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-676-768-38

Query Match 100.0%; Score 20; DB 4; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 208 TTGGGACCCCAACTACTC 189

RESULT 72  
US-09-034-205-26/c  
Sequence 26, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-26

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 208 TTGGGACCCCAACTACTC 189

RESULT 73  
US-09-034-205-27/c  
Sequence 27, Application US/09034205  
Patent No. 6194149

GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-27

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 208 TTGGGACCCCAACTACTC 189

RESULT 74  
US-09-034-205-29/c  
Sequence 29, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-29

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
|||||  
Db 208 TTGCGACCCCAACTACTC 189

RESULT 75  
US-09-034-205-31/c  
Sequence 31, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neil, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"  
US-09-034-205-31

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
|||||  
Db 208 TTGCGACCCCAACTACTC 189

RESULT 76  
US-08-934-097A-26/c  
Sequence 26, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neil, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
STRUCTURE PROBING WITH STRUCTURE-BRIDGING  
OLIGONUCLEOTIDES.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-26

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
|||||  
Db 208 TTGCGACCCCAACTACTC 189

RESULT 77  
US-08-934-097A-27/c  
Sequence 27, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.



APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-27

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 208 TTGCGACCCCAACTACTC 189

RESULT 78  
US-08-934-097A-29/C  
Sequence 29, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-29

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 208 TTGCGACCCCAACTACTC 189

RESULT 79  
US-08-934-097A-31/C  
Sequence 31, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-31

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGCGACCCCACTACTC 20  
Db 208 TTCGCGACCCCACTACTC 189

RESULT 80  
US-08-851-588-26/c  
Sequence 26, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-26

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGCGACCCCACTACTC 20  
Db 208 TTCGCGACCCCACTACTC 189

RESULT 81  
US-08-851-588-27/c  
Sequence 27, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:

APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-27

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGCGACCCCACTACTC 20  
Db 208 TTCGCGACCCCACTACTC 189

RESULT 82  
US-08-851-588-29/c  
Sequence 29, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-29

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 208 TTGCGACCCCAACTACTC 189

RESULT 83  
US-08-851-588-31/c  
Sequence 31, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-31

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 208 TTGCGACCCCAACTACTC 189

RESULT 84  
US-09-677-218B-26/c  
Sequence 26, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Neri, Bruce P.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Karlin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-09-677-218B-26

Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 208 TTGCGACCCCAACTACTC 189

RESULT 85

US-09-677-218B-27/c  
Sequence 27, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Fors, Lance  
Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-677-218B-27  
Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGACCCCAACTACTC 20  
Db 208 TTCCGACCCCAACTACTC 189  
RESULT 86  
US-09-677-218B-29/c  
Sequence 29, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Fors, Lance  
Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco

STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-677-218B-29  
Query Match 100.0%; Score 20; DB 3; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGACCCCAACTACTC 20  
Db 208 TTCCGACCCCAACTACTC 189  
RESULT 87  
US-09-677-218B-31/c  
Sequence 31, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Fors, Lance  
Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>

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ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-03268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 244 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-677-218b-31

Query Match          100.0%; Score 20; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 208 TTGGGACCCCAACTACTC 189

RESULT 88
US-09-677-192-26/c
; Sequence 26, Application US/09677192
; Patent No. 6358691
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
; TITLE OF INVENTION: OLIGONUCLEOTIDES
; FILE REFERENCE: FORS-04708
; CURRENT APPLICATION NUMBER: US/09/677,192
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/034,205
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-677-192-26

Query Match          100.0%; Score 20; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 208 TTGGGACCCCAACTACTC 189

RESULT 89
US-09-677-192-27/c
; Sequence 27, Application US/09677192
; Patent No. 6358691
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
; TITLE OF INVENTION: OLIGONUCLEOTIDES
; FILE REFERENCE: FORS-04708
; CURRENT APPLICATION NUMBER: US/09/677,192
; CURRENT FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 31
; LENGTH: 244
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CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/034,205
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 27
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-677-192-27

Query Match          100.0%; Score 20; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 208 TTGGGACCCCAACTACTC 189

RESULT 90
US-09-677-192-29/c
; Sequence 29, Application US/09677192
; Patent No. 6358691
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
; TITLE OF INVENTION: OLIGONUCLEOTIDES
; FILE REFERENCE: FORS-04708
; CURRENT APPLICATION NUMBER: US/09/677,192
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/034,205
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 29
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-677-192-29

Query Match          100.0%; Score 20; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 208 TTGGGACCCCAACTACTC 189

RESULT 91
US-09-677-192-31/c
; Sequence 31, Application US/09677192
; Patent No. 6358691
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING
; TITLE OF INVENTION: OLIGONUCLEOTIDES
; FILE REFERENCE: FORS-04708
; CURRENT APPLICATION NUMBER: US/09/677,192
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/034,205
; PRIOR FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 31
; LENGTH: 244
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; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-402-618B-27-31
Query Match      100.0%; Score 20; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20
Db 208 TTCCGACCCCAACTACTC 189

RESULT 92
US-09-402-618B-26/c
; Sequence 26, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-402-618B-26
Query Match      100.0%; Score 20; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20
Db 208 TTCCGACCCCAACTACTC 189

RESULT 93
US-09-402-618B-27/c
; Sequence 27, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-402-618B-27
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; ORGANISM: Hepatitis C virus
US-09-402-618B-27
Query Match      100.0%; Score 20; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20
Db 208 TTCCGACCCCAACTACTC 189

RESULT 94
US-09-402-618B-29/c
; Sequence 29, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-402-618B-29
Query Match      100.0%; Score 20; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20
Db 208 TTCCGACCCCAACTACTC 189

RESULT 95
US-09-402-618B-31/c
; Sequence 31, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-402-618B-31
```

US-09-402-618B-31

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
|||||  
Db 208 TTGGGACCCCACTACTC 189

RESULT 96

US-09-402-618B-124  
; Sequence 124, Application US/09402618B  
; Patent No. 6709815

GENERAL INFORMATION:

APPLICANT: Dong, Fang

APPLICANT: Lyamichev, Victor

APPLICANT: Prudent, James

APPLICANT: Fors, Lance

APPLICANT: Neri, Bruce

APPLICANT: Brow, Mary Ann

APPLICANT: Anderson, Todd

APPLICANT: Dahlberg, James

TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides

FILE REFERENCE: FORS-04012

CURRENT APPLICATION NUMBER: US/09/402,618B

CURRENT FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: PCT/US98/03194

PRIOR FILING DATE: 1998-05-05

NUMBER OF SEQ ID NOS: 128

SOFTWARE: PatentIn version 3.0

SEQ ID NO 124

LENGTH: 244

TYPE: DNA

ORGANISM: Hepatitis C virus

US-09-402-618B-124

Query Match 100.0%; Score 20; DB 4; Length 244;

Best Local Similarity 100.0%; Pred. No. 0.0029;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
|||||  
Db 37 TTGGGACCCCACTACTC 56

RESULT 97

US-09-402-618B-125  
; Sequence 125, Application US/09402618B  
; Patent No. 6709815

GENERAL INFORMATION:

APPLICANT: Dong, Fang

APPLICANT: Lyamichev, Victor

APPLICANT: Prudent, James

APPLICANT: Fors, Lance

APPLICANT: Neri, Bruce

APPLICANT: Brow, Mary Ann

APPLICANT: Anderson, Todd

APPLICANT: Dahlberg, James

TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides

FILE REFERENCE: FORS-04012

CURRENT APPLICATION NUMBER: US/09/402,618B

CURRENT FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: PCT/US98/03194

PRIOR FILING DATE: 1998-05-05

NUMBER OF SEQ ID NOS: 128

SOFTWARE: PatentIn version 3.0

SEQ ID NO 125

LENGTH: 244

TYPE: DNA

ORGANISM: Hepatitis C virus

US-09-402-618B-125

Query Match 100.0%; Score 20; DB 4; Length 244;

Best Local Similarity 100.0%; Pred. No. 0.0029;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
|||||  
Db 37 TTGGGACCCCACTACTC 56

RESULT 98

US-09-402-618B-127  
; Sequence 127, Application US/09402618B  
; Patent No. 6709815

GENERAL INFORMATION:

APPLICANT: Dong, Fang

APPLICANT: Lyamichev, Victor

APPLICANT: Prudent, James

APPLICANT: Fors, Lance

APPLICANT: Neri, Bruce

APPLICANT: Brow, Mary Ann

APPLICANT: Anderson, Todd

APPLICANT: Dahlberg, James

TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides

FILE REFERENCE: FORS-04012

CURRENT APPLICATION NUMBER: US/09/402,618B

CURRENT FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: PCT/US98/03194

PRIOR FILING DATE: 1998-05-05

NUMBER OF SEQ ID NOS: 128

SOFTWARE: PatentIn version 3.0

SEQ ID NO 127

LENGTH: 244

TYPE: DNA

ORGANISM: Hepatitis C virus

US-09-402-618B-127

Query Match 100.0%; Score 20; DB 4; Length 244;

Best Local Similarity 100.0%; Pred. No. 0.0029;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
|||||  
Db 37 TTGGGACCCCACTACTC 56

RESULT 99

US-09-402-618B-128  
; Sequence 128, Application US/09402618B  
; Patent No. 6709815

GENERAL INFORMATION:

APPLICANT: Dong, Fang

APPLICANT: Lyamichev, Victor

APPLICANT: Prudent, James

APPLICANT: Fors, Lance

APPLICANT: Neri, Bruce

APPLICANT: Brow, Mary Ann

APPLICANT: Anderson, Todd

APPLICANT: Dahlberg, James

TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides

FILE REFERENCE: FORS-04012

CURRENT APPLICATION NUMBER: US/09/402,618B

CURRENT FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: PCT/US98/03194

PRIOR FILING DATE: 1998-05-05

NUMBER OF SEQ ID NOS: 128

SOFTWARE: PatentIn version 3.0

SEQ ID NO 128

LENGTH: 244

TYPE: DNA

ORGANISM: Hepatitis C virus

US-09-402-618B-128

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 80.0%; Pred. No. 0.0029;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
Db 37 TTGGGACCCCAACTACTC 56

## RESULT 100

US-09-825-574-26/c

Sequence 26, Application US/09825574

Patent No. 6709819

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Fors, Lance P.

Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-02980

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 244 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-825-574-26

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
Db 208 TTGGGACCCCAACTACTC 189

## RESULT 101

US-09-825-574-27/c

Sequence 27, Application US/09825574

Patent No. 6709819

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Brow, Mary Ann D.

Fors, Lance P.

Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-02980

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 244 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 27:

US-09-825-574-27

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
Db 208 TTGGGACCCCAACTACTC 189

## RESULT 102

US-09-825-574-29/c

Sequence 29, Application US/09825574

Patent No. 6709819

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Fors, Lance P.

Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA



ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/09/825,574  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-825-574-29

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 208 TTGGGACCCCAACTACTC 189

RESULT 103  
US-09-825-574-31/c  
Sequence 31, Application US/09825574  
Patent No. 6709819  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:

NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-825-574-31

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 208 TTGGGACCCCAACTACTC 189

RESULT 104  
US-09-676-768-26/c  
Sequence 26, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 26;  
US-09-676-768-26

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGCGACCCCAACTACTC 20  
|||||  
Db 208 TTCGCGACCCCAACTACTC 189

## RESULT 105

US-09-676-768-27/c  
Sequence 27, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:

APPLICANT: Dong, Fang

Lyamichev, Victor I.

Prudent, James R.

Dahlberg, James E.

Fors, Lance

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/676,768

FILING DATE: 02-Oct-2000

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/851,588

FILING DATE: 05-May-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: FORS-02777

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 244 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 27:

US-09-676-768-27

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGCGACCCCAACTACTC 20  
|||||  
Db 208 TTCGCGACCCCAACTACTC 189

## RESULT 106

US-09-676-768-29/c

Sequence 29, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:

APPLICANT: Dong, Fang

Lyamichev, Victor I.

Prudent, James R.

Dahlberg, James E.

Fors, Lance

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/676,768

FILING DATE: 02-Oct-2000

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/851,588

FILING DATE: 05-May-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: FORS-02777

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 244 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 29:

US-09-676-768-29

Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCGCGACCCCAACTACTC 20  
|||||  
Db 208 TTCGCGACCCCAACTACTC 189

## RESULT 107

US-09-676-768-31/c  
Sequence 31, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:

APPLICANT: Dong, Fang

Lyamichev, Victor I.

Prudent, James R.

Dahlberg, James E.

Fors, Lance

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-676-768-31  
Query Match 100.0%; Score 20; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGGACCCCACTACTC 20  
DB 208 TTGGGACCCCACTACTC 189  
RESULT 108  
US-08-441-971-33/C  
Sequence 33, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-May-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:

APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE: (ATCC # 40394)  
INDIVIDUAL ISOLATE: hcvt  
US-08-441-971-33  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGGACCCCACTACTC 20  
DB 186 TTGGGACCCCACTACTC 167  
RESULT 109  
US-08-441-971-34/C  
Sequence 34, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-May-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: us5  
US-08-441-971-34

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCACTACTC 20  
Db 186 TTGCGACCCCACTACTC 167

RESULT 110  
US-08-441-971-35/c  
Sequence 35, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: aus1  
US-08-441-971-35

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGCGACCCCACTACTC 20

Db 186 TTGCGACCCCACTACTC 167

RESULT 111  
US-08-441-971-36/c  
Sequence 36, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: sp2  
US-08-441-971-36

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCACTACTC 20  
Db 186 TTGCGACCCCACTACTC 167

RESULT 112  
US-08-441-971-37/c  
Sequence 37, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
;; STREET: 600 Atlantic Avenue  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02210  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 5.25 inch  
;; COMPUTER: IBM compatible  
;; OPERATING SYSTEM: MS-DOS Version 3.3  
;; SOFTWARE: Wordperfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/441,971  
;; FILING DATE: 16-MAY-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/221,653  
;; FILING DATE:  
;; APPLICATION NUMBER: US/07/881,528  
;; FILING DATE:  
;; APPLICATION NUMBER: 07/697,326  
;; FILING DATE: 8 May 1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Janiuk, Anthony J.  
;; REGISTRATION NUMBER: 29,809  
;; REFERENCE/DOCKET NUMBER: C0772/7000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 720-3500  
;; TELEFAX: (617) 720-2441  
;; TELEX: EZEKIEL  
;; INFORMATION FOR SEQ. ID NO.: 37:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 252 nucleotides  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; ORIGINAL SOURCE:  
;; INDIVIDUAL ISOLATE: gm2  
;;  
;; US-08-441-971-37  
;;  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;;  
Qy 1 TTGCGACCCCAACTACTC 20  
Db 186 TTGCGACCCCAACTACTC 167  
;;  
RESULT 113  
US-08-441-971-38/c  
;; Sequence 38, Application US/08441971  
;; Patent No. 6071693  
;;  
;; GENERAL INFORMATION:  
;; APPLICANT: Tai-An Cha  
;; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
;; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
;; NUMBER OF SEQUENCES: 147  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
;; STREET: 600 Atlantic Avenue  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02210  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 5.25 inch  
;; COMPUTER: IBM compatible  
;; OPERATING SYSTEM: MS-DOS Version 3.3  
;; SOFTWARE: Wordperfect 5.1  
;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/441,971  
;; FILING DATE: 16-MAY-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/221,653  
;; FILING DATE:  
;; APPLICATION NUMBER: US/07/881,528  
;; FILING DATE:  
;; APPLICATION NUMBER: 07/697,326  
;; FILING DATE: 8 May 1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Janiuk, Anthony J.  
;; REGISTRATION NUMBER: 29,809  
;; REFERENCE/DOCKET NUMBER: C0772/7000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 720-3500  
;; TELEFAX: (617) 720-2441  
;; TELEX: EZEKIEL  
;; INFORMATION FOR SEQ. ID NO.: 38:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 252 nucleotides  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; ORIGINAL SOURCE:  
;; INDIVIDUAL ISOLATE: 121  
;;  
;; US-08-441-971-38  
;;  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;;  
Qy 1 TTGCGACCCCAACTACTC 20  
Db 186 TTGCGACCCCAACTACTC 167  
;;  
RESULT 114  
US-08-441-971-39/c  
;; Sequence 39, Application US/08441971  
;; Patent No. 6071693  
;;  
;; GENERAL INFORMATION:  
;; APPLICANT: Tai-An Cha  
;; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
;; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
;; NUMBER OF SEQUENCES: 147  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
;; STREET: 600 Atlantic Avenue  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02210  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 5.25 inch  
;; COMPUTER: IBM compatible  
;; OPERATING SYSTEM: MS-DOS Version 3.3  
;; SOFTWARE: Wordperfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/441,971  
;; FILING DATE: 16-MAY-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/221,653  
;; FILING DATE:  
;; APPLICATION NUMBER: US/07/881,528  
;; FILING DATE:  
;; APPLICATION NUMBER: 07/697,326  
;; FILING DATE: 8 May 1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Janiuk, Anthony J.  
;; REGISTRATION NUMBER: 29,809

REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: us4  
US-08-441-971-39

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
Db 186 TTCCGACCCCACTACTC 167

RESULT 115  
US-08-441-971-40/C  
Sequence 40, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: jh1  
US-08-441-971-40

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
Db 186 TTCCGACCCCACTACTC 167

RESULT 116  
US-08-441-971-41/C  
Sequence 41, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: nac5  
US-08-441-971-41

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
Db 186 TTCCGACCCCACTACTC 167

RESULT 117

US-08-441-971-42/c  
; Sequence 42, Application US/08441971  
; Patent No. 6071693  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,971  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIORITY INFORMATION:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; APPLICATION NUMBER: US/07/881,528  
; FILING DATE:  
; APPLICATION NUMBER: 07/697,326  
; FILING DATE: 8 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janiuk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: C0772/7000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
; TELEX: EZEKIEL  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: arg2  
; US-08-441-971-42  
  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Oy 1 TTGGGACCCCACTACTC 20  
Db 186 TTGGGACCCCACTACTC 167  
  
RESULT 118  
US-08-441-971-43/c  
; Sequence 43, Application US/08441971  
; Patent No. 6071693  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts

COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,971  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIORITY INFORMATION:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; APPLICATION NUMBER: US/07/881,528  
; FILING DATE:  
; APPLICATION NUMBER: 07/697,326  
; FILING DATE: 8 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janiuk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: C0772/7000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
; TELEX: EZEKIEL  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: spl  
; US-08-441-971-43  
  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Oy 1 TTGGGACCCCACTACTC 20  
Db 186 TTGGGACCCCACTACTC 167  
  
RESULT 119  
US-08-441-971-44/c  
; Sequence 44, Application US/08441971  
; Patent No. 6071693  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,971  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIORITY INFORMATION:  
; APPLICATION NUMBER: US/08/221,653

;; FILING DATE: US/07/881,528  
;; APPLICATION NUMBER: 07/697,326  
;; FILING DATE: 8 May 1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Janiuk, Anthony J.  
;; REGISTRATION NUMBER: 29,809  
;; REFERENCE/DOCKET NUMBER: C0772/7000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 720-3500  
;; TELEFAX: (617) 720-2441  
;; TELEX: EZEKIEL  
;; INFORMATION FOR SEQ ID NO: 44:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 252 nucleotides  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; ORIGINAL SOURCE:  
;; INDIVIDUAL ISOLATE: ghl  
US-08-441-971-44

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCAACTACTC 20  
Db 186 TTGGGACCCCAACTACTC 167

RESULT 120  
US-08-441-971-45/c  
; Sequence 45, Application US/08441971  
; Patent No. 6071693  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,971  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; APPLICATION NUMBER: US/07/881,528  
; FILING DATE:  
; APPLICATION NUMBER: 07/697,326  
; FILING DATE: 8 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janiuk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: C0772/7000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
; TELEX: EZEKIEL

;; INFORMATION FOR SEQ ID NO: 45:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 252 nucleotides  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; ORIGINAL SOURCE:  
;; INDIVIDUAL ISOLATE: i15  
US-08-441-971-45

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCAACTACTC 20  
Db 186 TTGGGACCCCAACTACTC 167

RESULT 121  
US-08-441-971-48/c  
; Sequence 48, Application US/08441971  
; Patent No. 6071693  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,971  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; APPLICATION NUMBER: US/07/881,528  
; FILING DATE:  
; APPLICATION NUMBER: 07/697,326  
; FILING DATE: 8 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janiuk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: C0772/7000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
; TELEX: EZEKIEL

;; INFORMATION FOR SEQ ID NO: 48:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 252 nucleotides  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; ORIGINAL SOURCE:  
;; INDIVIDUAL ISOLATE: 621  
US-08-441-971-48

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;



Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCACACTACTC 20  
|||||  
Db 186 TTGGGACCCACACTACTC 167

RESULT 122  
US-08-441-971-49/c  
; Sequence 49, Application US/08441971  
; Patent No. 6071693  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,971  
; FILING DATE: 16-May-1995  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; APPLICATION NUMBER: US/07/881,528  
; FILING DATE:  
; APPLICATION NUMBER: 07/697,326  
; FILING DATE: 8 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janiuk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: C0772/7000  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
; TELEX: EZEKIEL  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: GJ61329  
US-08-441-971-49

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCACACTACTC 20  
|||||  
Db 186 TTGGGACCCACACTACTC 167

RESULT 123  
US-08-221-653-33/c  
; Sequence 33, Application US/08221653  
; Patent No. 6190864  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha

;; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
;; DIAGNOSTICS AND THERAPEUTICS  
;; NUMBER OF SEQUENCES: 147  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
;; STREET: 600 Atlantic Avenue  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02210  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 5.25 inch  
;; OPERATING SYSTEM: MS-DOS Version 3.3  
;; SOFTWARE: WordPerfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/221,653  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIORITY APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/881,528  
;; FILING DATE:  
;; APPLICATION NUMBER: 07/697,326  
;; FILING DATE: 8 May 1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Janiuk, Anthony J.  
;; REGISTRATION NUMBER: 29,809  
;; REFERENCE/DOCKET NUMBER: C0772/7000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 720-3500  
;; TELEFAX: (617) 720-2441  
;; TELEX: EZEKIEL  
;; INFORMATION FOR SEQ ID NO: 33:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 252 nucleotides  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; ORIGINAL SOURCE: (ATCC # 40394)  
;; INDIVIDUAL ISOLATE: hcvi  
US-08-221-653-33

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCACACTACTC 20  
|||||  
Db 186 TTGGGACCCACACTACTC 167

RESULT 124  
US-08-221-653-34/c  
; Sequence 34, Application US/08221653  
; Patent No. 6190864  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: us5  
US-08-221-653-34

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGAGCCCACTACTC 20  
Db 186 TTGGGAGCCCACTACTC 167

RESULT 125  
US-08-221-653-35/c  
Sequence 35, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500

TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: aus1  
US-08-221-653-35

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGAGCCCACTACTC 20  
Db 186 TTGGGAGCCCACTACTC 167

RESULT 126  
US-08-221-653-36/c  
Sequence 36, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: sp2  
US-08-221-653-36

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 186 TTGGGACCCCAACTACTC 167

RESULT 127  
US-08-221-653-37/C  
Sequence 37, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: gm2  
US-08-221-653-37

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 186 TTGGGACCCCAACTACTC 167

RESULT 128  
US-08-221-653-38/C  
Sequence 38, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653

NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 121  
US-08-221-653-38

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 186 TTGGGACCCCAACTACTC 167

RESULT 129  
US-08-221-653-39/C  
Sequence 39, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653

;; FILING DATE: 07/697,326  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA: US/07/881,528  
;; APPLICATION NUMBER: 07/697,326  
;; FILING DATE: 8 May 1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Janiuk, Anthony J.  
;; REGISTRATION NUMBER: 29,809  
;; REFERENCE/DOCKET NUMBER: C0772/7000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 720-3500  
;; TELEFAX: (617) 720-2441  
;;  
;; INFORMATION FOR SEQ ID NO: 39:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 252 nucleotides  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; ORIGINAL SOURCE:  
;; INDIVIDUAL ISOLATE: us4  
;;  
US-08-221-653-39

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCACTACTC 20  
Db 186 TTGCGACCCCACTACTC 167

RESULT 130  
US-08-221-653-40/C  
; Sequence 40, Application US/08221653  
; Patent No. 6190864  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/881,528  
; FILING DATE:  
; APPLICATION NUMBER: 07/697,326  
; FILING DATE: 8 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janiuk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: C0772/7000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
;  
; TELER: EZEKIEL

;; INFORMATION FOR SEQ ID NO: 40:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 252 nucleotides  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; ORIGINAL SOURCE:  
;; INDIVIDUAL ISOLATE: jh1  
;;  
US-08-221-653-40

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCACTACTC 20  
Db 186 TTGCGACCCCACTACTC 167

RESULT 131  
US-08-221-653-41/C  
; Sequence 41, Application US/08221653  
; Patent No. 6190864  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/881,528  
; FILING DATE:  
; APPLICATION NUMBER: 07/697,326  
; FILING DATE: 8 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janiuk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: C0772/7000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
;  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: nac5  
;  
US-08-221-653-41

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCACACTACTC 20  
|||  
Db 186 TTGGGACCCACACTACTC 167

RESULT 132  
US-08-221-653-42/C  
; Sequence 42, Application US/08221653  
; Patent No. 6190864  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/881,528  
; FILING DATE:  
; APPLICATION NUMBER: 07/697,326  
; FILING DATE: 8 May 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Janiuk, Anthony J.  
; REGISTRATION NUMBER: 29,809  
; REFERENCE/DOCKET NUMBER: C0772/7000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 720-3500  
; TELEFAX: (617) 720-2441  
; TELEX: EZEKIEL  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 252 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: arg2  
; US-08-221-653-42  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCACACTACTC 20  
|||  
Db 186 TTGGGACCCACACTACTC 167

RESULT 134  
US-08-221-653-44/C  
; Sequence 44, Application US/08221653  
; Patent No. 6190864  
; GENERAL INFORMATION:  
; APPLICANT: Tai-An Cha  
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 147  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; CLASSIFICATION: 435  
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
; STREET: 600 Atlantic Avenue  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: MS-DOS Version 3.3  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,653  
; FILING DATE:  
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29, 809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: ghl  
US-08-221-653-44

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCACACTACTC 20  
DB 186 TTCCGACCCACACTACTC 167

RESULT 135  
US-08-221-653-45/c  
Sequence 45, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESS: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29, 809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:

LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 115  
US-08-221-653-45

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCACACTACTC 20  
DB 186 TTCCGACCCACACTACTC 167

RESULT 136  
US-08-221-653-48/c  
Sequence 48, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESS: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29, 809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 821  
US-08-221-653-48

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCACACTACTC 20

Db 186 TTCGCGACCCCAACTACTC 167

RESULT 137  
US-08-221-653-49/c  
Sequence 49, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacke, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: g161329  
US-08-221-653-49  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTCGCGACCCCAACTACTC 20  
Db 186 TTCGCGACCCCAACTACTC 167  
RESULT 138  
US-08-442-144A-33/c  
Sequence 33, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yalco Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: hcvi (ATCC# 40394)  
US-08-442-144A-33  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTCGCGACCCCAACTACTC 20  
Db 186 TTCGCGACCCCAACTACTC 167  
RESULT 139  
US-08-442-144A-34/c  
Sequence 34, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: us5  
US-08-442-144A-34

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCACACTACTC 20  
Db 186 TTGGGACCCACACTACTC 167

RESULT 140  
US-08-442-144A-35/C  
Sequence 35, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdrea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: aus1  
US-08-442-144A-35

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCACACTACTC 20  
Db 186 TTGGGACCCACACTACTC 167

RESULT 141  
US-08-442-144A-36/C  
Sequence 36, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdrea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: SP2  
US-08-442-144A-36



Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 186 TTGGGACCCCAACTACTC 167

## RESULT 142

US-08-442-144A-37/c  
; Sequence 37, Application US/08442144A  
; Patent No. 6214583

## GENERAL INFORMATION:

APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994

## ATTORNEY/AGENT INFORMATION:

NAME: Doreen Yalco Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:

## INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: gm2  
US-08-442-144A-37

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 186 TTGGGACCCCAACTACTC 167

## RESULT 143

US-08-442-144A-38/c  
; Sequence 38, Application US/08442144A  
; Patent No. 6214583

## GENERAL INFORMATION:

APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994

## ATTORNEY/AGENT INFORMATION:

NAME: Doreen Yalco Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:

## INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 121  
US-08-442-144A-38

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 186 TTGGGACCCCAACTACTC 167

## RESULT 144

US-08-442-144A-39/c  
; Sequence 39, Application US/08442144A  
; Patent No. 6214583

## GENERAL INFORMATION:

APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville

STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: us4  
US-08-442-144A-39

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCACACTACTC 20  
Db 186 TTGCGACCCACACTACTC 167

RESULT 145  
US-08-442-144A-40/c  
Sequence 40, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: jh1  
US-08-442-144A-40

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCACACTACTC 20  
Db 186 TTGCGACCCACACTACTC 167

RESULT 146  
US-08-442-144A-41/c  
Sequence 41, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides

TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: nacs  
US-08-442-144A-41

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 186 TTGGGACCCCAACTACTC 167

RESULT 147  
US-08-442-144A-42/c  
Sequence 42, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Udea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko Ttuji110  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: arg2  
US-08-442-144A-42

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 186 TTGGGACCCCAACTACTC 20

DB 186 TTGGGACCCCAACTACTC 167

RESULT 148  
US-08-442-144A-43/c  
Sequence 43, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Udea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yacko Ttuji110  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: epl  
US-08-442-144A-43

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 186 TTGGGACCCCAACTACTC 167

RESULT 149  
US-08-442-144A-44/c  
Sequence 44, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg

APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yanko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: ghl  
US-08-442-144A-44

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCACTACTC 20  
DB 186 TTGCGACCCCACTACTC 167

RESULT 150  
US-08-442-144A-45/C  
Sequence 45, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch

COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yanko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 115  
US-08-442-144A-45

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGCGACCCCACTACTC 20  
DB 186 TTGCGACCCCACTACTC 167

RESULT 151  
US-08-442-144A-48/C  
Sequence 48, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yanko Trujillo  
REGISTRATION NUMBER: 35,719

REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 821  
US-08-442-144A-48

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 186 TTGGGACCCCAACTACTC 167

RESULT 152  
US-08-442-144A-49/C  
Sequence 49, Application US/08442144A  
Patent No. 6214583  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
APPLICANT: Eileen Beall  
APPLICANT: Bruce Irvine  
APPLICANT: Janice Kolberg  
APPLICANT: Michael S. Urdea  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows NT  
SOFTWARE: Microsoft Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/442,144A  
FILING DATE: MAY 16, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/221,653  
FILING DATE: APRIL 1, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yalco Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: CHIR-0121  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
TELEX:  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 Nucleotides  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: 9j61329  
US-08-442-144A-49

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 186 TTGGGACCCCAACTACTC 167

RESULT 153  
US-08-441-970-33/C  
Sequence 33, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacke, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE: (ATCC # 40394)  
INDIVIDUAL ISOLATE: hc1  
US-08-441-970-33

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 186 TTGGGACCCCAACTACTC 167

RESULT 154  
US-08-441-970-34/C  
Sequence 34, Application US/08441970

Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: us5  
US-08-441-970-34  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTCCGACCCCACTACTC 20  
Db 186 TTCCGACCCCACTACTC 167  
RESULT 155  
US-08-441-970-35/c  
Sequence 35, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch

COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: aus1  
US-08-441-970-35

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTCCGACCCCACTACTC 20  
Db 186 TTCCGACCCCACTACTC 167

RESULT 156  
US-08-441-970-36/c  
Sequence 36, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809

REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: SP2  
US-08-441-970-36

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCACTACTC 20  
DB 186 TTGCGACCCCACTACTC 167

RESULT 157  
US-08-441-970-37/c  
Sequence 37, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: gm2  
US-08-441-970-37

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCACTACTC 20  
DB 186 TTGCGACCCCACTACTC 167

RESULT 158  
US-08-441-970-38/c  
Sequence 38, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 121  
US-08-441-970-38

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCACTACTC 20  
DB 186 TTGCGACCCCACTACTC 167

RESULT 159  
US-08-441-970-39/c  
Sequence 39, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:

APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29, 809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: us4  
US-08-441-970-39  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 TTGCGACCCCACTACTC 20  
Db 186 TTGCGACCCCACTACTC 167  
RESULT 160  
US-08-441-970-40/c  
Sequence 40, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29, 809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:

SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29, 809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: jh1  
US-08-441-970-40  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 TTGCGACCCCACTACTC 20  
Db 186 TTGCGACCCCACTACTC 167  
RESULT 161  
US-08-441-970-41/c  
Sequence 41, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29, 809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:



TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: nacs  
US-08-441-970-41

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 186 TTGCGACCCCAACTACTC 167

RESULT 162  
US-08-441-970-42/C  
Sequence 42, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: arg2  
US-08-441-970-42  
Query Match 100.0%; Score 20; DB 3; Length 252;

Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 186 TTGCGACCCCAACTACTC 167

RESULT 163  
US-08-441-970-43/C  
Sequence 43, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: spi  
US-08-441-970-43  
Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 186 TTGCGACCCCAACTACTC 167

RESULT 164  
US-08-441-970-44/C  
Sequence 44, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: ghl  
US-08-441-970-44

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20  
DB 186 TTCCGACCCCACTACTC 167

RESULT 165  
US-08-441-970-45/C  
Sequence 45, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: i15  
US-08-441-970-45

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20  
DB 186 TTCCGACCCCACTACTC 167

RESULT 166  
US-08-441-970-48/C  
Sequence 48, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441

TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 821  
US-08-441-970-48

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 186 TTGCGACCCCAACTACTC 167

RESULT 167  
US-08-441-970-49/c  
Sequence 49, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441, 970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29, 809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 9161329  
US-08-441-970-49

Query Match 100.0%; Score 20; DB 3; Length 252;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 186 TTGCGACCCCAACTACTC 167

RESULT 168  
US-08-483-695-1/c  
Sequence 1, Application US/08483695  
Patent No. 5866139  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremdorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3335  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,695  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,265  
FILING DATE: 18-MAR-1993  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4000  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: cDNA to genomic RNA  
US-08-483-695-1

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
Db 193 TTGCGACCCCAACTACTC 174

RESULT 169  
US-08-483-695-24/c  
Sequence 24, Application US/08483695  
Patent No. 5866139  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremdorf, Dina

APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,695.  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,285  
FILING DATE: 18-MAR-1993  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: CDNA to genomic RNA  
US-08-483-695-24  
Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 TTGGGACCCCACTACTC 20  
Db 193 TTGGGACCCCACTACTC 174  
RESULT 170  
US-08-483-695-25/c  
Sequence 25, Application US/08483695  
Patent No. 5866139  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremendorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,695  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,285  
FILING DATE: 18-MAR-1993  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: CDNA to genomic RNA  
US-08-483-695-25  
Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 TTGGGACCCCACTACTC 20  
Db 193 TTGGGACCCCACTACTC 174  
RESULT 171  
US-08-483-695-26/c  
Sequence 26, Application US/08483695  
Patent No. 5866139  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremendorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,695  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,285  
FILING DATE: 18-MAR-1993  
APPLICATION NUMBER: FR 91 06 882

FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: cDNA to genomic RNA  
US-08-483-695-26

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 193 TTGCGACCCCAACTACTC 174

RESULT 172  
US-07-965-285-1/c  
Sequence 1, Application US/07965285  
Patent No. 5879904  
GENERAL INFORMATION:  
APPLICANT: Brecht, Christian  
APPLICANT: Kremendorf, Dina  
TITLE OF INVENTION: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,285  
FILING DATE: 18-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other

DESCRIPTION: cDNA to genomic RNA  
US-07-965-285-1  
Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 193 TTGCGACCCCAACTACTC 174

RESULT 173  
US-07-965-285-24/c  
Sequence 24, Application US/07965285  
Patent No. 5879904  
GENERAL INFORMATION:  
APPLICANT: Brecht, Christian  
APPLICANT: Kremendorf, Dina  
TITLE OF INVENTION: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,285  
FILING DATE: 18-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: cDNA to genomic RNA  
US-07-965-285-24

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 193 TTGCGACCCCAACTACTC 174

RESULT 174  
US-07-965-285-25/c  
Sequence 25, Application US/07965285

Patent No. 5879904  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremsdorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,285  
FILING DATE: 18-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: CDNA to genomic RNA  
US-07-965-285-25

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCACTACTC 20  
|||||  
Db 193 TTGCGACCCCACTACTC 174

RESULT 175  
US-07-965-285-26/C  
Sequence 26, Application US/07965285  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremsdorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC

COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,285  
FILING DATE: 18-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: CDNA to genomic RNA  
US-07-965-285-26

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCACTACTC 20  
|||||  
Db 193 TTGCGACCCCACTACTC 174

RESULT 176  
US-08-487-231-1/C  
Sequence 1, Application US/08487231  
Patent No. 5919454  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremsdorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,231  
FILING DATE: 07-JUNE-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/965,285  
FILING DATE: 18-MAR-1993  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: CDNA to genomic RNA  
US-08-487-231-1

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCAACTACTC 20  
Db 193 TTGCGACCCCAACTACTC 174

RESULT 177  
US-08-487-231-24/c  
Sequence 24, Application US/08487231  
Patent No. 5919454  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremendorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,231  
FILING DATE: 07-JUNE-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/965,285  
FILING DATE: 18-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: CDNA to genomic RNA  
US-08-487-231-24

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCAACTACTC 20  
Db 193 TTGCGACCCCAACTACTC 174

RESULT 178  
US-08-487-231-25/c  
Sequence 25, Application US/08487231  
Patent No. 5919454  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremendorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,231  
FILING DATE: 07-JUNE-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/965,285  
FILING DATE: 18-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-02000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: CDNA to genomic RNA  
US-08-487-231-25

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
Db 193 TTCCGACCCCAACTACTC 174

## RESULT 179

US-08-487-231-26/c  
; Sequence 26, Application US/08487231  
; Patent No. 5919454  
; GENERAL INFORMATION:  
; APPLICANT: Brechot, Christian  
; APPLICANT: Kremsdorf, Dina  
; APPLICANT: Porchon, Colette  
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS: 46  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,231  
; FILING DATE: 07-JUNE-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/965,285  
; FILING DATE: 18-MAR-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 91 06 882  
; FILING DATE: 06-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 05286-0001-02000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 256 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other  
; DESCRIPTION: cDNA to genomic RNA  
US-08-487-231-26

Query Match 100.0%; Score 20; DB 2; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
Db 193 TTCCGACCCCAACTACTC 174

RESULT 180  
US-09-201-912-1/c  
; Sequence 1, Application US/09201912  
; Patent No. 6210962

## GENERAL INFORMATION:

; APPLICANT: Brechot, Christian  
; APPLICANT: Kremsdorf, Dina  
; APPLICANT: Porchon, Colette  
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS: 46  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/201,912  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/965,285  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 05286-0001-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 256 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other  
; DESCRIPTION: cDNA to genomic RNA  
US-09-201-912-1

Query Match 100.0%; Score 20; DB 3; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCAACTACTC 20  
Db 193 TTCCGACCCCAACTACTC 174

## RESULT 181

US-09-201-912-24/c  
; Sequence 24, Application US/09201912  
; Patent No. 6210962  
; GENERAL INFORMATION:  
; APPLICANT: Brechot, Christian  
; APPLICANT: Kremsdorf, Dina  
; APPLICANT: Porchon, Colette  
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS: 46  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA



ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/201,912  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,285  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: cDNA to genomic RNA  
US-09-201-912-24

Query Match 100.0%; Score 20; DB 3; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCACACTACTC 20  
Db 193 TTGGGACCCACACTACTC 174

RESULT 182  
US-09-201-912-25/C  
Sequence 25, Application US/09201912  
Patent No. 6210962  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremesdorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/201,912  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,285  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: cDNA to genomic RNA  
US-09-201-912-25

Query Match 100.0%; Score 20; DB 3; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCACACTACTC 20  
Db 193 TTGGGACCCACACTACTC 174

RESULT 183  
US-09-201-912-26/C  
Sequence 26, Application US/09201912  
Patent No. 6210962  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Kremesdorf, Dina  
APPLICANT: Porchon, Colette  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
TITLE OF INVENTION: Applications  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/201,912  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/965,285  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: cDNA to genomic RNA  
US-09-201-912-26

Query Match 100.0%; Score 20; DB 3; Length 256;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCACTACTC 20  
DB 193 TTGGGACCCCACTACTC 174

RESULT 184  
US-08-757-653-121/c

Sequence 121, Application US/08757653  
Patent No. 5843669

GENERAL INFORMATION:

APPLICANT: Kaiser, Michael W.

APPLICANT: Lyamichev, Victor I.

APPLICANT: Lyamichev, Natasha

TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States Of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757,653

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: FORS-02565

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 121:

SEQUENCE CHARACTERISTICS:

LENGTH: 281 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-757-653-121

Query Match 100.0%; Score 20; DB 2; Length 281;

Best Local Similarity 100.0%; Pred. No. 0.0029;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCACTACTC 20

DB 218 TTGGGACCCCACTACTC 199

RESULT 185  
US-08-757-653-123/c

Sequence 123, Application US/08757653  
Patent No. 5843669

GENERAL INFORMATION:

APPLICANT: Kaiser, Michael W.

APPLICANT: Lyamichev, Victor I.

APPLICANT: Lyamichev, Natasha

TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States Of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757,653

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: FORS-02565

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 123:

SEQUENCE CHARACTERISTICS:

LENGTH: 281 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-757-653-123

Query Match 100.0%; Score 20; DB 2; Length 281;

Best Local Similarity 100.0%; Pred. No. 0.0029;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCACTACTC 20

DB 218 TTGGGACCCCACTACTC 199

RESULT 186  
US-08-757-653-126/c

Sequence 126, Application US/08757653  
Patent No. 5843669

GENERAL INFORMATION:

APPLICANT: Kaiser, Michael W.

APPLICANT: Lyamichev, Victor I.

APPLICANT: Lyamichev, Natasha

TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States Of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757,653

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: FORS-02565

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 126:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-757-653-126

Query Match 100.0%; Score 20; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCCGGACCCCACTACTC 20  
Db 218 TTCCGGACCCCACTACTC 199

RESULT 187  
US-08-757-653-127

; Sequence 127, Application US/08757653  
; Patent No. 5843669

; GENERAL INFORMATION:

; APPLICANT: Kaiser, Michael W.  
; APPLICANT: Lyamichev, Victor I.

; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

; NUMBER OF INVENTIONS: Thermostable FEN-1 Endonucleases

; NUMBER OF SEQUENCES: 190

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Medlen & Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States Of America

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/757,653

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Ingolia, Diane E.

; REGISTRATION NUMBER: 40,027

; REFERENCE/DOCKET NUMBER: FORS-02565

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 705-8410

; TELEFAX: (415) 397-8338

; INFORMATION FOR SEQ ID NO: 127:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 281 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-757-653-127

Query Match 100.0%; Score 20; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCCGGACCCCACTACTC 20  
Db 64 TTCCGGACCCCACTACTC 83

RESULT 188  
US-08-757-653-128

; Sequence 128, Application US/08757653  
; Patent No. 5843669

; GENERAL INFORMATION:

; APPLICANT: Kaiser, Michael W.

; APPLICANT: Lyamichev, Victor I.

; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

; NUMBER OF INVENTIONS: Thermostable FEN-1 Endonucleases

; NUMBER OF SEQUENCES: 190

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Medlen & Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States Of America

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/757,653

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Ingolia, Diane E.

; REGISTRATION NUMBER: 40,027

; REFERENCE/DOCKET NUMBER: FORS-02565

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 705-8410

; TELEFAX: (415) 397-8338

; INFORMATION FOR SEQ ID NO: 128:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 281 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-757-653-128

Query Match 100.0%; Score 20; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTCCGGACCCCACTACTC 20  
Db 64 TTCCGGACCCCACTACTC 83

RESULT 189

US-08-757-653-129

; Sequence 129, Application US/08757653

; Patent No. 5843669

; GENERAL INFORMATION:

; APPLICANT: Kaiser, Michael W.

; APPLICANT: Lyamichev, Victor I.

; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

; NUMBER OF INVENTIONS: Thermostable FEN-1 Endonucleases

; NUMBER OF SEQUENCES: 190

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Medlen & Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States Of America

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/757,653  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Ingolia, Diane E.  
;; REGISTRATION NUMBER: 40,027  
;; REFERENCE/DOCKET NUMBER: FORS-02565  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 705-8410  
;; TELEFAX: (415) 397-8338  
;; INFORMATION FOR SEQ ID NO: 129:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 281 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-757-653-129

Query Match 100.0%; Score 20; DB 2; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 64 TTGGGACCCCACTACTC 83

RESULT 190  
US-08-757-653-132  
;; Sequence 132, Application US/08757653  
;; Patent No. 5843669  
;; GENERAL INFORMATION:  
;; APPLICANT: Kaiser, Michael W.  
;; APPLICANT: Lyamichev, Victor I.  
;; APPLICANT: Lyamichev, Natasha  
;; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using  
;; NUMBER OF SEQUENCES: 190  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Medlen & Carroll, LLP  
;; STREET: 220 Montgomery Street, Suite 2200  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: United States Of America  
;; ZIP: 94104  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/757,653  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Ingolia, Diane E.  
;; REGISTRATION NUMBER: 40,027  
;; REFERENCE/DOCKET NUMBER: FORS-02565  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 705-8410  
;; TELEFAX: (415) 397-8338  
;; INFORMATION FOR SEQ ID NO: 132:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 281 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-757-653-132

Query Match 100.0%; Score 20; DB 2; Length 281;

Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTGGGACCCCACTACTC 20  
Db 64 TTGGGACCCCACTACTC 83

RESULT 191  
US-08-520-946-121/c  
;; Sequence 121, Application US/08520946  
;; Patent No. 6372424  
;; GENERAL INFORMATION:  
;; APPLICANT: BROW, MARY ANN D.  
;; APPLICANT: LYAMICHEV, VICTOR I.  
;; APPLICANT: OLIVE, DAVID M.  
;; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
;; NUMBER OF SEQUENCES: 160  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: MEDLEN & CARROLL  
;; STREET: 220 MONTGOMERY STREET, SUITE 2200  
;; CITY: SAN FRANCISCO  
;; STATE: CALIFORNIA  
;; COUNTRY: UNITED STATES OF AMERICA  
;; ZIP: 94104  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/520,946  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: CARROLL, PETER G.  
;; REGISTRATION NUMBER: 32,837  
;; REFERENCE/DOCKET NUMBER: FORS-01756  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 705-8410  
;; TELEFAX: (415) 397-8338  
;; INFORMATION FOR SEQ ID NO: 121:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 281 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-520-946-121

Query Match 100.0%; Score 20; DB 3; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 218 TTGGGACCCCACTACTC 199

RESULT 192  
US-08-520-946-123/c  
;; Sequence 123, Application US/08520946  
;; Patent No. 6372424  
;; GENERAL INFORMATION:  
;; APPLICANT: BROW, MARY ANN D.  
;; APPLICANT: LYAMICHEV, VICTOR I.  
;; APPLICANT: OLIVE, DAVID M.  
;; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
;; NUMBER OF SEQUENCES: 160  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: MEDLEN & CARROLL

```
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,946
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-520-946-123

Query Match          100.0%; Score 20; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20
DB 218 TTGCGACCCCAACTACTC 199

RESULT 193
US-08-520-946-126/c
Sequence 126, Application US/08520946
Patent No. 6372424
GENERAL INFORMATION:
APPLICANT: BROW, MARY ANN D.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
TITLE OF INVENTION: PATHOGENS
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,946
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
```

```
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-520-946-126

Query Match          100.0%; Score 20; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20
DB 218 TTGCGACCCCAACTACTC 199

RESULT 194
US-08-520-946-127
Sequence 127, Application US/08520946
Patent No. 6372424
GENERAL INFORMATION:
APPLICANT: BROW, MARY ANN D.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
TITLE OF INVENTION: PATHOGENS
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,946
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
TELEFAX: (415) 705-8410
INFORMATION FOR SEQ ID NO: 127:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-520-946-127

Query Match          100.0%; Score 20; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20
DB 64 TTGCGACCCCAACTACTC 83

RESULT 195
US-08-520-946-128
Sequence 128, Application US/08520946
```

Patent No. 6372424  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
APPLICANT: LYAMICHEV, VICTOR I.  
APPLICANT: OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
TITLE OF INVENTION: PATHOGENS  
NUMBER OF SEQUENCES: 160  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,946  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 128:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-520-946-128

Query Match 100.0%; Score 20; DB 3; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 TTGGGACCCACACTACTC 20  
DB 64 TTGGGACCCACACTACTC 83

RESULT 196  
US-08-520-946-129  
Sequence 129; Application US/08520946  
Patent No. 6372424  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
APPLICANT: LYAMICHEV, VICTOR I.  
APPLICANT: OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
TITLE OF INVENTION: PATHOGENS  
NUMBER OF SEQUENCES: 160  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/520,946  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 129:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-520-946-129

Query Match 100.0%; Score 20; DB 3; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 TTGGGACCCACACTACTC 20  
DB 64 TTGGGACCCACACTACTC 83

RESULT 197  
US-08-520-946-132  
Sequence 132; Application US/08520946  
Patent No. 6372424  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
APPLICANT: LYAMICHEV, VICTOR I.  
APPLICANT: OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
TITLE OF INVENTION: PATHOGENS  
NUMBER OF SEQUENCES: 160  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/520,946  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 132:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-520-946-132

Query Match 100.0%; Score 20; DB 3; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.0029;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
Db 64 TTGGGACCCCACTACTC 83

## RESULT 198

US-09-655-378A-121/C

Sequence 121, Application US/09655378A

Patent No. 6673616

GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.

LYAMICHEV, VICTOR I.

OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF

PATHOGENS

NUMBER OF SEQUENCES: 165

CORRESPONDENCE ADDRESS:

ADDRESSER: MEDLEN &amp; CARROLL

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/655,378A

FILING DATE: 05-Sep-2000

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: FORS-01756

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 121:

SEQUENCE CHARACTERISTICS:

LENGTH: 281 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 121:

US-09-655-378A-121

Query Match 100.0%; Score 20; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.0029;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
Db 218 TTGGGACCCCACTACTC 199

## RESULT 199

US-09-655-378A-123/C

Sequence 123, Application US/09655378A

Patent No. 6673616

GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.

LYAMICHEV, VICTOR I.

OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF

PATHOGENS

NUMBER OF SEQUENCES: 165

CORRESPONDENCE ADDRESS:

ADDRESSER: MEDLEN &amp; CARROLL

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/655,378A

FILING DATE: 05-Sep-2000

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: FORS-01756

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 123:

SEQUENCE CHARACTERISTICS:

LENGTH: 281 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 123:

US-09-655-378A-123

Query Match 100.0%; Score 20; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.0029;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCACTACTC 20  
Db 218 TTGGGACCCCACTACTC 199

## RESULT 200

US-09-655-378A-126/C

Sequence 126, Application US/09655378A

Patent No. 6673616

GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.

LYAMICHEV, VICTOR I.

OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF

PATHOGENS

NUMBER OF SEQUENCES: 165

CORRESPONDENCE ADDRESS:

ADDRESSER: MEDLEN &amp; CARROLL

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/655,378A

FILING DATE: 05-Sep-2000

CLASSIFICATION: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: FORS-01756

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 126:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 281 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 126:  
US-09-655-378A-126.

Query Match 100.0%; Score 20; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred.No. 0.0029;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 218 TTGCGAGCCCAACTACTC 199

Search completed: April 25, 2005, 13:47:39  
Job time : 104.316 secs



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OM nucleic - nucleic search, using bw model

Run on: April 25, 2005, 13:45:46 ; Search time 280.526 Seconds

(Without alignments)  
432.833 Million cell updates/sec

Title: US-08-887-505B-28

Perfect score: 20

Sequence: 1 TTCGGACCCACACTACTC 20

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 5633728 seqs, 3035525691 residues

Word size : 0

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Minimum DB seq length: 0

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Post-Processing: Listing first 1000 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 94	20	100.0	281	10	US-09-941-193A-126	Sequence 126, App	C 167	20	100.0	5860	16	US-10-734-801-17	Sequence 17, Appl
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C 98	20	100.0	281	10	US-09-941-193A-132	Sequence 132, App	C 171	20	100.0	7992	13	US-10-005-469-1	Sequence 1, Appl
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C 101	20	100.0	282	10	US-09-941-193A-124	Sequence 124, App	C 174	20	100.0	7992	13	US-10-005-469-5	Sequence 5, Appl
C 102	20	100.0	282	10	US-09-941-193A-130	Sequence 130, App	C 175	20	100.0	7992	13	US-10-005-469-6	Sequence 6, Appl
C 103	20	100.0	286	9	US-09-825-574-21	Sequence 21, App	C 176	20	100.0	7992	17	US-10-434-842-1	Sequence 1, Appl
C 104	20	100.0	286	10	US-09-882-945A-21	Sequence 21, App	C 177	20	100.0	7992	17	US-10-434-842-2	Sequence 2, Appl
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C 133	20	100.0	337	17	US-10-356-861-45	Sequence 45, App	C 206	20	100.0	8642	13	US-10-029-907-2	Sequence 2, Appl
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C 135	20	100.0	337	18	US-10-897-793-45	Sequence 45, App	C 208	20	100.0	8642	18	US-10-309-561-2	Sequence 2, Appl
C 136	20	100.0	337	19	US-10-783-557-45	Sequence 45, App	C 209	20	100.0	8642	18	US-10-686-835-2	Sequence 2, Appl
C 137	20	100.0	341	9	US-09-814-297-44	Sequence 44, App	C 210	20	100.0	8643	13	US-10-686-835-2	Sequence 2, Appl
C 138	20	100.0	341	10	US-09-814-357-3	Sequence 3, Appl	C 211	20	100.0	8643	13	US-10-029-907-4	Sequence 4, Appl
C 139	20	100.0	341	15	US-09-814-351-3	Sequence 3, Appl	C 212	20	100.0	8643	18	US-10-309-561-4	Sequence 4, Appl
C 140	20	100.0	341	15	US-10-259-275-35	Sequence 35, App	C 213	20	100.0	8643	18	US-10-789-335-4	Sequence 4, Appl
C 141	20	100.0	347	15	US-10-132-295-1	Sequence 1, App	C 214	20	100.0	8643	18	US-10-686-835-4	Sequence 4, Appl
C 142	20	100.0	366	9	US-09-877-526A-48	Sequence 48, App	C 215	20	100.0	8648	13	US-10-029-907-5	Sequence 5, Appl
C 143	20	100.0	366	10	US-09-992-160-48	Sequence 48, App	C 216	20	100.0	8648	15	US-10-309-561-5	Sequence 5, Appl
C 144	20	100.0	366	10	US-09-740-332-9701	Sequence 9701, App	C 217	20	100.0	8648	18	US-10-789-335-5	Sequence 5, Appl
C 145	20	100.0	366	14	US-09-817-879-9701	Sequence 9701, App	C 218	20	100.0	9353	18	US-10-686-835-5	Sequence 5, Appl
C 146	20	100.0	366	14	US-10-056-761-48	Sequence 48, App	C 219	20	100.0	9353	18	US-10-475-024-17	Sequence 17, App
C 147	20	100.0	366	17	US-10-422-050-48	Sequence 48, App	C 220	20	100.0	9365	10	US-09-827-668-7	Sequence 7, App
C 148	20	100.0	366	18	US-10-669-841-1618	Sequence 1618, App	C 221	20	100.0	9411	18	US-09-816-359-1	Sequence 1, App
C 149	20	100.0	374	17	US-10-334-4098-32	Sequence 32, App	C 222	20	100.0	9411	18	US-10-448-774-1	Sequence 1, App
C 150	20	100.0	383	19	US-10-626-879-9	Sequence 9, App	C 223	20	100.0	9413	10	US-09-827-668-6	Sequence 6, App
C 151	20	100.0	384	17	US-10-332-626-1	Sequence 1, App	C 224	20	100.0	9416	9	US-09-818-076-19	Sequence 19, App
C 152	20	100.0	386	10	US-09-940-925A-122	Sequence 122, App	C 225	20	100.0	9416	10	US-09-929-955-13	Sequence 13, App
C 153	20	100.0	386	15	US-09-941-193A-122	Sequence 122, App	C 226	20	100.0	9416	10	US-09-929-955-13	Sequence 13, App
C 154	20	100.0	393	15	US-10-276-513-5	Sequence 5, App	C 227	20	100.0	9416	13	US-10-104-966-13	Sequence 13, App
C 155	20	100.0	412	15	US-10-276-513-4	Sequence 4, App	C 228	20	100.0	9416	17	US-10-719-619-13	Sequence 13, App
C 156	20	100.0	652	9	US-09-851-138-59	Sequence 59, App	C 229	20	100.0	9416	18	US-10-817-591-13	Sequence 13, App
C 157	20	100.0	685	10	US-09-853-409-37	Sequence 37, App	C 230	20	100.0	9599	17	US-10-189-359-13	Sequence 13, App

C 231	20	100.0	9605	17	US-10-467-000-2	Sequence 2, Appli	C 304	19	95.0	177	9	US-09-899-302-69	Sequence 69, Appl
C 232	20	100.0	9609	18	US-10-333-449A-33	Sequence 33, Appl	C 305	19	95.0	177	9	US-09-899-302-70	Sequence 70, Appl
C 233	20	100.0	9632	18	US-10-475-989-2	Sequence 2, Appli	C 306	19	95.0	177	9	US-09-899-302-71	Sequence 71, Appl
C 234	20	100.0	9646	9	US-09-742-659-3	Sequence 3, Appli	C 307	19	95.0	177	9	US-09-899-302-72	Sequence 72, Appl
C 235	20	100.0	9646	9	US-09-238-076-1	Sequence 1, Appli	C 308	19	95.0	177	9	US-09-899-302-73	Sequence 73, Appl
C 236	20	100.0	9646	10	US-09-995-937-1	Sequence 1, Appli	C 309	19	95.0	177	9	US-09-899-302-74	Sequence 74, Appl
C 237	20	100.0	9646	14	US-09-917-563-1	Sequence 1, Appli	C 310	19	95.0	177	9	US-09-899-302-75	Sequence 75, Appl
C 238	20	100.0	10690	10	US-10-125-940-1	Sequence 1, Appli	C 311	19	95.0	177	9	US-09-899-302-76	Sequence 76, Appl
C 239	20	100.0	10690	16	US-10-125-920-1	Sequence 1, Appli	C 312	19	95.0	177	9	US-09-899-302-77	Sequence 77, Appl
C 240	20	100.0	10690	17	US-10-467-000-3	Sequence 3, Appli	C 313	19	95.0	177	9	US-09-899-302-78	Sequence 78, Appl
C 241	20	100.0	10803	9	US-09-747-419-1	Sequence 17, Appl	C 314	19	95.0	177	9	US-09-899-302-79	Sequence 79, Appl
C 242	20	100.0	10803	15	US-10-259-275-17	Sequence 17, Appl	C 315	19	95.0	177	10	US-09-899-044-57	Sequence 57, Appl
C 243	20	100.0	12305	18	US-10-422-323A-2	Sequence 2, Appli	C 316	19	95.0	177	10	US-09-899-044-58	Sequence 58, Appl
C 244	20	100.0	12315	18	US-10-422-323A-1	Sequence 5, Appli	C 317	19	95.0	177	10	US-09-899-044-61	Sequence 61, Appl
C 245	20	100.0	12980	9	US-09-238-076-5	Sequence 5, Appli	C 318	19	95.0	177	10	US-09-899-044-62	Sequence 62, Appl
C 246	20	100.0	12980	10	US-09-995-937-5	Sequence 5, Appli	C 319	19	95.0	177	10	US-09-899-044-65	Sequence 65, Appl
C 247	20	100.0	12980	10	US-09-917-563-5	Sequence 5, Appli	C 320	19	95.0	177	10	US-09-899-044-66	Sequence 66, Appl
C 248	20	100.0	12980	8	US-08-887-505-111	Sequence 11, App	C 321	19	95.0	177	10	US-09-899-044-67	Sequence 67, Appl
C 249	19	95.0	19	8	US-08-887-505-114	Sequence 114, App	C 322	19	95.0	177	10	US-09-899-044-68	Sequence 68, Appl
C 250	19	95.0	19	9	US-09-930-781-2	Sequence 2, Appli	C 323	19	95.0	177	10	US-09-899-044-69	Sequence 69, Appl
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C 252	19	95.0	19	18	US-10-667-271-158	Sequence 158, App	C 325	19	95.0	177	10	US-09-899-044-72	Sequence 72, Appl
C 253	19	95.0	19	18	US-10-667-271-166	Sequence 166, App	C 326	19	95.0	177	10	US-09-899-044-73	Sequence 73, Appl
C 254	19	95.0	19	18	US-10-667-271-854	Sequence 854, App	C 327	19	95.0	177	10	US-09-899-044-74	Sequence 74, Appl
C 255	19	95.0	19	18	US-10-667-271-862	Sequence 862, App	C 328	19	95.0	177	10	US-09-899-044-75	Sequence 75, Appl
C 256	19	95.0	19	18	US-10-819-564-2	Sequence 2, Appli	C 329	19	95.0	177	10	US-09-899-044-76	Sequence 76, Appl
C 257	19	95.0	40	18	US-10-318-416B-25	Sequence 25, Appl	C 330	19	95.0	177	10	US-09-899-044-77	Sequence 77, Appl
C 258	19	95.0	177	9	US-09-294-121A-57	Sequence 57, Appl	C 331	19	95.0	177	10	US-09-899-044-78	Sequence 78, Appl
C 259	19	95.0	177	9	US-09-294-121A-58	Sequence 58, Appl	C 332	19	95.0	177	10	US-09-899-044-79	Sequence 79, Appl
C 260	19	95.0	177	9	US-09-294-121A-61	Sequence 61, Appl	C 333	19	95.0	177	10	US-09-899-044-80	Sequence 80, Appl
C 261	19	95.0	177	9	US-09-294-121A-62	Sequence 62, Appl	C 334	19	95.0	177	18	US-10-822-711-57	Sequence 57, Appl
C 262	19	95.0	177	9	US-09-294-121A-65	Sequence 65, Appl	C 335	19	95.0	177	18	US-10-822-711-58	Sequence 58, Appl
C 263	19	95.0	177	9	US-09-294-121A-66	Sequence 66, Appl	C 336	19	95.0	177	18	US-10-822-711-61	Sequence 61, Appl
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C 266	19	95.0	177	9	US-09-294-121A-69	Sequence 69, Appl	C 339	19	95.0	177	18	US-10-822-711-66	Sequence 66, Appl
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C 268	19	95.0	177	9	US-09-294-121A-72	Sequence 72, Appl	C 341	19	95.0	177	18	US-10-822-711-68	Sequence 68, Appl
C 269	19	95.0	177	9	US-09-294-121A-73	Sequence 73, Appl	C 342	19	95.0	177	18	US-10-822-711-69	Sequence 69, Appl
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C 271	19	95.0	177	9	US-09-294-121A-75	Sequence 75, Appl	C 344	19	95.0	177	18	US-10-822-711-72	Sequence 72, Appl
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C 275	19	95.0	177	9	US-09-294-121A-79	Sequence 79, Appl	C 348	19	95.0	177	18	US-10-822-711-76	Sequence 76, Appl
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C 281	19	95.0	177	9	US-09-899-082A-65	Sequence 65, Appl	C 354	19	95.0	178	9	US-09-294-121A-60	Sequence 60, Appl
C 282	19	95.0	177	9	US-09-899-082A-66	Sequence 66, Appl	C 355	19	95.0	178	9	US-09-294-121A-71	Sequence 71, Appl
C 283	19	95.0	177	9	US-09-899-082A-67	Sequence 67, Appl	C 356	19	95.0	178	9	US-09-294-121A-81	Sequence 81, Appl
C 284	19	95.0	177	9	US-09-899-082A-68	Sequence 68, Appl	C 357	19	95.0	178	9	US-09-899-082A-59	Sequence 59, Appl
C 285	19	95.0	177	9	US-09-899-082A-69	Sequence 69, Appl	C 358	19	95.0	178	9	US-09-899-082A-60	Sequence 60, Appl
C 286	19	95.0	177	9	US-09-899-082A-70	Sequence 70, Appl	C 359	19	95.0	178	9	US-09-899-082A-71	Sequence 71, Appl
C 287	19	95.0	177	9	US-09-899-082A-72	Sequence 72, Appl	C 360	19	95.0	178	9	US-09-899-082A-81	Sequence 81, Appl
C 288	19	95.0	177	9	US-09-899-082A-73	Sequence 73, Appl	C 361	19	95.0	178	9	US-09-899-302-59	Sequence 59, Appl
C 289	19	95.0	177	9	US-09-899-082A-74	Sequence 74, Appl	C 362	19	95.0	178	9	US-09-899-302-60	Sequence 60, Appl
C 290	19	95.0	177	9	US-09-899-082A-75	Sequence 75, Appl	C 363	19	95.0	178	9	US-09-899-302-71	Sequence 71, Appl
C 291	19	95.0	177	9	US-09-899-082A-76	Sequence 76, Appl	C 364	19	95.0	178	9	US-09-899-302-81	Sequence 81, Appl
C 292	19	95.0	177	9	US-09-899-082A-77	Sequence 77, Appl	C 365	19	95.0	178	10	US-09-899-044-59	Sequence 59, Appl
C 293	19	95.0	177	9	US-09-899-082A-78	Sequence 78, Appl	C 366	19	95.0	178	10	US-09-899-044-60	Sequence 60, Appl
C 294	19	95.0	177	9	US-09-899-082A-79	Sequence 79, Appl	C 367	19	95.0	178	10	US-09-899-044-71	Sequence 71, Appl
C 295	19	95.0	177	9	US-09-899-082A-80	Sequence 80, Appl	C 368	19	95.0	178	10	US-09-899-044-81	Sequence 81, Appl
C 296	19	95.0	177	9	US-09-899-302-57	Sequence 57, Appl	C 369	19	95.0	178	10	US-10-822-711-59	Sequence 59, Appl
C 297	19	95.0	177	9	US-09-899-302-58	Sequence 58, Appl	C 370	19	95.0	178	18	US-10-822-711-61	Sequence 61, Appl
C 298	19	95.0	177	9	US-09-899-302-61	Sequence 61, Appl	C 371	19	95.0	178	18	US-10-822-711-71	Sequence 71, Appl
C 299	19	95.0	177	9	US-09-899-302-62	Sequence 62, Appl	C 372	19	95.0	178	18	US-10-822-711-81	Sequence 81, Appl
C 300	19	95.0	177	9	US-09-899-302-65	Sequence 65, Appl	C 373	18	90.0	18	8	US-08-887-505-112	Sequence 112, App
C 301	19	95.0	177	9	US-09-899-302-66	Sequence 66, Appl	C 374	18	90.0	18	8	US-08-887-505-115	Sequence 115, App
C 302	19	95.0	177	9	US-09-899-302-67	Sequence 67, Appl	C 375	18	90.0	19	18	US-10-667-271-150	Sequence 150, App
C 303	19	95.0	177	9	US-09-899-302-68	Sequence 68, Appl	C 376	18	90.0	19	18	US-10-667-271-151	Sequence 151, App

377	18	90.0	19	18	US-10-667-271-846	Sequence 846, App	C 450	14	70.0	17	18	US-10-669-841-2649	Sequence 2649, App
378	18	90.0	19	18	US-10-667-271-847	Sequence 847, App	C 451	14	70.0	17	18	US-10-667-271-161	Sequence 161, App
379	18	90.0	20	8	US-08-887-505-27	Sequence 27, Appl	C 452	14	70.0	19	18	US-10-667-271-177	Sequence 177, App
380	18	90.0	20	8	US-08-887-505-29	Sequence 29, Appl	C 453	14	70.0	19	18	US-10-667-271-857	Sequence 857, App
381	18	90.0	20	10	US-09-888-164-9	Sequence 9, Appl	C 454	14	70.0	19	18	US-10-667-271-857	Sequence 873, App
382	18	90.0	20	18	US-10-318-41GB-20	Sequence 20, Appl	C 455	14	70.0	20	8	US-08-887-505-25	Sequence 25, Appl
383	18	90.0	25	18	US-10-318-41GB-8	Sequence 8, Appl	C 456	14	70.0	20	8	US-08-887-505-11	Sequence 31, Appl
384	18	90.0	39	9	US-09-292-563-9	Sequence 9, Appl	C 457	14	70.0	23	18	US-10-318-41GB-29	Sequence 29, Appl
385	18	90.0	39	9	US-09-979-999-9	Sequence 9, Appl	C 458	14	70.0	31	18	US-10-782-646-6	Sequence 6, Appl
386	17	85.0	17	8	US-08-887-505-113	Sequence 113, App	C 459	14	70.0	31	17	US-10-782-646-7	Sequence 7, Appl
387	17	85.0	17	8	US-08-887-505-116	Sequence 116, App	C 460	14	70.0	431	17	US-10-424-599-12626	Sequence 12626, App
388	17	85.0	17	10	US-09-740-333-4498	Sequence 4498, App	C 461	14	70.0	454	18	US-10-425-115-12339	Sequence 12339, A
389	17	85.0	17	10	US-09-817-879-4498	Sequence 4498, App	C 462	14	70.0	482	17	US-10-424-599-115670	Sequence 115670, A
390	17	85.0	17	18	US-10-669-841-7091	Sequence 7091, App	C 463	14	70.0	486	13	US-10-027-632-177422	Sequence 177422, A
C 391	17	85.0	17	18	US-10-667-271-153	Sequence 153, App	C 464	14	70.0	486	17	US-10-027-632-177422	Sequence 177422, A
C 392	17	85.0	19	18	US-10-667-271-156	Sequence 156, App	C 465	14	70.0	592	18	US-10-425-115-100618	Sequence 100618, A
C 393	17	85.0	19	18	US-10-667-271-849	Sequence 849, App	C 466	14	70.0	765	18	US-10-425-115-100618	Sequence 100618, A
C 394	17	85.0	19	18	US-10-667-271-852	Sequence 852, App	C 467	14	70.0	924	17	US-10-282-115-108563	Sequence 108563, A
C 395	17	85.0	20	8	US-08-887-505-117	Sequence 117, App	C 468	14	70.0	1634	18	US-10-282-122A-34798	Sequence 34798, A
C 396	17	85.0	17	16	US-10-336-964-18	Sequence 117, App	C 469	14	70.0	1634	19	US-10-363-345A-35714	Sequence 35714, A
C 397	16	80.0	16	8	US-08-887-505-76	Sequence 76, Appl	C 470	14	70.0	1634	19	US-10-363-483A-35714	Sequence 35714, A
C 398	16	80.0	17	10	US-09-740-332-57	Sequence 57, Appl	C 471	14	70.0	1634	19	US-10-363-483A-35714	Sequence 35714, A
C 399	16	80.0	17	10	US-09-740-332-58	Sequence 58, Appl	C 472	14	70.0	2000	11	US-09-938-842A-4582	Sequence 4582, App
C 400	16	80.0	17	10	US-09-817-879-57	Sequence 57, Appl	C 473	14	70.0	2000	11	US-10-151-666-14	Sequence 14, Appl
C 401	16	80.0	17	10	US-09-817-879-58	Sequence 58, Appl	C 474	14	70.0	2352	13	US-10-424-599-82545	Sequence 82545, A
C 402	16	80.0	17	18	US-10-669-841-2650	Sequence 2650, App	C 475	14	70.0	3270	17	US-10-473-126-245	Sequence 1272, App
C 403	16	80.0	17	18	US-10-669-841-2651	Sequence 2651, App	C 476	14	70.0	5020	18	US-10-311-455-11712	Sequence 1279, App
C 404	16	80.0	19	18	US-10-667-271-146	Sequence 146, App	C 477	14	70.0	5506	15	US-10-311-455-1179	Sequence 1281, App
C 405	16	80.0	19	18	US-10-667-271-164	Sequence 164, App	C 478	14	70.0	6175	15	US-10-311-455-1179	Sequence 55, Appl
C 406	16	80.0	19	18	US-10-667-271-842	Sequence 842, App	C 479	14	70.0	6224	15	US-10-311-455-1181	Sequence 1394, App
C 407	16	80.0	19	18	US-10-667-271-860	Sequence 860, App	C 480	14	70.0	6224	16	US-10-240-455-55	Sequence 1667, App
C 408	16	80.0	20	8	US-08-887-505-26	Sequence 26, Appl	C 481	14	70.0	9707	15	US-10-311-455-1194	Sequence 1394, App
C 409	16	80.0	20	8	US-08-887-505-30	Sequence 30, Appl	C 482	14	70.0	10717	15	US-10-311-455-1667	Sequence 1538, App
C 410	16	80.0	20	16	US-09-888-164-11	Sequence 11, Appl	C 483	14	70.0	15609	18	US-10-302-547-131	Sequence 548, App
C 411	16	80.0	20	16	US-10-080-979-13	Sequence 11, Appl	C 484	14	70.0	17959	15	US-10-311-455-548	Sequence 2, Appl
C 412	16	80.0	20	17	US-10-443-824-1	Sequence 13, Appl	C 485	14	70.0	17959	16	US-10-240-455-42	Sequence 42, App
C 413	16	80.0	20	18	US-10-780-439-13	Sequence 13, Appl	C 486	14	70.0	23663	15	US-10-240-455-42	Sequence 42, App
C 414	16	80.0	25	8	US-08-887-505-133	Sequence 133, App	C 487	14	70.0	49600	17	US-10-459-262A-2	Sequence 175, App
C 415	15	75.0	15	9	US-09-504-231A-39	Sequence 39, Appl	C 488	13	65.0	13	10	US-09-740-332-4585	Sequence 4585, App
C 416	15	75.0	15	9	US-09-274-553D-39	Sequence 39, Appl	C 489	13	65.0	13	10	US-09-740-332-4611	Sequence 4611, App
C 417	15	75.0	15	10	US-09-740-332-4584	Sequence 4584, App	C 490	13	65.0	13	10	US-09-817-879-4585	Sequence 4585, App
C 418	15	75.0	15	10	US-09-740-332-4586	Sequence 4586, App	C 491	13	65.0	13	10	US-09-817-879-4611	Sequence 4611, App
C 419	15	75.0	15	10	US-09-817-879-4584	Sequence 4584, App	C 492	13	65.0	13	18	US-10-669-841-7178	Sequence 7178, App
C 420	15	75.0	15	18	US-09-817-879-4586	Sequence 4586, App	C 493	13	65.0	13	18	US-10-669-841-7204	Sequence 7204, App
C 421	15	75.0	15	18	US-10-669-841-7177	Sequence 7177, App	C 494	13	65.0	13	18	US-10-257-017B-65153	Sequence 65153, A
C 422	15	75.0	15	18	US-10-669-841-7179	Sequence 7179, App	C 495	13	65.0	13	18	US-10-257-017B-65154	Sequence 65154, A
C 423	15	75.0	16	10	US-09-825-805-14	Sequence 14, Appl	C 496	13	65.0	15	9	US-09-504-231A-11	Sequence 11, Appl
C 424	15	75.0	17	10	US-09-740-332-4497	Sequence 4497, App	C 497	13	65.0	15	9	US-09-740-332-4610	Sequence 4610, App
C 425	15	75.0	17	10	US-09-740-332-4499	Sequence 4499, App	C 498	13	65.0	15	10	US-09-817-879-4610	Sequence 4610, App
C 426	15	75.0	17	10	US-09-817-879-4497	Sequence 4497, App	C 499	13	65.0	15	10	US-10-569-841-1203	Sequence 7203, App
C 427	15	75.0	17	10	US-09-817-879-4499	Sequence 4499, App	C 500	13	65.0	17	10	US-09-888-164-12	Sequence 12, Appl
C 428	15	75.0	17	18	US-10-669-841-7090	Sequence 7090, App	C 501	13	65.0	17	10	US-09-388-164-13	Sequence 13, Appl
C 429	15	75.0	19	18	US-10-667-271-154	Sequence 7092, App	C 502	13	65.0	17	10	US-09-740-332-59	Sequence 59, Appl
C 430	15	75.0	19	18	US-10-667-271-170	Sequence 154, App	C 503	13	65.0	17	10	US-09-817-879-459	Sequence 59, Appl
C 431	15	75.0	19	18	US-10-667-271-850	Sequence 170, App	C 504	13	65.0	17	10	US-10-669-841-2652	Sequence 2652, App
C 432	15	75.0	19	18	US-10-667-271-850	Sequence 850, App	C 505	13	65.0	18	9	US-09-782-361-4	Sequence 4, Appl
C 433	15	75.0	20	10	US-10-667-271-866	Sequence 866, App	C 506	13	65.0	18	9	US-09-802-110B-75	Sequence 75, App
C 434	15	75.0	25	15	US-10-098-2638-54576	Sequence 290, App	C 507	13	65.0	19	10	US-10-667-271-157	Sequence 157, App
C 435	15	75.0	45	9	US-09-728-265-23	Sequence 54576, A	C 508	13	65.0	19	18	US-10-667-271-165	Sequence 165, App
C 436	15	75.0	45	9	US-09-978-261A-23	Sequence 23, Appl	C 509	13	65.0	19	18	US-10-667-271-853	Sequence 853, App
C 437	15	75.0	45	16	US-10-309-438-23	Sequence 23, Appl	C 510	13	65.0	19	18	US-10-667-271-861	Sequence 861, App
C 438	15	75.0	45	16	US-10-719-480-23	Sequence 23, Appl	C 511	13	65.0	19	18	US-10-667-271-861	Sequence 861, App
C 439	15	75.0	45	16	US-10-719-480-23	Sequence 23, Appl	C 512	13	65.0	21	19	US-10-478-633A-86	Sequence 86, Appl
C 440	15	75.0	639	18	US-10-425-115-129831	Sequence 129831, A	C 513	13	65.0	21	19	US-10-478-633A-86	Sequence 86, Appl
C 441	15	75.0	2445	17	US-10-425-114-25176	Sequence 49248, A	C 514	13	65.0	24	18	US-10-318-41GB-31	Sequence 31, Appl
C 442	15	75.0	3177	18	US-10-425-115-49248	Sequence 49248, A	C 515	13	65.0	24	18	US-10-318-41GB-31	Sequence 31, Appl
C 443	14	70.0	15	9	US-09-504-231A-1546	Sequence 1546, App	C 516	13	65.0	25	15	US-10-098-2638-21034	Sequence 21034, A
C 444	14	70.0	15	9	US-09-274-553D-1546	Sequence 1546, App	C 517	13	65.0	25	15	US-09-817-879-526A-28	Sequence 28, Appl
C 445	14	70.0	16	10	US-09-825-805-15	Sequence 15, Appl	C 518	13	65.0	54	9	US-09-992-160-28	Sequence 28, Appl
C 446	14	70.0	17	10	US-09-740-332-56	Sequence 56, Appl	C 519	13	65.0	54	10	US-10-056-761-28	Sequence 28, Appl
C 447	14	70.0	17	10	US-09-817-879-56	Sequence 56, Appl	C 520	13	65.0	54	14	US-10-422-050-28	Sequence 28, Appl
C 448	14	70.0	17	15	US-10-150-779A-7	Sequence 7, Appl	C 521	13	65.0	72	9	US-09-877-526A-29	Sequence 29, Appl
C 449	14	70.0	17	16	US-10-080-979-67	Sequence 67, Appl	C 522	13	65.0	72	9	US-09-877-526A-29	Sequence 29, Appl



C 669	13	65.0	68571	17	US-10-401-194-1	Sequence 1, Appl1	742	12	60.0	275	18	US-10-425-115-133389	Sequence 133389,
C 670	13	65.0	107280	18	US-10-322-281-155	Sequence 155, App	743	12	60.0	277	9	US-09-563-817-486	Sequence 486, App
C 671	13	65.0	149062	18	US-10-367-094-93	Sequence 93, Appl	744	12	60.0	284	17	US-10-424-599-97282	Sequence 97282, A
C 672	13	65.0	216929	18	US-10-741-601-5727	Sequence 5727, Ap	745	12	60.0	284	18	US-10-767-701-173168	Sequence 173168, A
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C 674	13	65.0	430442	18	US-10-417-375-128	Sequence 128, App	747	12	60.0	311	18	US-10-425-115-17829	Sequence 17829, A
C 675	13	65.0	786452	18	US-10-719-993-682	Sequence 682, App	748	12	60.0	311	18	US-10-425-115-147841	Sequence 147841, A
C 676	13	65.0	2731748	18	US-10-297-465A-1	Sequence 1, Appl1	749	12	60.0	315	10	US-09-803-119-1583	Sequence 1583, Ap
C 677	13	65.0	2731748	18	US-10-297-465A-1	Sequence 1, Appl1	750	12	60.0	323	18	US-10-425-115-143680	Sequence 143680, A
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C 684	12	60.0		13	US-09-817-879-4609	Sequence 4609, Ap	757	12	60.0	339	10	US-09-814-353-845	Sequence 845, App
C 685	12	60.0		13	US-10-669-841-7202	Sequence 7202, Ap	758	12	60.0	345	18	US-10-425-115-120304	Sequence 120304, A
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C 693	12	60.0		15	US-09-817-879-4587	Sequence 4587, Ap	766	12	60.0	396	17	US-10-424-599-108535	Sequence 108535, A
C 694	12	60.0		15	US-10-669-841-7180	Sequence 7180, Ap	767	12	60.0	402	17	US-10-424-599-118001	Sequence 118001, A
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C 701	12	60.0		18	US-10-478-126-1040	Sequence 1040, Ap	774	12	60.0	435	18	US-10-425-115-128880	Sequence 128880, A
C 702	12	60.0		18	US-10-478-126-1040	Sequence 1040, Ap	775	12	60.0	440	18	US-10-425-115-128880	Sequence 128880, A
C 703	12	60.0		18	US-10-478-126-1040	Sequence 1040, Ap	776	12	60.0	444	18	US-10-425-115-128880	Sequence 128880, A
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C 706	12	60.0		19	US-10-667-271-167	Sequence 167, App	779	12	60.0	466	17	US-10-424-599-73674	Sequence 73674, A
C 707	12	60.0		19	US-10-667-271-167	Sequence 167, App	780	12	60.0	466	17	US-10-424-599-73674	Sequence 73674, A
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C 710	12	60.0		25	US-10-098-263B-52517	Sequence 32, Appl1	783	12	60.0	470	14	US-10-092-154-1658	Sequence 1658, Ap
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C 736	12	60.0		25	US-10-098-263B-52517	Sequence 32, Appl1	809	12	60.0	470	14	US-10-092-154-1658	Sequence 1658, Ap
C 737	12	60.0		25	US-10-098-263B-52517	Sequence 32, Appl1	810	12	60.0	470	14	US-10-092-154-1658	Sequence 1658, Ap
C 738	12	60.0		25	US-10-098-263B-52517	Sequence 32, Appl1	811	12	60.0	470	14	US-10-092-154-1658	Sequence 1658, Ap
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C 740	12	60.0		25	US-10-098-263B-52517	Sequence 32, Appl1	813	12	60.0	470	14	US-10-092-154-1658	Sequence 1658, Ap
C 741	12	60.0		25	US-10-098-263B-52517	Sequence 32, Appl1	814	12	60.0	470	14	US-10-092-154-1658	Sequence 1658, Ap



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C 819	12	60.0	555 9	US-09-811-284-24	Sequence 24, Appl	C 892	12	60.0	669 18	US-10-767-701-2277	Sequence 2277, Ap
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C 822	12	60.0	557 18	US-10-021-323-13604	Sequence 13604, A	C 895	12	60.0	670 18	US-10-363-345A-20166	Sequence 20166, A
C 823	12	60.0	558 18	US-10-767-701-20602	Sequence 20602, A	C 896	12	60.0	670 19	US-10-363-483A-20165	Sequence 20165, A
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C 839	12	60.0	586 13	US-10-027-632-136577	Sequence 136577, A	C 912	12	60.0	728 19	US-10-766-970A-166	Sequence 166, App
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C 841	12	60.0	592 18	US-10-425-115-16185	Sequence 16185, A	C 914	12	60.0	729 17	US-10-027-632-20710	Sequence 20710, A
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C 843	12	60.0	603 18	US-10-021-323-15606	Sequence 15606, A	C 916	12	60.0	733 18	US-10-363-345A-28728	Sequence 28728, A
C 844	12	60.0	603 18	US-10-021-323-15606	Sequence 15606, A	C 917	12	60.0	733 19	US-10-363-345A-28728	Sequence 28728, A
C 845	12	60.0	604 18	US-10-653-047-1261	Sequence 1261, Ap	C 918	12	60.0	733 19	US-10-363-483A-28728	Sequence 28728, A
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C 847	12	60.0	604 19	US-10-363-483A-19575	Sequence 19575, A	C 920	12	60.0	737 18	US-10-363-345A-25331	Sequence 25331, A
C 848	12	60.0	604 19	US-10-363-483A-19575	Sequence 19575, A	C 921	12	60.0	737 18	US-10-363-345A-25331	Sequence 25331, A
C 849	12	60.0	607 19	US-10-363-483A-19575	Sequence 19575, A	C 922	12	60.0	737 19	US-10-363-483A-25331	Sequence 25331, A
C 850	12	60.0	611 13	US-10-027-632-198236	Sequence 198236, A	C 923	12	60.0	737 19	US-10-363-483A-25331	Sequence 25331, A
C 851	12	60.0	611 17	US-10-027-632-198236	Sequence 198236, A	C 924	12	60.0	738 18	US-10-363-483A-25332	Sequence 25332, A
C 852	12	60.0	614 18	US-10-363-345A-18775	Sequence 18775, A	C 925	12	60.0	738 19	US-10-767-701-10846	Sequence 10846, A
C 853	12	60.0	614 18	US-10-363-345A-18775	Sequence 18775, A	C 926	12	60.0	740 13	US-10-427-928-1521	Sequence 1521, Ap
C 854	12	60.0	614 18	US-10-363-345A-22779	Sequence 22779, A	C 927	12	60.0	740 17	US-10-027-632-13903	Sequence 13903, A
C 855	12	60.0	614 19	US-10-363-345A-22780	Sequence 22780, A	C 928	12	60.0	741 18	US-10-027-632-13903	Sequence 13903, A
C 856	12	60.0	614 19	US-10-363-483A-18775	Sequence 18775, A	C 929	12	60.0	744 18	US-10-437-963-31641	Sequence 31641, A
C 857	12	60.0	614 19	US-10-363-483A-18776	Sequence 18776, A	C 930	12	60.0	744 18	US-10-363-345A-3533	Sequence 3533, Ap
C 858	12	60.0	614 19	US-10-363-483A-22779	Sequence 22779, A	C 931	12	60.0	744 18	US-10-363-483A-3533	Sequence 3533, Ap
C 859	12	60.0	614 19	US-10-363-483A-22780	Sequence 22780, A	C 932	12	60.0	744 19	US-10-363-483A-3533	Sequence 3533, Ap
C 860	12	60.0	624 13	US-10-027-632-179841	Sequence 179841, A	C 933	12	60.0	748 18	US-10-363-483A-3534	Sequence 3534, Ap
C 861	12	60.0	624 17	US-10-027-632-179842	Sequence 179842, A	C 934	12	60.0	751 18	US-10-363-483A-3534	Sequence 3534, Ap
C 862	12	60.0	624 17	US-10-027-632-179842	Sequence 179842, A	C 935	12	60.0	751 18	US-10-363-483A-13523	Sequence 13523, A
C 863	12	60.0	624 17	US-10-027-632-179842	Sequence 179842, A	C 936	12	60.0	751 18	US-10-363-483A-13523	Sequence 13523, A
C 864	12	60.0	629 13	US-10-027-632-306581	Sequence 306581, A	C 937	12	60.0	751 19	US-10-363-483A-13524	Sequence 13524, A
C 865	12	60.0	629 17	US-10-027-632-306581	Sequence 306581, A	C 938	12	60.0	754 18	US-10-363-483A-20871	Sequence 20871, A
C 866	12	60.0	633 13	US-10-027-632-253403	Sequence 253403, A	C 939	12	60.0	754 18	US-10-363-483A-20871	Sequence 20871, A
C 867	12	60.0	633 17	US-10-027-632-253403	Sequence 253403, A	C 940	12	60.0	754 19	US-10-363-483A-20871	Sequence 20871, A
C 868	12	60.0	635 18	US-10-363-345A-33523	Sequence 33523, A	C 941	12	60.0	754 19	US-10-363-483A-20872	Sequence 20872, A
C 869	12	60.0	635 19	US-10-363-345A-33524	Sequence 33524, A	C 942	12	60.0	755 13	US-10-027-632-135398	Sequence 135398, A
C 870	12	60.0	635 19	US-10-363-483A-33524	Sequence 33524, A	C 943	12	60.0	755 17	US-10-027-632-135398	Sequence 135398, A
C 871	12	60.0	635 19	US-10-363-483A-33524	Sequence 33524, A	C 944	12	60.0	769 18	US-10-363-483A-5145	Sequence 5145, Ap
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C 873	12	60.0	636 18	US-10-363-345A-2102	Sequence 2102, Ap	C 946	12	60.0	769 19	US-10-363-483A-5146	Sequence 5146, Ap
C 874	12	60.0	636 19	US-10-363-483A-2101	Sequence 2101, Ap	C 947	12	60.0	769 19	US-10-363-483A-5146	Sequence 5146, Ap
C 875	12	60.0	636 19	US-10-363-483A-2102	Sequence 2102, Ap	C 948	12	60.0	769 19	US-10-363-483A-5146	Sequence 5146, Ap
C 876	12	60.0	645 17	US-10-425-115-19395	Sequence 19395, A	C 949	12	60.0	786 18	US-10-425-115-14379	Sequence 14379, A
C 877	12	60.0	645 17	US-10-425-115-19395	Sequence 19395, A	C 950	12	60.0	786 18	US-10-767-701-24	Sequence 24, Appl
C 878	12	60.0	645 18	US-10-363-345A-31819	Sequence 31819, A	C 951	12	60.0	790 13	US-10-027-632-169961	Sequence 169961, A
C 879	12	60.0	645 19	US-10-363-345A-31820	Sequence 31820, A	C 952	12	60.0	790 13	US-10-027-632-169962	Sequence 169962, A
C 880	12	60.0	645 19	US-10-363-483A-31819	Sequence 31819, A	C 953	12	60.0	790 17	US-10-027-632-169963	Sequence 169963, A
C 881	12	60.0	646 18	US-10-363-483A-31820	Sequence 31820, A	C 954	12	60.0	790 17	US-10-027-632-169963	Sequence 169963, A
C 882	12	60.0	646 18	US-10-425-115-183881	Sequence 183881, A	C 955	12	60.0	790 17	US-10-027-632-169962	Sequence 169962, A
C 883	12	60.0	649 18	US-10-767-795-724	Sequence 724, App	C 956	12	60.0	791 17	US-10-027-632-169963	Sequence 169963, A
C 884	12	60.0	649 18	US-10-767-795-2840	Sequence 2840, App	C 957	12	60.0	791 18	US-10-363-345A-40093	Sequence 40093, A
C 885	12	60.0	654 17	US-10-282-122A-14881	Sequence 14881, A	C 958	12	60.0	791 18	US-10-363-345A-40094	Sequence 40094, A
C 886	12	60.0	661 18	US-10-363-345A-2279	Sequence 2279, Ap	C 959	12	60.0	791 19	US-10-363-483A-40094	Sequence 40094, A
C 887	12	60.0	661 19	US-10-363-483A-2279	Sequence 2279, Ap	C 960	12	60.0	798 15	US-10-238-075-1154	Sequence 1154, Ap

C 961 12 60.0 807 18 US-10-363-345A-17135 Sequence 17135, A  
C 962 12 60.0 807 18 US-10-363-345A-17136 Sequence 17136, A  
C 963 12 60.0 807 19 US-10-363-483A-17135 Sequence 17135, A  
C 964 12 60.0 807 19 US-10-363-483A-17136 Sequence 17136, A  
C 965 12 60.0 812 18 US-10-363-345A-21711 Sequence 21711, A  
C 966 12 60.0 812 18 US-10-363-345A-21712 Sequence 21712, A  
C 967 12 60.0 812 19 US-10-363-483A-21711 Sequence 21711, A  
C 968 12 60.0 812 19 US-10-363-483A-21712 Sequence 21712, A  
C 969 12 60.0 817 18 US-10-363-345A-22095 Sequence 22095, A  
C 970 12 60.0 817 18 US-10-363-345A-22096 Sequence 22096, A  
C 971 12 60.0 817 19 US-10-363-483A-22095 Sequence 22095, A  
C 972 12 60.0 817 19 US-10-363-483A-22096 Sequence 22096, A  
C 973 12 60.0 822 17 US-10-363-483A-22096 Sequence 22096, A  
C 974 12 60.0 825 17 US-10-424-599-87321 Sequence 87321, A  
C 975 12 60.0 826 18 US-10-425-115-52498 Sequence 52498, A  
C 976 12 60.0 826 18 US-10-425-115-52498 Sequence 52498, A  
C 977 12 60.0 828 17 US-10-027-632-14440 Sequence 14440, A  
C 978 12 60.0 828 17 US-10-027-632-14440 Sequence 14440, A  
C 979 12 60.0 863 13 US-10-027-632-261783 Sequence 261783, A  
C 980 12 60.0 863 13 US-10-027-632-261784 Sequence 261784, A  
C 981 12 60.0 863 13 US-10-027-632-261784 Sequence 261784, A  
C 982 12 60.0 863 13 US-10-027-632-261785 Sequence 261785, A  
C 983 12 60.0 863 17 US-10-027-632-261782 Sequence 261782, A  
C 984 12 60.0 863 17 US-10-027-632-261783 Sequence 261783, A  
C 985 12 60.0 863 17 US-10-027-632-261784 Sequence 261784, A  
C 986 12 60.0 870 11 US-09-997-722-3 Sequence 261785, A  
C 987 12 60.0 876 13 US-10-024-066-1 Sequence 3, Appl  
C 988 12 60.0 880 18 US-10-425-115-111217 Sequence 111217, A  
C 989 12 60.0 916 18 US-10-363-345A-26589 Sequence 26589, A  
C 990 12 60.0 916 18 US-10-363-345A-26590 Sequence 26590, A  
C 991 12 60.0 916 19 US-10-363-483A-26589 Sequence 26589, A  
C 992 12 60.0 916 19 US-10-363-483A-26590 Sequence 26590, A  
C 993 12 60.0 917 18 US-10-767-701-9820 Sequence 9820, Ap  
C 994 12 60.0 930 18 US-09-510-332-61 Sequence 61, Appl  
C 995 12 60.0 930 18 US-10-770-127-61 Sequence 61, Appl  
C 996 12 60.0 930 18 US-10-962-365-61 Sequence 61, Appl  
C 997 12 60.0 954 9 US-09-938-842A-2570 Sequence 2570, Ap  
C 998 12 60.0 954 11 US-09-938-842A-2570 Sequence 2570, Ap  
C 999 12 60.0 962 18 US-10-363-345A-18907 Sequence 18907, A  
1000 12 60.0 962 18 US-10-363-345A-18908 Sequence 18908, A

## ALIGNMENTS

RESULT 1  
US-08-887-505-28  
Sequence 28, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner Ann-Louise  
REGISTRATION NUMBER: 33,523  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-5000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-28

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TTGGCGACCCGACACTACTC 20  
Db 1 TTGGCGACCCGACACTACTC 20

RESULT 2  
US-08-887-505-119  
Sequence 119, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP



TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 119:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-119

Query Match  
Best Local Similarity 100.0%; Score 20; DB 8; Length 20;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCAACTACTC 20  
Db 1 TTGCGACCCCAACTACTC 20

RESULT 3  
US-08-887-505-120  
Sequence 120, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A11 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
TITLE OF INVENTION: HEPATITIS C VIRUS  
CORRESPONDENCE ADDRESS:  
ADDRESS: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Keirner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 120:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO

ANTI-SENSE: YES  
US-08-887-505-120

Query Match  
Best Local Similarity 100.0%; Score 20; DB 8; Length 20;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCAACTACTC 20  
Db 1 TTGCGACCCCAACTACTC 20

RESULT 4  
US-08-887-505-121  
Sequence 121, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A11 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
TITLE OF INVENTION: HEPATITIS C VIRUS  
CORRESPONDENCE ADDRESS:  
ADDRESS: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Keirner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-121

Query Match  
Best Local Similarity 100.0%; Score 20; DB 8; Length 20;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCAACTACTC 20  
Db 1 TTGCGACCCCAACTACTC 20

RESULT 5  
US-08-887-505-122  
Sequence 122, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Keener, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 122:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-122

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 80.0%; Pred. No. 0.017;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCGACACTACTC 20  
Db 1 TTGGGACCCGACACTACTC 20

RESULT 6  
US-08-887-505-123  
Sequence 123, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.

APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Keener, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 123:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-123

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 80.0%; Pred. No. 0.017;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCGACACTACTC 20  
Db 1 TTGGGACCCGACACTACTC 20

RESULT 7  
US-08-887-505-124  
Sequence 124, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA

COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 124:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-124

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 80.0%; Pred. No. 0.017;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTGGGACCCCACTACTC 20  
Db 1 UUCGGACCCCACTACTC 20

RESULT 8  
US-08-887-505-125  
Sequence 125, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 125:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-125

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 80.0%; Pred. No. 0.017;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTGGGACCCCACTACTC 20  
Db 1 UUCGGACCCCACTACTC 20

RESULT 9  
US-08-887-505-126  
Sequence 126, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 126:

SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-126

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
Db 1 TTGGGACCCCAACTACTC 20

## RESULT 10

US-08-887-505-127  
Sequence 127, Application US/08887505  
Publication No. US20020081577A1

## GENERAL INFORMATION:

APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
TITLE OF INVENTION: HEPATITIS C VIRUS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:

## CLASSIFICATION: 514

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995

## ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523

REFERENCE/DOCKET NUMBER: HYZ-040CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 526-5000

TELEFAX: (617) 526-6000

INFORMATION FOR SEQ ID NO: 127:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA/RNA

HYPOTHETICAL: NO

ANTI-SENSE: YES

US-08-887-505-127

Query Match 100.0%; Score 20; DB 8; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
Db 1 TTGGGACCCCAACTACTC 20

## RESULT 11

US-08-887-505-128

Sequence 128, Application US/08887505  
Publication No. US20020081577A1

## GENERAL INFORMATION:

APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
TITLE OF INVENTION: HEPATITIS C VIRUS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000

INFORMATION FOR SEQ ID NO: 128:

## SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA/RNA

HYPOTHETICAL: NO

ANTI-SENSE: YES

US-08-887-505-128

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
Db 1 TTGGGACCCCAACTACTC 20

## RESULT 12

US-08-887-505-129

Sequence 129, Application US/08887505

Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Keiner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 129:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-129

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20  
DB 1 TTCCGACCCCACTACTC 20

RESULT 13  
US-08-887-505-130  
Sequence 130, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR

TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Keiner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 130:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-130

Query Match 100.0%; Score 20; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20  
DB 1 TTCCGACCCCACTACTC 20

RESULT 14  
US-08-887-505-75  
Sequence 75, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-75

Query Match 100.0%; Score 20; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACTACTC 20  
DB 3 TTGCGAGCCCAACTACTC 22

RESULT 15  
US-08-887-505-131  
Sequence 131, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 131:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-131

Query Match 100.0%; Score 20; DB 8; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACTACTC 20  
DB 1 TTGCGAGCCCAACTACTC 20

RESULT 16  
US-10-407-952-4/c  
Sequence 4, Application US/10407952  
Publication No. US20030232074A1  
GENERAL INFORMATION:  
APPLICANT: Lipford, Grayson  
APPLICANT: Bauer, Stefan  
TITLE OF INVENTION: Immunostimulatory G,U-Containing Oligoribonucleotides  
FILE REFERENCE: C01041.70037 US  
CURRENT APPLICATION NUMBER: US/10/407,952  
CURRENT FILING DATE: 2003-04-04  
PRIOR APPLICATION NUMBER: US 60/421,966  
PRIOR FILING DATE: 2002-10-29  
PRIOR APPLICATION NUMBER: US 60/370,515  
PRIOR FILING DATE: 2002-04-04  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 27  
TYPE: RNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide  
US-10-407-952-4

Query Match 100.0%; Score 20; DB 17; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACTACTC 20  
DB 23 TTGCGAGCCCAACTACTC 4

RESULT 17  
US-10-475-024-20/c  
Sequence 20, Application US/10475024  
Publication No. US20040219545A1  
GENERAL INFORMATION:  
APPLICANT: Rando, Robert F.  
APPLICANT: Welch, Ellen  
TITLE OF INVENTION: METHODS FOR IDENTIFYING SMALL MOLECULES THAT BIND SPECIFIC RNA  
FILE REFERENCE: 10589-007-999  
CURRENT APPLICATION NUMBER: US/10/475,024  
CURRENT FILING DATE: 2003-10-10  
PRIOR APPLICATION NUMBER: 60/282,965

PRIOR FILING DATE: 2001-04-11  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 20  
LENGTH: 27  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-10-475-024-20

Query Match 100.0%; Score 20; DB 18; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 23 TTGGGACCCCAACTACTC 4

## RESULT 18

US-08-887-505-68  
Sequence 68, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-68  
Query Match 100.0%; Score 20; DB 8; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 1 TTGGGACCCCAACTACTC 20

## RESULT 19

US-08-887-505-74  
Sequence 74, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-74  
Query Match 100.0%; Score 20; DB 8; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 5 TTGGGACCCCAACTACTC 24

## RESULT 20

US-10-332-626-3/c  
Sequence 3, Application US/10332626  
Publication No. US20040073380A1

GENERAL INFORMATION:  
APPLICANT: Joseph D. Puglisi  
TITLE OF INVENTION: Structural Targets of Hepatitis C Virus  
FILE REFERENCE: STAN-196  
CURRENT FILING DATE: 2003-09-08  
PRIOR APPLICATION NUMBER: PCT/US01/21871  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,673  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 29  
TYPE: RNA  
ORGANISM: Hepatitis C virus  
US-10-332-626-3

Query Match 100.0%; Score 20; DB 17; Length 29;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 24 TTGGGACCCCAACTACTC 5

## RESULT 21

US-09-790-417-181/c  
Sequence 181, Application US/09790417  
Patent No. US20010031470A1  
GENERAL INFORMATION:  
APPLICANT: Shultz, John W  
APPLICANT: Lewis, Martin K.  
APPLICANT: Liepke, Donna  
APPLICANT: Mandrekas, Michelle  
APPLICANT: Kephart, Daniel B.  
APPLICANT: Andrews, Christine A.  
APPLICANT: Hartnett, James R.  
APPLICANT: Gu, Trent  
APPLICANT: Olson, Ryan J.  
APPLICANT: Wood, Keith W.  
APPLICANT: Welch, Roy  
TITLE OF INVENTION: Nucleic Acid Detection  
FILE REFERENCE: Pro-103 6868/75528  
CURRENT APPLICATION NUMBER: US/09/790,417  
CURRENT FILING DATE: 2001-02-22  
PRIOR APPLICATION NUMBER: 09/358,972  
PRIOR FILING DATE: 1999-07-21  
PRIOR APPLICATION NUMBER: 09/042,287  
PRIOR FILING DATE: 1998-03-13  
NUMBER OF SEQ ID NOS: 290  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 181  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
FEATURE:  
OTHER INFORMATION: probe for Hepatitis C  
US-09-790-417-181

Query Match 100.0%; Score 20; DB 9; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 29 TTGGGACCCCAACTACTC 10

## RESULT 22

US-09-780-863-43/c  
Sequence 43, Application US/09780863  
Publication No. US2003020358A1  
GENERAL INFORMATION:  
APPLICANT: Shultz, John W  
APPLICANT: Lewis, Martin K  
APPLICANT: Liepke, Donna  
APPLICANT: Mandrekas, Michelle  
APPLICANT: Kephart, Daniel  
APPLICANT: Rhodes, Richard B  
APPLICANT: Andrews, Christine A  
APPLICANT: Hartnett, James R  
APPLICANT: Gu, Trent  
APPLICANT: Wood, Keith V  
APPLICANT: Welch, Roy  
TITLE OF INVENTION: EXOGENOUS NUCLEIC ACID DETECTION  
FILE REFERENCE: EXOGENOUS NUCLEIC ACID DETECTION  
CURRENT APPLICATION NUMBER: US/09/780,863  
CURRENT FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/406,147  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-27  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/252,436  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/042,287  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-13  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 43  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-780-863-43

Query Match 100.0%; Score 20; DB 10; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 29 TTGGGACCCCAACTACTC 10

## RESULT 23

US-10-318-416B-6/c  
Sequence 6, Application US/10318416B  
Publication No. US20040115643A1  
GENERAL INFORMATION:  
APPLICANT: Lizardi, Paul M.  
APPLICANT: Grishanov, Oleg G.  
TITLE OF INVENTION: THERMODYNAMIC EQUILIBRIUM EXTENSION OF  
FILE REFERENCE: 25006.001201  
CURRENT APPLICATION NUMBER: US/10/318,416B  
CURRENT FILING DATE: 2002-12-12  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:/note =  
US-10-318-416B-6

Query Match 100.0%; Score 20; DB 18; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.016;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 31 TTGGGACCCCAACTACTC 12



```
RESULT 24
US-10-318-416B-18/c
; Sequence 18, Application US/10318416B
; Publication No. US20040115643A1
; GENERAL INFORMATION:
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Gribanov, Oleg G.
; TITLE OF INVENTION: THERMODYNAMIC EQUILIBRIUM EXTENSION OF
; TITLE OF INVENTION: PRIMERS
; FILE REFERENCE: 25006.001201
; CURRENT APPLICATION NUMBER: US/10/318,416B
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
US-10-318-416B-18

Query Match      100.0%; Score 20; DB 18; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGAGCCCAACACTACTC 20
Db 31 TTGGGAGCCCAACACTACTC 12

RESULT 25
US-10-318-416B-19/c
; Sequence 19, Application US/10318416B
; Publication No. US20040115643A1
; GENERAL INFORMATION:
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Gribanov, Oleg G.
; TITLE OF INVENTION: THERMODYNAMIC EQUILIBRIUM EXTENSION OF
; TITLE OF INVENTION: PRIMERS
; FILE REFERENCE: 25006.001201
; CURRENT APPLICATION NUMBER: US/10/318,416B
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
US-10-318-416B-19

Query Match      100.0%; Score 20; DB 18; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGAGCCCAACACTACTC 20
Db 31 TTGGGAGCCCAACACTACTC 12

RESULT 26
US-09-870-939-1/c
; Sequence 1, Application US/09870939
; Publication No. US20020192650A1
; GENERAL INFORMATION:
; APPLICANT: AMORESE, DOUGLAS A.
; APPLICANT: SHANNON, KAREN W.
; APPLICANT: COLLINS, PATRICK J.
```

```
; APPLICANT: WOLBER, PAUL. K.
; TITLE OF INVENTION: COMPOSITE ARRAYS
; FILE REFERENCE: 10010791-1
; CURRENT APPLICATION NUMBER: US/09/870,939
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-870-939-1

Query Match      100.0%; Score 20; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGAGCCCAACACTACTC 20
Db 24 TTGGGAGCCCAACACTACTC 5

RESULT 27
US-09-728-265-31
; Sequence 31, Application US/09728265
; Publication No. US20020182598A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, David Y.
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHOD:
; TITLE OF INVENTION: RAMIFICATION-EXTENSION AMPLIFICATION METHOD (RAM)
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroock & Stroock & Lavan
; STREET: 180 Maiden Lane
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10038
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PCDOS/MSDOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/728,265
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pokocillow, Steven B.
; REGISTRATION NUMBER: 26,405
; REFERENCE/DOCKET NUMBER: Old 29545APCT/USA-B // New 251305/0018
; TELEPHONE: 212806-6663
; TELEFAX: 2128066006
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..108
US-09-728-265-31

Query Match      100.0%; Score 20; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGAGCCCAACACTACTC 20
Db 4 TTGGGAGCCCAACACTACTC 23
```

```
RESULT 28
US-09-978-261A-31
; Sequence 31, Application US/09978261A
; Publication No. US20030175706A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, David Y.
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION METHODS
; FILE REFERENCE: A29545-A-PCT-USA-A 070165.0601
; CURRENT APPLICATION NUMBER: US/09/978,261A
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 08/263,937
; PRIOR FILING DATE: 1994-06-22
; PRIOR APPLICATION NUMBER: 08/596,331
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: 08/690,495
; PRIOR FILING DATE: 1996-07-31
; PRIOR APPLICATION NUMBER: 08/909,031
; PRIOR FILING DATE: 1997-08-11
; PRIOR APPLICATION NUMBER: 09/728,265
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-09-978-261A-31

Query Match          100.0%; Score 20; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCACTACTC 20
DB 4 TTGCGAGCCCACTACTC 23

RESULT 29
US-10-309-438-31
; Sequence 31, Application US/10309438
; Publication No. US20030190604A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, David Y.
; APPLICANT: Brandwein, Marageth
; APPLICANT: Hsueh, Terence C.H.
; TITLE OF INVENTION: Nucleic Acid Amplification Method: Ramification-extension
; FILE REFERENCE: 251305/0031
; CURRENT APPLICATION NUMBER: US/10/309,438
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 09/299,217
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 08/690,494
; PRIOR FILING DATE: 1996-07-31
; PRIOR APPLICATION NUMBER: US 08/596,331
; PRIOR FILING DATE: 1996-05-20
; PRIOR APPLICATION NUMBER: PCT/US95/07671
; PRIOR FILING DATE: 1995-06-14
; PRIOR APPLICATION NUMBER: 08/263,937
; PRIOR FILING DATE: 1994-06-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-10-309-438-31
```

```
Query Match          100.0%; Score 20; DB 16; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCACTACTC 20
DB 4 TTGCGAGCCCACTACTC 23

RESULT 30
US-10-719-480-31
; Sequence 31, Application US/10719480
; Publication No. US20040137484A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, David Y.
; APPLICANT: Yi, Jizuo
; APPLICANT: Zhang, Mandi
; TITLE OF INVENTION: Nucleic Acid Amplification Methods
; FILE REFERENCE: 251305/0040
; CURRENT APPLICATION NUMBER: US/10/719,480
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 09/978,261
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/US02/32754
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-10-719-480-31

Query Match          100.0%; Score 20; DB 18; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCACTACTC 20
DB 4 TTGCGAGCCCACTACTC 23

RESULT 31
US-10-396-964-12/C
; Sequence 12, Application US/10396964
; Publication No. US20030198946A1
; GENERAL INFORMATION:
; APPLICANT: Simmonds, Peter
; APPLICANT: Chan, Shiu-Wan
; APPLICANT: Yap, Peng L.
; TITLE OF INVENTION: Hepatitis-C Virus Testing
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Selzer, Park & Gibson, P.A.
; STREET: 1211 East Morehead Street
; CITY: Charlotte
; STATE: NO. US20030198946A1th Carolina
; COUNTRY: United States
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/396,964
; FILING DATE: 23-MARCH-2003
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,116B
```

```

; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02143
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 1749-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 704-377-1561
; TELEFAX: 704-334-2014
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Hepatitis-C virus
;
US-10-396-964-12

Query Match      100.0%; Score 20; DB 16; Length 194;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  TTCCGACCCCAACTACTC 20
        ||||||||||||||||
Db      189 TTCCGACCCCAACTACTC 170

RESULT 32
US-10-688-272-19/c
; Sequence 19, Application US/10688272
; Publication No. US20040091924A1
; GENERAL INFORMATION:
; APPLICANT: Genematrix Inc.; Kim, Nam-Keun
; TITLE OF INVENTION: Method for detecting base mutation
; FILE REFERENCE: 11281-014-999
; CURRENT APPLICATION NUMBER: US/10/688,272
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: KR2002-0063832
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: KR2003-0061066
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Koparentin 1.71
; SEQ ID NO 19
; LENGTH: 226
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Resulting PCR fragment
;
US-10-688-272-19

Query Match      100.0%; Score 20; DB 17; Length 226;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  TTCCGACCCCAACTACTC 20
        ||||||||||||||||
Db      200 TTCCGACCCCAACTACTC 181

RESULT 33
US-10-688-272-22/c
; Sequence 22, Application US/10688272
; Publication No. US20040091924A1
; GENERAL INFORMATION:
; APPLICANT: Genematrix Inc.; Kim, Nam-Keun
```

```

; TITLE OF INVENTION: Method for detecting base mutation
; FILE REFERENCE: 11281-014-999
; CURRENT APPLICATION NUMBER: US/10/688,272
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: KR2002-0063832
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: KR2003-0061066
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Koparentin 1.71
; SEQ ID NO 22
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Resulting PCR fragment
;
US-10-688-272-22

Query Match      100.0%; Score 20; DB 17; Length 230;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  TTCCGACCCCAACTACTC 20
        ||||||||||||||||
Db      204 TTCCGACCCCAACTACTC 185

RESULT 34
US-10-688-272-23
; Sequence 23, Application US/10688272
; Publication No. US20040091924A1
; GENERAL INFORMATION:
; APPLICANT: Genematrix Inc.; Kim, Nam-Keun
; TITLE OF INVENTION: Method for detecting base mutation
; FILE REFERENCE: 11281-014-999
; CURRENT APPLICATION NUMBER: US/10/688,272
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: KR2002-0063832
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: KR2003-0061066
; PRIOR FILING DATE: 2003-09-02
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Koparentin 1.71
; SEQ ID NO 23
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Resulting PCR fragment
;
US-10-688-272-23

Query Match      100.0%; Score 20; DB 17; Length 230;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  TTCCGACCCCAACTACTC 20
        ||||||||||||||||
Db      27  TTCCGACCCCAACTACTC 46

RESULT 35
US-09-825-574-37/c
; Sequence 37, Application US/09825574
; Patent No. US20020119454A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
;           Brow, Mary Ann D.
;           Fors, Lance
;           Neil, Bruce P.
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
;                   Structure Probing With Structure-Bridging
;                   Oligonucleotides.
; NUMBER OF SEQUENCES: 51
```

CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-09-825-574-37

Query Match  
Best Local Similarity 100.0%; Score 20; DB 9; Length 232;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 199 TTGGGACCCCAACTACTC 180

RESULT 36  
US-09-882-945A-37/c  
Sequence 37, Application US/09882945A  
Publication No. US20030143535A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor  
APPLICANT: Allawi, Hatim  
APPLICANT: Dong, Fang  
APPLICANT: Neri, Bruce  
APPLICANT: Vener, Tatiana  
TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
FILE REFERENCE: FORS-04586  
CURRENT APPLICATION NUMBER: US/09/882,945A  
CURRENT FILING DATE: 2001-06-15  
NUMBER OF SEQ ID NOS: 334  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 37  
LENGTH: 232  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-882-945A-37

Query Match  
Best Local Similarity 100.0%; Score 20; DB 10; Length 232;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 199 TTGGGACCCCAACTACTC 180

RESULT 37  
US-10-807-114-37/c  
Sequence 37, Application US/10807114  
Publication No. US20040235024A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor  
APPLICANT: Allawi, Hatim  
APPLICANT: Dong, Fang  
APPLICANT: Neri, Bruce  
APPLICANT: Vener, Tatiana  
TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
FILE REFERENCE: FORS-04586  
CURRENT APPLICATION NUMBER: US/10/807,114  
CURRENT FILING DATE: 2004-03-23  
PRIOR APPLICATION NUMBER: US/09/882,945  
PRIOR FILING DATE: 2001-06-15  
NUMBER OF SEQ ID NOS: 334  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 37  
LENGTH: 232  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-807-114-37

Query Match  
Best Local Similarity 100.0%; Score 20; DB 18; Length 232;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 199 TTGGGACCCCAACTACTC 180

RESULT 38  
US-10-655-362-37/c  
Sequence 37, Application US/10655362  
Publication No. US2005014163A1  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Andersson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/10/655,362  
CURRENT FILING DATE: 2003-09-04  
PRIOR APPLICATION NUMBER: US/09/402,618B  
PRIOR FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 37  
LENGTH: 232  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-10-655-362-37

Query Match  
Best Local Similarity 100.0%; Score 20; DB 19; Length 232;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 199 TTGGGACCCCAACTACTC 180

## RESULT 39

US-09-825-574-32/c

Sequence 32, Application US/09825574

Patent No. US20020119454A1

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Brow, Mary Ann D.

Fors, Lance

Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid

Structure Probing With Structure-Bridging

Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN &amp; CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Macknight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 239 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-09-825-574-32

Query Match 100.0%; Score 20; DB 9; Length 239;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20

|||||

Db 206 TTGGGACCCCAACTACTC 187

## RESULT 40

US-09-825-574-36/c

Sequence 36, Application US/09825574

Patent No. US20020119454A1

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Brow, Mary Ann D.

Fors, Lance

Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid

Structure Probing With Structure-Bridging

Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN &amp; CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Macknight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 239 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 36:

US-09-825-574-36

Query Match 100.0%; Score 20; DB 9; Length 239;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20

|||||

Db 206 TTGGGACCCCAACTACTC 187

## RESULT 41

US-09-882-945A-32/c

Sequence 32, Application US/09882945A

Patent No. US20030143535A1

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor

APPLICANT: Allawi, Halim

APPLICANT: Dong, Fang

APPLICANT: Neri, Bruce

APPLICANT: Vener, Tatiana

TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites

FILE REFERENCE: FORS-04586

CURRENT APPLICATION NUMBER: US/09/882,945A

NUMBER OF SEQ ID NOS: 334

SOFTWARE: Patentin version 3.0

SEQ ID NO: 32

LENGTH: 239

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-09-882-945A-32

Query Match 100.0%; Score 20; DB 10; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 206 TTGGGACCCCAACTACTC 187

RESULT 42  
US-09-882-945A-36/c  
; Sequence 36, Application US/09882945A  
; Publication No. US2003014355A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang  
; APPLICANT: Neri, Bruce  
; APPLICANT: Vener, Tatiana

FILE REFERENCE: Nucleic Acid Accessible Hybridization Sites  
CURRENT APPLICATION NUMBER: US/09/882,945A  
CURRENT FILING DATE: 2001-06-15  
NUMBER OF SEQ ID NOS: 334  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 36  
LENGTH: 239  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-882-945A-36

Query Match 100.0%; Score 20; DB 10; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 206 TTGGGACCCCAACTACTC 187

RESULT 43  
US-10-807-114-32/c

; Sequence 32, Application US/10807114  
; Publication No. US20040235024A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang  
; APPLICANT: Neri, Bruce  
; APPLICANT: Vener, Tatiana  
TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
FILE REFERENCE: FORS-04586  
CURRENT APPLICATION NUMBER: US/10/807,114  
CURRENT FILING DATE: 2004-03-23  
PRIOR APPLICATION NUMBER: US/09/882,945  
PRIOR FILING DATE: 2001-06-15  
NUMBER OF SEQ ID NOS: 334  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 32  
LENGTH: 239  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-807-114-32

Query Match 100.0%; Score 20; DB 19; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 206 TTGGGACCCCAACTACTC 187

RESULT 44  
US-10-807-114-36/c  
; Sequence 36, Application US/10807114  
; Publication No. US20040235024A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang  
; APPLICANT: Neri, Bruce  
; APPLICANT: Vener, Tatiana  
TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
FILE REFERENCE: FORS-04586  
CURRENT APPLICATION NUMBER: US/10/807,114  
CURRENT FILING DATE: 2004-03-23  
PRIOR APPLICATION NUMBER: US/09/882,945  
PRIOR FILING DATE: 2001-06-15  
NUMBER OF SEQ ID NOS: 334  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 36  
LENGTH: 239  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-807-114-36

Query Match 100.0%; Score 20; DB 18; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 206 TTGGGACCCCAACTACTC 187

RESULT 45  
US-10-655-362-32/c  
; Sequence 32, Application US/10655362  
; Publication No. US20050014163A1  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce  
; APPLICANT: Brow, Mary Ann  
; APPLICANT: Anderson, Todd  
; APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/10/655,362  
CURRENT FILING DATE: 2003-09-04  
PRIOR APPLICATION NUMBER: US/09/402,618B  
PRIOR FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 32  
LENGTH: 239  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-10-655-362-32

Query Match 100.0%; Score 20; DB 19; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
Db 206 TTGGGACCCCAACTACTC 187

## RESULT 46

US-10-655-362-36/C  
; Sequence 36, Application US/10655362  
; Publication No. US20050014163A1  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce  
; APPLICANT: Brow, Mary Ann  
; APPLICANT: Anderson, Todd  
; APPLICANT: Dahlberg, James  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/10/655,362  
; CURRENT FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: US/09/402,618B  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/03194  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 239  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-10-655-362-36

Query Match 100.0%; Score 20; DB 19; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
Db 206 TTGGGACCCCAACTACTC 187

## RESULT 47

US-10-927-520-9/C  
; Sequence 9, Application US/10927520  
; Publication No. US20050069870A1  
; GENERAL INFORMATION:  
; APPLICANT: Innogenetics N.V.  
; TITLE OF INVENTION: New HCV clade and prototype sequences thereof  
; FILE REFERENCE: 157  
; CURRENT APPLICATION NUMBER: US/10/927,520  
; CURRENT FILING DATE: 2004-08-27  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 239  
; TYPE: DNA  
; ORGANISM: hepatitis C virus  
US-10-927-520-9

Query Match 100.0%; Score 20; DB 19; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
Db 200 TTGGGACCCCAACTACTC 181

## RESULT 48

US-10-927-520-10/C

; Sequence 10, Application US/10927520  
; Publication No. US20050069870A1  
; GENERAL INFORMATION:  
; APPLICANT: Innogenetics N.V.  
; TITLE OF INVENTION: New HCV clade and prototype sequences thereof  
; FILE REFERENCE: 157  
; CURRENT APPLICATION NUMBER: US/10/927,520  
; CURRENT FILING DATE: 2004-08-27  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 239  
; TYPE: DNA  
; ORGANISM: hepatitis C virus  
US-10-927-520-10

Query Match 100.0%; Score 20; DB 19; Length 239;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
Db 200 TTGGGACCCCAACTACTC 181

## RESULT 49

US-09-825-574-33/C  
; Sequence 33, Application US/09825574  
; Patent No. US20020119454A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce P.  
; APPLICANT: Brow, Mary Ann D.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA

COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Macknight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:

US-09-825-574-33

Query Match 100.0%; Score 20; DB 9; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 207 TTGGGACCCCAACTACTC 188

RESULT 50  
US-09-825-574-35/c

Sequence 35, Application US/09825574  
Patent No. US20020119454A1

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Brow, Mary Ann D.

Fors, Lance

Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN &amp; CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Macknight, Kamrin T.

REGISTRATION NUMBER: 38,230

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 240 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 35:

US-09-825-574-35

Query Match 100.0%; Score 20; DB 9; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 207 TTGGGACCCCAACTACTC 188

RESULT 51

US-09-825-574-38/c  
Sequence 38, Application US/09825574

Patent No. US20020119454A1

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Brow, Mary Ann D.

Fors, Lance

Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN &amp; CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Macknight, Kamrin T.

REGISTRATION NUMBER: 38,230

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 240 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-09-825-574-38

Query Match 100.0%; Score 20; DB 9; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 208 TTGGGACCCCAACTACTC 189

RESULT 52

US-09-882-945A-33/c

Sequence 33, Application US/09882945A

Publication No. US20030143535A1

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor

APPLICANT: Allawi, Hatim

APPLICANT: Dong, Fang

APPLICANT: Neri, Bruce

APPLICANT: Vener, Tatiana

TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites

FILE REFERENCE: FORS-04586

CURRENT APPLICATION NUMBER: US/09/882,945A

CURRENT FILING DATE: 2001-06-15

NUMBER OF SEQ ID NOS: 334

SOFTWARE: PatentIn version 3.0

SEQ ID NO 33



LENGTH: 240  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-882-945A-33

Query Match 100.0%; Score 20; DB 10; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 207 TTGGGACCCCAACTACTC 188

RESULT 53  
US-09-882-945A-35/c  
Sequence 35, Application US/09882945A  
Publication No. US2003014353A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor  
APPLICANT: Allawi, Hatim  
APPLICANT: Dong, Fang  
APPLICANT: Neri, Bruce  
APPLICANT: Vener, Tatiana  
TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
FILE REFERENCE: FORS-04586  
CURRENT APPLICATION NUMBER: US/09/882,945A  
CURRENT FILING DATE: 2001-06-15  
NUMBER OF SEQ ID NOS: 334  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 35  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-882-945A-35

Query Match 100.0%; Score 20; DB 10; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 207 TTGGGACCCCAACTACTC 188

RESULT 54  
US-09-882-945A-38/c  
Sequence 38, Application US/09882945A  
Publication No. US2003014353A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor  
APPLICANT: Allawi, Hatim  
APPLICANT: Dong, Fang  
APPLICANT: Neri, Bruce  
APPLICANT: Vener, Tatiana  
TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
FILE REFERENCE: FORS-04586  
CURRENT APPLICATION NUMBER: US/09/882,945A  
CURRENT FILING DATE: 2001-06-15  
NUMBER OF SEQ ID NOS: 334  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 38  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-882-945A-38

Query Match 100.0%; Score 20; DB 10; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 208 TTGGGACCCCAACTACTC 189

RESULT 55  
US-10-807-114-33/c  
Sequence 33, Application US/10807114  
Publication No. US20040235024A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor  
APPLICANT: Allawi, Hatim  
APPLICANT: Dong, Fang  
APPLICANT: Neri, Bruce  
APPLICANT: Vener, Tatiana  
TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
FILE REFERENCE: FORS-04586  
CURRENT APPLICATION NUMBER: US/10/807,114  
CURRENT FILING DATE: 2004-03-23  
PRIOR APPLICATION NUMBER: US/09/882,945  
PRIOR FILING DATE: 2001-06-15  
NUMBER OF SEQ ID NOS: 334  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 33  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-807-114-33

Query Match 100.0%; Score 20; DB 18; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 207 TTGGGACCCCAACTACTC 188

RESULT 56  
US-10-807-114-35/c  
Sequence 35, Application US/10807114  
Publication No. US20040235024A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor  
APPLICANT: Allawi, Hatim  
APPLICANT: Dong, Fang  
APPLICANT: Neri, Bruce  
APPLICANT: Vener, Tatiana  
TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
FILE REFERENCE: FORS-04586  
CURRENT APPLICATION NUMBER: US/10/807,114  
CURRENT FILING DATE: 2004-03-23  
PRIOR APPLICATION NUMBER: US/09/882,945  
PRIOR FILING DATE: 2001-06-15  
NUMBER OF SEQ ID NOS: 334  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 35  
LENGTH: 240  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-807-114-35

Query Match 100.0%; Score 20; DB 18; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
|||||  
Db 207 TTCCGACCCCACTACTC 188

## RESULT 57

US-10-807-114-38/c  
; Sequence 38, Application US/10807114  
; Publication No. US20040235024A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang  
; APPLICANT: Neri, Bruce  
; APPLICANT: Vener, Tatiana  
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
; FILE REFERENCE: FORS-04586  
; CURRENT APPLICATION NUMBER: US/10/807,114  
; PRIOR FILING DATE: 2004-03-23  
; PRIOR APPLICATION NUMBER: US/09/882,945  
; PRIOR FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 38  
; LENGTH: 240  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-807-114-38

Query Match 100.0%; Score 20; DB 18; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
|||||  
Db 208 TTCCGACCCCACTACTC 189

## RESULT 58

US-10-655-362-33/c  
; Sequence 33, Application US/10655362  
; Publication No. US20050014163A1  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce  
; APPLICANT: Brow, Mary Ann  
; APPLICANT: Anderson, Todd  
; APPLICANT: Dahlberg, James  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/10/655,362  
; PRIOR FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: US/09/402,618B  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/03194  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 33  
; LENGTH: 240  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-10-655-362-33

Query Match 100.0%; Score 20; DB 19; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
|||||  
Db 207 TTCCGACCCCACTACTC 188

## RESULT 59

US-10-655-362-35/c  
; Sequence 35, Application US/10655362  
; Publication No. US20050014163A1  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce  
; APPLICANT: Brow, Mary Ann  
; APPLICANT: Anderson, Todd  
; APPLICANT: Dahlberg, James  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleor  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/10/655,362  
; PRIOR FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: US/09/402,618B  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/03194  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35  
; LENGTH: 240  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-10-655-362-35

Query Match 100.0%; Score 20; DB 19; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTCCGACCCCACTACTC 20  
|||||  
Db 207 TTCCGACCCCACTACTC 188

## RESULT 60

US-10-655-362-38/c  
; Sequence 38, Application US/10655362  
; Publication No. US20050014163A1  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce  
; APPLICANT: Brow, Mary Ann  
; APPLICANT: Anderson, Todd  
; APPLICANT: Dahlberg, James  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/10/655,362  
; PRIOR FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: US/09/402,618B  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/03194  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 38  
; LENGTH: 240  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-10-655-362-38

Query Match 100.0%; Score 20; DB 19; Length 240;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACACTACTC 20  
DB 208 TTGCGAGCCCAACACTACTC 189

RESULT 61  
US-10-087-631B-10/c

Sequence 10, Application US/10087631B  
Publication No. US20030054372A1  
GENERAL INFORMATION:

APPLICANT: JAEGER, STEPHAN  
TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A  
FILE REFERENCE: 1803-335-999  
CURRENT APPLICATION NUMBER: US/10/087,631B  
CURRENT FILING DATE: 2002-03-01  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 241  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNA sequence derived by  
US-10-087-631B-10

Query Match 100.0%; Score 20; DB 14; Length 241;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACACTACTC 20  
DB 208 TTGCGAGCCCAACACTACTC 189

RESULT 62  
US-10-419-022-10/c

Sequence 10, Application US/10419022  
Publication No. US20030165982A1  
GENERAL INFORMATION:

APPLICANT: JAEGER, STEPHAN  
TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A  
FILE REFERENCE: 1803-335-999  
CURRENT APPLICATION NUMBER: US/10/419,022  
CURRENT FILING DATE: 2003-04-17  
PRIOR APPLICATION NUMBER: US/10/087,631B  
PRIOR FILING DATE: 2002-03-01  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 241  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNA sequence derived by  
US-10-419-022-10

Query Match 100.0%; Score 20; DB 16; Length 241;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACACTACTC 20  
DB 208 TTGCGAGCCCAACACTACTC 189

RESULT 63  
US-09-825-574-26/c

Sequence 26, Application US/09825574  
Patent No. US20020119454A1  
GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance P.  
Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA

ZIP: 94104  
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-825-574-26

Query Match 100.0%; Score 20; DB 9; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGAGCCCAACACTACTC 20  
DB 208 TTGCGAGCCCAACACTACTC 189

RESULT 64  
US-09-825-574-27/c

Sequence 27, Application US/09825574  
Patent No. US20020119454A1  
GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance P.  
Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:

ADDRESS: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-825-574-27

Query Match 100.0%; Score 20; DB 9; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 208 TTGGGACCCCACTACTC 189

RESULT 65  
US-09-825-574-29/c  
Sequence 29, Application US/09825574  
Patent No. US20020119454A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance P.  
Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-825-574-29

Query Match 100.0%; Score 20; DB 9; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 208 TTGGGACCCCACTACTC 189

RESULT 66  
US-09-825-574-31/c  
Sequence 31, Application US/09825574  
Patent No. US20020119454A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance P.  
Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs

TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-825-574-31

Query Match 100.0%; Score 20; DB 9; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 208 TTGGGACCCCAACTACTC 189

RESULT 67  
US-09-882-945A-26/c  
; Sequence 26, Application US/09882945A  
; Publication No. US20030143535A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang  
; APPLICANT: Neri, Bruce  
; APPLICANT: Vener, Tatiana  
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
; FILE REFERENCE: FORS-04586  
; CURRENT APPLICATION NUMBER: US/09/882,945A  
; CURRENT FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 26  
; LENGTH: 244  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-882-945A-26

Query Match 100.0%; Score 20; DB 10; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 208 TTGGGACCCCAACTACTC 189

RESULT 68  
US-09-882-945A-27/c  
; Sequence 27, Application US/09882945A  
; Publication No. US20030143535A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang  
; APPLICANT: Neri, Bruce  
; APPLICANT: Vener, Tatiana  
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
; FILE REFERENCE: FORS-04586  
; CURRENT APPLICATION NUMBER: US/09/882,945A  
; CURRENT FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 27  
; LENGTH: 244  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-882-945A-27

Query Match 100.0%; Score 20; DB 10; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 208 TTGGGACCCCAACTACTC 189

RESULT 69  
US-09-882-945A-29/c  
; Sequence 29, Application US/09882945A  
; Publication No. US20030143535A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang  
; APPLICANT: Neri, Bruce  
; APPLICANT: Vener, Tatiana  
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
; FILE REFERENCE: FORS-04586  
; CURRENT APPLICATION NUMBER: US/09/882,945A  
; CURRENT FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 29  
; LENGTH: 244  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-882-945A-29

Query Match 100.0%; Score 20; DB 10; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 208 TTGGGACCCCAACTACTC 189

RESULT 70  
US-09-882-945A-31/c  
; Sequence 31, Application US/09882945A  
; Publication No. US20030143535A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang  
; APPLICANT: Neri, Bruce  
; APPLICANT: Vener, Tatiana  
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
; FILE REFERENCE: FORS-04586  
; CURRENT APPLICATION NUMBER: US/09/882,945A  
; CURRENT FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 31  
; LENGTH: 244  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-882-945A-31

Query Match 100.0%; Score 20; DB 10; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20

Db 208 TTGGGACCCCAACTACTC 189

RESULT 71  
US-10-688-272-16/c

; Sequence 16, Application US/10688272

; Publication No. US20040091924A1

; GENERAL INFORMATION:

; APPLICANT: Genentech Inc.; Klm, Nam-Keun

; TITLE OF INVENTION: Method for detecting base mutation

; FILE REFERENCE: 11281-014-999

; CURRENT FILING DATE: 2003-10-17

; PRIOR FILING DATE: 2002-10-18

; PRIOR APPLICATION NUMBER: KR2002-0063832

; PRIOR FILING DATE: 2003-09-02

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Kopatentlin 1.71

; SEQ ID NO 16

; LENGTH: 244

; TYPE: DNA

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: 5' Noncoding region of HCV

US-10-688-272-16

Query Match

Best Local Similarity 100.0%; Score 20; DB 17; Length 244;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20

Db 208 TTGGGACCCCAACTACTC 189

RESULT 72

US-10-807-114-26/c

; Sequence 26, Application US/10807114

; Publication No. US20040235024A1

; GENERAL INFORMATION:

; APPLICANT: Lyamichev, Victor

; APPLICANT: Allawi, Hatim

; APPLICANT: Dong, Fang

; APPLICANT: Neri, Bruce

; APPLICANT: Vener, Tatiana

; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites

; FILE REFERENCE: FORS-04586

; CURRENT FILING DATE: 2004-03-23

; PRIOR FILING DATE: 2001-06-15

; NUMBER OF SEQ ID NOS: 334

; SOFTWARE: Patentlin version 3.0

; SEQ ID NO 26

; LENGTH: 244

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-807-114-26

Query Match

Best Local Similarity 100.0%; Score 20; DB 18; Length 244;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20

Db 208 TTGGGACCCCAACTACTC 189

RESULT 73

US-10-807-114-27/c

; Sequence 27, Application US/10807114

; Publication No. US20040235024A1

; GENERAL INFORMATION:

; APPLICANT: Lyamichev, Victor

; APPLICANT: Allawi, Hatim

; APPLICANT: Dong, Fang

; APPLICANT: Neri, Bruce

; APPLICANT: Vener, Tatiana

; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites

; FILE REFERENCE: FORS-04586

; CURRENT FILING DATE: 2004-03-23

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: US/09/882,945

; NUMBER OF SEQ ID NOS: 334

; SOFTWARE: Patentlin version 3.0

; SEQ ID NO 27

; LENGTH: 244

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-807-114-27

Query Match

Best Local Similarity 100.0%; Score 20; DB 18; Length 244;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20

Db 208 TTGGGACCCCAACTACTC 189

RESULT 74

US-10-807-114-29/c

; Sequence 29, Application US/10807114

; Publication No. US20040235024A1

; GENERAL INFORMATION:

; APPLICANT: Lyamichev, Victor

; APPLICANT: Allawi, Hatim

; APPLICANT: Dong, Fang

; APPLICANT: Neri, Bruce

; APPLICANT: Vener, Tatiana

; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites

; FILE REFERENCE: FORS-04586

; CURRENT FILING DATE: 2004-03-23

; PRIOR FILING DATE: 2001-06-15

; NUMBER OF SEQ ID NOS: 334

; SOFTWARE: Patentlin version 3.0

; SEQ ID NO 29

; LENGTH: 244

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-807-114-29

Query Match

Best Local Similarity 100.0%; Score 20; DB 18; Length 244;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20

Db 208 TTGGGACCCCAACTACTC 189

RESULT 75

US-10-807-114-31/c

; Sequence 31, Application US/10807114

; Publication No. US20040235024A1

; GENERAL INFORMATION:

```

; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neil, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; PRIOR FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-807-114-31
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Query Match          100.0%; Score 20; DB 18; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 TTCCGACCCCAACTACTC 20
          |||||
Db      208 TTCCGACCCCAACTACTC 189
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RESULT 76
US-10-655-362-26/c
; Sequence 26, Application US/10655362
; Publication No. US20050014163A1
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleo
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/10/655,362
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/402,618B
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-655-362-26
```

```

Query Match          100.0%; Score 20; DB 19; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTCCGACCCCAACTACTC 20
          |||||
Db      208 TTCCGACCCCAACTACTC 189
```

```

RESULT 77
US-10-655-362-27/c
; Sequence 27, Application US/10655362
; Publication No. US20050014163A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleo
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/10/655,362
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/402,618B
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-655-362-27
```

```

Query Match          100.0%; Score 20; DB 19; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTCCGACCCCAACTACTC 20
          |||||
Db      208 TTCCGACCCCAACTACTC 189
```

```

RESULT 78
US-10-655-362-29/c
; Sequence 29, Application US/10655362
; Publication No. US20050014163A1
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleo
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/10/655,362
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/402,618B
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-655-362-29
```

```

Query Match          100.0%; Score 20; DB 19; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTCCGACCCCAACTACTC 20
          |||||
Db      208 TTCCGACCCCAACTACTC 189
```

```

RESULT 79
US-10-655-362-31/c
```

```
; Sequence 31, Application US/10655362
; Publication No. US20050014163A1
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/10/655,362
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/402,618B
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-655-362-31
```

```
Query Match 100.0%; Score 20; DB 19; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TTGGGACCCCAACTACTC 20
Db 208 TTGGGACCCCAACTACTC 189
```

```
RESULT 80
US-10-655-362-124
; Sequence 124, Application US/10655362
; Publication No. US20050014163A1
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/10/655,362
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/402,618B
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 124
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-655-362-124
```

```
Query Match 100.0%; Score 20; DB 19; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TTGGGACCCCAACTACTC 20
Db 37 TTGGGACCCCAACTACTC 56
```

```
RESULT 81
US-10-655-362-125
; Sequence 125, Application US/10655362
; Publication No. US20050014163A1
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/10/655,362
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/402,618B
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 125
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-655-362-125
```

```
Query Match 100.0%; Score 20; DB 19; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TTGGGACCCCAACTACTC 20
Db 37 TTGGGACCCCAACTACTC 56
```

```
RESULT 82
US-10-655-362-127
; Sequence 127, Application US/10655362
; Publication No. US20050014163A1
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/10/655,362
; PRIOR FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/402,618B
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 127
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-655-362-127
```

```
Query Match 100.0%; Score 20; DB 19; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TTGGGACCCCAACTACTC 20
```



DB 37 TTGGGACCCCAACTACTC 56

RESULT 83  
US-10-655-362-128  
; Sequence 128, Application US/10655362  
; Publication No. US20050014163A1  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neel, Bruce  
; APPLICANT: Brown, Mary Ann  
; APPLICANT: Anderson, Todd  
; APPLICANT: Dahlberg, James  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/10/655,362  
; CURRENT FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: US/09/402,618B  
; PRIOR FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/03194  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 128  
; LENGTH: 244  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-10-655-362-128

Query Match 100.0%; Score 20; DB 19; Length 244;  
Best Local Similarity 80.0%; Pred. No. 0.014;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 37 TTGGGACCCCAACTACTC 56  
RESULT 84  
US-10-292-129-13/c  
; Sequence 13, Application US/10292129  
; Publication No. US20030148267A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmidt, Emmett Vance  
; APPLICANT: Chung, Raymond Taeyong  
; TITLE OF INVENTION: SCREENING ASSAY FOR HEPATITIS C VIRUS  
; FILE REFERENCE: 00786-539001  
; CURRENT APPLICATION NUMBER: US/10/292,129  
; CURRENT FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: US 60/345,405  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 263  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-292-129-13

Query Match 100.0%; Score 20; DB 15; Length 263;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 217 TTGGGACCCCAACTACTC 198

RESULT 85  
US-09-940-925A-121/c  
; Sequence 121, Application US/09940925A  
; Publication No. US20030054338A1  
; GENERAL INFORMATION:  
; APPLICANT: BROW, MARY ANN D.  
; APPLICANT: LYAMICHEV, VICTOR I.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS

NUMBER OF SEQUENCES: 165

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/940,925A

FILING DATE: 10-Jun-2002

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.

REGISTRATION NUMBER: 32,837

REFERENCE/DOCKET NUMBER: FORS-01756

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 121:

SEQUENCE CHARACTERISTICS:

LENGTH: 281 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 121:

US-09-940-925A-121

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
DB 218 TTGGGACCCCAACTACTC 199

RESULT 86  
US-09-940-925A-123/c

; Sequence 123, Application US/09940925A

; Publication No. US20030054338A1

; GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.

LYAMICHEV, VICTOR I.

OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS

NUMBER OF SEQUENCES: 165

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: Version #1.30  
APPLICATION NUMBER: US/09/940,925A  
FILING DATE: 10-Jun-2002  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 123:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 123:  
US-09-940-925A-123

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACTACTC 20  
DB 218 TTGCGACCCACACTACTC 199

RESULT 87  
US-09-940-925A-126/c  
Sequence 126, Application US/09940925A  
Publication No. US20030054338A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
OLIVE, DAVID M.  
LYAMICHEV, VICTOR I.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: Version #1.30  
APPLICATION NUMBER: US/09/940,925A  
FILING DATE: 10-Jun-2002  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 126:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 126:  
US-09-940-925A-126

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACTACTC 20  
DB 218 TTGCGACCCACACTACTC 199

RESULT 88  
US-09-940-925A-127  
Sequence 127, Application US/09940925A  
Publication No. US20030054338A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
OLIVE, DAVID M.  
LYAMICHEV, VICTOR I.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: Version #1.30  
APPLICATION NUMBER: US/09/940,925A  
FILING DATE: 10-Jun-2002  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 127:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 127:  
US-09-940-925A-127

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCACACTACTC 20  
DB 64 TTGCGACCCACACTACTC 83

RESULT 89  
US-09-940-925A-128  
Sequence 128, Application US/09940925A  
Publication No. US20030054338A1  
GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940,925A  
FILING DATE: 10-Jun-2002  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 128:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 128:  
US-09-940-925A-128  
Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGGACCCCACTACTC 20  
Db 64 TTGGGACCCCACTACTC 83  
RESULT 90  
US-09-940-925A-129  
Sequence 129, Application US/09940925A  
Publication No. US20030054338A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940,925A

FILING DATE: 10-Jun-2002  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 129:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 129:  
US-09-940-925A-129  
Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTGGGACCCCACTACTC 20  
Db 64 TTGGGACCCCACTACTC 83  
RESULT 91  
US-09-940-925A-132  
Sequence 132, Application US/09940925A  
Publication No. US20030054338A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940,925A  
FILING DATE: 10-Jun-2002  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 132:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 132:  
US-09-940-925A-132  
Query Match 100.0%; Score 20; DB 10; Length 281;

Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 64 TTGGGACCCCACTACTC 83

## RESULT 92

US-09-941-193A-121/c

; Sequence 121, Application US/09941193A  
; Publication No. US20030108873A1  
; GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.  
OLIVE, DAVID M.  
LYAMICHEV, VICTOR I.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS

NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/941,193A  
FILING DATE: 28-Aug-2001  
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 121:

SEQUENCE CHARACTERISTICS:

LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 121:  
US-09-941-193A-121

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 218 TTGGGACCCCACTACTC 199

## RESULT 93

US-09-941-193A-123/c

; Sequence 123, Application US/09941193A  
; Publication No. US20030108873A1  
; GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.  
OLIVE, DAVID M.  
LYAMICHEV, VICTOR I.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS

NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/941,193A  
FILING DATE: 28-Aug-2001  
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 123:

SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 123:  
US-09-941-193A-123

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 218 TTGGGACCCCACTACTC 199

## RESULT 94

US-09-941-193A-126/c

; Sequence 126, Application US/09941193A  
; Publication No. US20030108873A1  
; GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.  
OLIVE, DAVID M.  
LYAMICHEV, VICTOR I.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS

NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/941,193A  
FILING DATE: 28-Aug-2001  
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 126:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 126:  
US-09-941-193A-126

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
DB 218 TTCCGACCCCAACTACTC 199

RESULT 95  
US-09-941-193A-127  
Sequence 127, Application US/09941193A  
Publication No. US20030108873A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/941,193A  
FILING DATE: 28-Aug-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 127:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 127:  
US-09-941-193A-127

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TTCCGACCCCAACTACTC 20  
DB 64 TTCCGACCCCAACTACTC 83

RESULT 96  
US-09-941-193A-128  
Sequence 128, Application US/09941193A  
Publication No. US20030108873A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS

NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/941,193A  
FILING DATE: 28-Aug-2001  
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 128:

SEQUENCE CHARACTERISTICS:

LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 128:  
US-09-941-193A-128

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
DB 64 TTCCGACCCCAACTACTC 83

RESULT 97  
US-09-941-193A-129

Sequence 129, Application US/09941193A  
Publication No. US20030108873A1  
GENERAL INFORMATION:

APPLICANT: BROW, MARY ANN D.

LYAMICHEV, VICTOR I.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS

NUMBER OF SEQUENCES: 165

CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO

STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/941,193A  
FILING DATE: 28-Aug-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 129:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 129:  
US-09-941-193A-129

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACACTACTC 20  
Db 64 TTGGGACCCCAACACTACTC 83

RESULT 98  
US-09-941-193A-132  
Sequence 132, Application US/09941193A  
Publication No. US20030108673A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
OLIVE, DAVID M.  
LYAMICHEV, VICTOR I.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/941,193A  
FILING DATE: 28-Aug-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 132:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 281 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 132:  
US-09-941-193A-132

Query Match 100.0%; Score 20; DB 10; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACACTACTC 20  
Db 64 TTGGGACCCCAACACTACTC 83

RESULT 99  
US-09-940-925A-124/c  
Sequence 124, Application US/09940925A  
Publication No. US20030054338A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
OLIVE, DAVID M.  
LYAMICHEV, VICTOR I.

TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940,925A  
FILING DATE: 10-Jun-2002  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 124:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 124:  
US-09-940-925A-124

Query Match 100.0%; Score 20; DB 10; Length 282;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACACTACTC 20  
Db 219 TTGGGACCCCAACACTACTC 200

RESULT 100  
US-09-940-925A-130  
Sequence 130, Application US/09940925A  
Publication No. US20030054338A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.

LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/940,925A  
FILING DATE: 10-Jun-2002  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 130:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 130:  
US-09-940-925A-130

Query Match 100.0%; Score 20; DB 10; Length 282;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 64 TTGGGACCCCACTACTC 83

RESULT 101  
US-09-941-193A-124/C  
Sequence 124, Application US/09941193A  
Publication No. US20030108873A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
OLIVE, DAVID M.  
LYAMICHEV, VICTOR I.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/941,193A  
FILING DATE: 28-Aug-2001

CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 124:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 124:  
US-09-941-193A-124

Query Match 100.0%; Score 20; DB 10; Length 282;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
Db 219 TTGGGACCCCACTACTC 200

RESULT 102  
US-09-941-193A-130  
Sequence 130, Application US/09941193A  
Publication No. US20030108873A1  
GENERAL INFORMATION:  
APPLICANT: BROW, MARY ANN D.  
OLIVE, DAVID M.  
LYAMICHEV, VICTOR I.  
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/941,193A  
FILING DATE: 28-Aug-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: CARROLL, PETER G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: FORS-01756  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 130:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 130:  
US-09-941-193A-130

Query Match 100.0%; Score 20; DB 10; Length 282;  
Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
64 TTGGGACCCCAACTACTC 83

## RESULT 103

US-09-825-574-21/c  
; Sequence 21, Application US/09825574  
; Patent No. US20020119454A1

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Brow, Mary Ann D.

Fors, Lance

Neri, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid

Structure Probing With Structure-Bridging

Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8358

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 286 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-09-825-574-21

Query Match 100.0%; Score 20; DB 9; Length 286;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
222 TTGGGACCCCAACTACTC 203

## RESULT 104

US-09-882-945A-21/c

; Sequence 21, Application US/09882945A

; Publication No. US20030143535A1

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor

APPLICANT: Allawi, Hatim

APPLICANT: Dong, Fang

APPLICANT: Neri, Bruce

APPLICANT: Vener, Tatiana

TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites

FILE REFERENCE: FORS-04586

CURRENT APPLICATION NUMBER: US/09/882,945A

CURRENT FILING DATE: 2001-06-15

NUMBER OF SEQ ID NOS: 334

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 21

LENGTH: 286

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-09-882-945A-21

Query Match 100.0%; Score 20; DB 10; Length 286;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
222 TTGGGACCCCAACTACTC 203

## RESULT 105

US-10-807-114-21/c

; Sequence 21, Application US/10807114

; Publication No. US2004023502A1

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor

APPLICANT: Allawi, Hatim

APPLICANT: Dong, Fang

APPLICANT: Neri, Bruce

APPLICANT: Vener, Tatiana

TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites

FILE REFERENCE: FORS-04586

CURRENT APPLICATION NUMBER: US/10/807,114

CURRENT FILING DATE: 2004-03-23

PRIOR APPLICATION NUMBER: US/09/882,945

PRIOR FILING DATE: 2001-06-15

NUMBER OF SEQ ID NOS: 334

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 21

LENGTH: 286

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-10-807-114-21

Query Match 100.0%; Score 20; DB 18; Length 286;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20  
|||||  
222 TTGGGACCCCAACTACTC 203

## RESULT 106

US-10-655-362-21/c

; Sequence 21, Application US/10655362

; Publication No. US20050014163A1

GENERAL INFORMATION:

APPLICANT: Dong, Fang

APPLICANT: Lyamichev, Victor

APPLICANT: Prudent, James

APPLICANT: Fors, Lance

APPLICANT: Neri, Bruce

APPLICANT: Brow, Mary Ann

APPLICANT: Anderson, Todd



APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/10/655,362  
CURRENT FILING DATE: 2003-09-04  
PRIOR APPLICATION NUMBER: US/09/402,618B  
PRIOR FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 21  
LENGTH: 286  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-10-655-362-21

Query Match 100.0%; Score 20; DB 19; Length 286;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 222 TTGGGACCCCAACTACTC 203

RESULT 107  
US-09-825-574-20/c  
Sequence 20, Application US/09825574  
Patent No. US20020119454A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Fors, Lance P.  
Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESS: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 289 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-09-825-574-20

Query Match 100.0%; Score 20; DB 9; Length 289;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 222 TTGGGACCCCAACTACTC 203

RESULT 108  
US-09-825-574-23/c  
Sequence 23, Application US/09825574  
Patent No. US20020119454A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Fors, Lance P.  
Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESS: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 289 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

US-09-825-574-23

Query Match 100.0%; Score 20; DB 9; Length 289;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 222 TTGGGACCCCAACTACTC 203

RESULT 109  
US-09-882-945A-20/c

```
; Sequence 20, Application US/09882945A
; Publication No. US20030143535A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-882-945A-20
```

```
Query Match          100.0%; Score 20; DB 10; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGGGACCCCAACTACTC 20
         |||||
Db       222 TTGGGACCCCAACTACTC 203
```

```
RESULT 110
US-09-882-945A-23/C
; Sequence 23, Application US/09882945A
; Publication No. US20030143535A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-882-945A-23
```

```
Query Match          100.0%; Score 20; DB 10; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 TTGGGACCCCAACTACTC 20
         |||||
Db       222 TTGGGACCCCAACTACTC 203
```

```
RESULT 111
US-10-807-114-20/C
; Sequence 20, Application US/10807114
; Publication No. US20040235024A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
```

```
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-807-114-20
```

```
Query Match          100.0%; Score 20; DB 18; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGGGACCCCAACTACTC 20
         |||||
Db       222 TTGGGACCCCAACTACTC 203
```

```
RESULT 112
US-10-807-114-23/C
; Sequence 23, Application US/10807114
; Publication No. US20040235024A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-807-114-23
```

```
Query Match          100.0%; Score 20; DB 18; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGGGACCCCAACTACTC 20
         |||||
Db       222 TTGGGACCCCAACTACTC 203
```

```
RESULT 113
US-10-655-362-20/C
; Sequence 20, Application US/10655362
; Publication No. US20050014163A1
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
```

```

; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/10/655,362
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/402,618B
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 20
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-655-362-20

Query Match      100.0%; Score 20; DB 19; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTGGGACCCCAACTACTC 20
DB      222 TTGGGACCCCAACTACTC 203

RESULT 114
US-10-655-362-23/c
; Sequence 23, Application US/10655362
; Publication No. US20050014163A1
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neill, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/10/655,362
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/402,618B
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 23
; LENGTH: 289
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-655-362-23

Query Match      100.0%; Score 20; DB 19; Length 289;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTGGGACCCCAACTACTC 20
DB      222 TTGGGACCCCAACTACTC 203

RESULT 115
US-09-345-761-7/c
; Sequence 7, Application US/09345761
; Patent No. US20010053518A1
; GENERAL INFORMATION:
; APPLICANT: ISHIGURO, Takahiko
; APPLICANT: SAITOH, Juichi
```

```

; APPLICANT: ISHIZUKA, Tetsuya
; TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID
; FILE REFERENCE: Q54969
; CURRENT APPLICATION NUMBER: US/09/345,761
; CURRENT FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: JP 10-186434
; PRIOR FILING DATE: 1998-07-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 7
; LENGTH: 298
; TYPE: RNA
; ORGANISM: Synthetic Construct
US-09-345-761-7

Query Match      100.0%; Score 20; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTGGGACCCCAACTACTC 20
DB      261 TTGGGACCCCAACTACTC 242

RESULT 116
US-10-687-588-7/c
; Sequence 7, Application US/10687588
; Publication No. US20040115718A1
; GENERAL INFORMATION:
; APPLICANT: ISHIGURO, Takahiko
; APPLICANT: SAITOH, Juichi
; APPLICANT: ISHIZUKA, Tetsuya
; TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID
; FILE REFERENCE: Q54969
; CURRENT APPLICATION NUMBER: US/10/687,588
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US/09/345,761
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: JP 10-186434
; PRIOR FILING DATE: 1998-07-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 7
; LENGTH: 298
; TYPE: RNA
; ORGANISM: Synthetic Construct
US-10-687-588-7

Query Match      100.0%; Score 20; DB 18; Length 298;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTGGGACCCCAACTACTC 20
DB      261 TTGGGACCCCAACTACTC 242

RESULT 117
US-10-230-381-1/c
; Sequence 1, Application US/10230381
; Publication No. US20030152591A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: New hepatitis C virus genotype 13, and its use as prophylactic,
; FILE REFERENCE: INNX-124-BP
; CURRENT APPLICATION NUMBER: US/10/230,381
; CURRENT FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 1
; LENGTH: 299
; TYPE: DNA
```

; ORGANISM: hepatitis C virus  
US-10-230-381-1

Query Match 100.0%; Score 20; DB 16; Length 299;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 233 TTGGGACCCCAACTACTC 214

## RESULT 118

US-09-345-761-6/c  
; Sequence 6, Application US/09345761  
; Patent No. US2001005318A1  
; GENERAL INFORMATION:  
; APPLICANT: ISHIGURO, Takahiko  
; APPLICANT: SAITOH, Juichi  
; APPLICANT: ISHIZUKA, Tetsuya  
; TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID  
; FILE REFERENCE: 054969  
; CURRENT APPLICATION NUMBER: US/09/345,761  
; CURRENT FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: JP 10-186434  
; PRIOR FILING DATE: 1998-07-01  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 315  
; TYPE: DNA  
; ORGANISM: Synthetic Construct  
US-09-345-761-6

Query Match 100.0%; Score 20; DB 9; Length 315;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 278 TTGGGACCCCAACTACTC 259

## RESULT 119

US-10-687-588-6/c  
; Sequence 6, Application US/10687588  
; Publication No. US20040115718A1  
; GENERAL INFORMATION:  
; APPLICANT: ISHIGURO, Takahiko  
; APPLICANT: SAITOH, Juichi  
; APPLICANT: ISHIZUKA, Tetsuya  
; TITLE OF INVENTION: METHOD OF ASSAY OF TARGET NUCLEIC ACID  
; FILE REFERENCE: 054969  
; CURRENT APPLICATION NUMBER: US/10/687,588  
; CURRENT FILING DATE: 2003-10-20  
; PRIOR APPLICATION NUMBER: US/09/345,761  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: JP 10-186434  
; PRIOR FILING DATE: 1998-07-01  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 315  
; TYPE: DNA  
; ORGANISM: Synthetic Construct  
US-10-687-588-6

Query Match 100.0%; Score 20; DB 18; Length 315;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||

Db 278 TTGGGACCCCAACTACTC 259

## RESULT 120

US-09-882-945A-240/c  
; Sequence 240, Application US/09882945A  
; Publication No. US20030143535A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang  
; APPLICANT: Neri, Bruce  
; APPLICANT: Vener, Tatiana  
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
; FILE REFERENCE: FORS-04586  
; CURRENT APPLICATION NUMBER: US/09/882,945A  
; CURRENT FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 240  
; LENGTH: 328  
; TYPE: RNA  
; ORGANISM: Hepatitis C virus  
US-09-882-945A-240

Query Match 100.0%; Score 20; DB 10; Length 328;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 257 TTGGGACCCCAACTACTC 238

## RESULT 121

US-09-882-945A-242/c  
; Sequence 242, Application US/09882945A  
; Publication No. US20030143535A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang  
; APPLICANT: Neri, Bruce  
; APPLICANT: Vener, Tatiana  
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites  
; FILE REFERENCE: FORS-04586  
; CURRENT APPLICATION NUMBER: US/09/882,945A  
; CURRENT FILING DATE: 2001-06-15  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 242  
; LENGTH: 328  
; TYPE: RNA  
; ORGANISM: Hepatitis C virus  
US-09-882-945A-242

Query Match 100.0%; Score 20; DB 10; Length 328;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
|||||  
Db 257 TTGGGACCCCAACTACTC 238

## RESULT 122

US-09-882-945A-245/c  
; Sequence 245, Application US/09882945A  
; Publication No. US20030143535A1  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Dong, Fang

```

; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 245
; LENGTH: 328
; TYPE: RNA
; ORGANISM: Hepatitis C virus
US-09-882-945A-245

Query Match          100.0%; Score 20; DB 10; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCAACTACTC 20
Db 257 TTGGGACCCCAACTACTC 238

RESULT 123
US-10-475-024-18/c
; Sequence 18, Application US/10475024
; Publication No. US20040219545A1
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Welch, Ellen
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SMALL MOLECULES THAT BIND SPECIFIC RNA
; FILE REFERENCE: 10589-007-999
; CURRENT APPLICATION NUMBER: US/10/475,024
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/282,965
; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 328
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-475-024-18

Query Match          100.0%; Score 20; DB 18; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCAACTACTC 20
Db 263 TTGGGACCCCAACTACTC 244

RESULT 124
US-10-807-114-240/c
; Sequence 240, Application US/10807114
; Publication No. US20040235024A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 240
```

```

; LENGTH: 328
; TYPE: RNA
; ORGANISM: Hepatitis C virus
US-10-807-114-240

Query Match          100.0%; Score 20; DB 18; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCAACTACTC 20
Db 257 TTGGGACCCCAACTACTC 238

RESULT 125
US-10-807-114-242/c
; Sequence 242, Application US/10807114
; Publication No. US20040235024A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 242
; LENGTH: 328
; TYPE: RNA
; ORGANISM: Hepatitis C virus
US-10-807-114-242

Query Match          100.0%; Score 20; DB 18; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTGGGACCCCAACTACTC 20
Db 257 TTGGGACCCCAACTACTC 238

RESULT 126
US-10-807-114-245/c
; Sequence 245, Application US/10807114
; Publication No. US20040235024A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/10/807,114
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US/09/882,945
; PRIOR FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 245
; LENGTH: 328
; TYPE: RNA
; ORGANISM: Hepatitis C virus
US-10-807-114-245

Query Match          100.0%; Score 20; DB 18; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.014;
```

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 257 TTGCGACCCCAACTACTC 238

## RESULT 127

US-09-940-244-45/C  
Sequence 45, Application US/09940244  
Publication No. US2003004796A1  
GENERAL INFORMATION:  
APPLICANT: Neri, Bruce P.  
APPLICANT: Hall, Jeff G.  
APPLICANT: Lyamachev, Victor  
APPLICANT: Smith, Lloyd M.  
TITLE OF INVENTION: Reactions on Dendrimers  
FILE REFERENCE: FORS-06478  
CURRENT APPLICATION NUMBER: US/09/940,244  
CURRENT FILING DATE: 2002-05-06  
NUMBER OF SEQ ID NOS: 422  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 45  
LENGTH: 337  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-940-244-45

Query Match 100.0%; Score 20; DB 10; Length 337;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 274 TTGCGACCCCAACTACTC 255

## RESULT 128

US-09-982-667-56/C  
Sequence 56, Application US/09982667  
Publication No. US20030096245A1  
GENERAL INFORMATION:  
APPLICANT: Prudent, James R.  
Hall, Jeff G.  
Lyamachev, Victor I.

TITLE OF INVENTION: Invasive Cleavage Of Nucleic Acids  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medien & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States Of America  
ZIP: 94104

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/982,667  
FILING DATE: 18-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/756,386  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/682,853  
FILING DATE: 12-JUL-1996  
APPLICATION NUMBER: US 08/599,491  
FILING DATE: 24-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027

NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02564  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 337 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: RNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 56:  
US-09-982-667-56

Query Match 100.0%; Score 20; DB 10; Length 337;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGCGACCCCAACTACTC 20  
DB 274 TTGCGACCCCAACTACTC 255

## RESULT 129

US-10-033-297-45/C  
Sequence 45, Application US/10033297  
Publication No. US20020187486A1  
GENERAL INFORMATION:  
APPLICANT: Hall, Jeff G.  
Lyamachev, Victor I.  
Macl, Andrea L.  
Brow, Mary Ann D.

TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple  
Sequential Invasive Cleavages

NUMBER OF SEQUENCES: 163  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medien & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States Of America  
ZIP: 94104

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/033,297  
FILING DATE: 12-No. US20020187486A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/350,597  
FILING DATE: 09-Jul-1999  
APPLICATION NUMBER: US/08/823,516  
FILING DATE: 24-MAR-1997  
APPLICATION NUMBER: PCT/US97/01072  
FILING DATE: 21-JAN-1997  
APPLICATION NUMBER: US 08/759,038  
FILING DATE: 02-DEC-1996  
APPLICATION NUMBER: US 08/758,314  
FILING DATE: 02-DEC-1996  
APPLICATION NUMBER: US 08/756,386  
FILING DATE: 29-NOV-1996  
APPLICATION NUMBER: US 08/682,853  
FILING DATE: 12-JUL-1996  
APPLICATION NUMBER: US 08/599,491  
FILING DATE: 24-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: FORS-02736  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 337 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: No. US20020187486A1 Relevant  
TOPOLOGY: No. US20020187486A1 Relevant  
SEQUENCE DESCRIPTION: SEQ ID NO: 45:  
US-10-033-297-45

Query Match 100.0%; Score 20; DB 13; Length 337;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 274 TTGGGACCCCAACTACTC 255

RESULT 130  
US-10-081-806-56/c  
Sequence 56, Application US/10081806  
Publication No. US20020197623A1  
GENERAL INFORMATION:  
APPLICANT: Prudent, James R.  
Hall, Jeff G.  
Lyamichiev, Victor I.  
TITLE OF INVENTION: Invasive Cleavage Of Nucleic Acids  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: United States Of America  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/081,806  
FILING DATE: 22-Feb-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/756,386  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/682,853  
FILING DATE: 12-JUL-1996  
APPLICATION NUMBER: US 08/599,491  
FILING DATE: 24-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02564  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 337 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: No. US20020197623A1 Relevant  
TOPOLOGY: No. US20020197623A1 Relevant  
SEQUENCE DESCRIPTION: SEQ ID NO: 56:  
US-10-081-806-56

Query Match 100.0%; Score 20; DB 13; Length 337;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 274 TTGGGACCCCAACTACTC 255

RESULT 131  
US-10-142-283-136/c  
Sequence 136, Application US/10142283  
Publication No. US20030152942A1  
GENERAL INFORMATION:  
APPLICANT: Fors, Lance  
Neel, Bruce P.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: de Arruda Indig, Monika  
APPLICANT: Roeven, Robert  
TITLE OF INVENTION: Nucleic Acid Detection in Pooled Samples  
FILE REFERENCE: FORS-07219  
CURRENT APPLICATION NUMBER: US/10/142,283  
CURRENT FILING DATE: 2002-12-10  
PRIOR APPLICATION NUMBER: 60/326,549  
PRIOR FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: 60/289,764  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 139  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 136  
LENGTH: 337  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-10-142-283-136

Query Match 100.0%; Score 20; DB 16; Length 337;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 274 TTGGGACCCCAACTACTC 255

RESULT 132  
US-10-290-386-45/c  
Sequence 45, Application US/10290386  
Publication No. US2003015297A1  
GENERAL INFORMATION:  
APPLICANT: Lyamichiev, Victor  
Neel, Bruce P.  
APPLICANT: Hall, Jeff G.  
APPLICANT: Lukowiak, Andrew A.  
TITLE OF INVENTION: Methods and Compositions for Detecting Target Sequences  
FILE REFERENCE: FORS-07459  
CURRENT APPLICATION NUMBER: US/10/290,386  
CURRENT FILING DATE: 2002-11-07  
PRIOR APPLICATION NUMBER: 60/361,060  
PRIOR FILING DATE: 2002-02-27  
PRIOR APPLICATION NUMBER: 60/344,946  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: 09/713,601  
PRIOR FILING DATE: 2000-11-15  
PRIOR APPLICATION NUMBER: 09/381,212  
PRIOR FILING DATE: 2000-02-08  
PRIOR APPLICATION NUMBER: 09/350,309  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: 08/823,516  
PRIOR FILING DATE: 1997-03-24  
PRIOR APPLICATION NUMBER: 08/759,038  
PRIOR FILING DATE: 1996-12-02

```
; PRIOR APPLICATION NUMBER: 08/556,386
; PRIOR FILING DATE: 1996-11-26
; PRIOR APPLICATION NUMBER: 08/682,853
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 08/599,491
; PRIOR FILING DATE: 1996-01-24
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 337
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-290-386-45

Query Match          100.0%; Score 20; DB 16; Length 337;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20
    |||
Db 274 TTCCGACCCCACTACTC 255

RESULT 133
US-10-356-861-45/C
; Sequence 45, Application US/10356861
; Publication No. US20040072182A1
; GENERAL INFORMATION:
; APPLICANT: Victor, Lyamichev
; APPLICANT: Neri, Bruce P.
; APPLICANT: Hall, Jeff
; APPLICANT: Lukowiak, Andrew A.
; TITLE OF INVENTION: Methods and Compositions for Detecting Target Sequences
; FILE REFERENCE: FORS-07813
; CURRENT APPLICATION NUMBER: US/10/356,861
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 337
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-356-861-45

Query Match          100.0%; Score 20; DB 17; Length 337;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20
    |||
Db 274 TTCCGACCCCACTACTC 255

RESULT 134
US-10-309-584-45/C
; Sequence 45, Application US/10309584
; Publication No. US20040214174A1
; GENERAL INFORMATION:
; APPLICANT: Neri, Bruce P.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Smith, Lloyd M.
; TITLE OF INVENTION: Reactions on Dendrimers
; FILE REFERENCE: FORS-06478
; CURRENT APPLICATION NUMBER: US/10/309,584
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US/09/940,244
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 422
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-309-584-45

Query Match          100.0%; Score 20; DB 18; Length 337;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCACTACTC 20
    |||
Db 274 TTCCGACCCCACTACTC 255

RESULT 135
US-10-897-793-45/C
; Sequence 45, Application US/10897793
; Publication No. US20050003432A1
; GENERAL INFORMATION:
; APPLICANT: Hall, Jeff G.
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Mast, Andrea L.
; APPLICANT: Brow, Mary Ann D.
; TITLE OF INVENTION: Detection Of Nucleic Acids By Multiple
;                               Sequential Invasive Cleavages
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/897,793
; FILING DATE: 23-Jul-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/01072
; FILING DATE: 21-JAN-1997
; APPLICATION NUMBER: US 08/759,038
; FILING DATE: 02-DEC-1996
; APPLICATION NUMBER: US 08/758,314
; FILING DATE: 02-DEC-1996
; APPLICATION NUMBER: US 08/756,386
; FILING DATE: 29-NOV-1996
; APPLICATION NUMBER: US 08/682,853
; FILING DATE: 12-JUL-1996
; APPLICATION NUMBER: US 08/599,491
; FILING DATE: 24-JAN-1996
; APPLICATION NUMBER: US 08/323,516
; FILING DATE: 24-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: McKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-03295
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
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TOPOLOGY: not relevant  
MOLECULE TYPE: RNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 45:  
US-10-897-793-45

Query Match 100.0%; Score 20; DB 18; Length 337;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
DB 274 TTGGGACCCCAACTACTC 255

RESULT 136  
US-10-783-557-45/c  
Sequence 45, Application US/10783557  
Publication No. US20050048527A1  
GENERAL INFORMATION:  
APPLICANT: Allawi, Hatim T.  
APPLICANT: Kaiser, Michael W.  
APPLICANT: Ma, Wu-Po  
APPLICANT: Neel, Bruce P.  
APPLICANT: Lyamichev, Victor I.  
TITLE OF INVENTION: Endonuclease-Substrate Complexes  
FILE REFERENCE: FORS-08907  
CURRENT APPLICATION NUMBER: US/10/783,557  
CURRENT FILING DATE: 2004-02-20  
NUMBER OF SEQ ID NOS: 533  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 45  
LENGTH: 337  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-783-557-45

Query Match 100.0%; Score 20; DB 19; Length 337;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
DB 274 TTGGGACCCCAACTACTC 255

RESULT 137  
US-09-814-292-44/c  
Sequence 44, Application US/09814292  
Patent No. US20020120117A1  
GENERAL INFORMATION:  
APPLICANT: Yu, De-Chao  
APPLICANT: Zhang, Hong  
APPLICANT: Henderson, Daniel R.  
TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN  
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY SEQUENCES, VECTORS COMPRISING  
TITLE OF INVENTION: UROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND  
FILE REFERENCE: 348022001500  
CURRENT APPLICATION NUMBER: US/09/814,292  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 60/191,861  
PRIOR FILING DATE: 2000-03-24  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 44  
LENGTH: 341  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: 5' UTR region of HCV  
US-09-814-292-44

Query Match 100.0%; Score 20; DB 9; Length 341;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
DB 275 TTGGGACCCCAACTACTC 256

RESULT 138  
US-09-814-357-3/c  
Sequence 3, Application US/09814357  
Publication No. US20030068307A1  
GENERAL INFORMATION:  
APPLICANT: Yu, De-Chao  
APPLICANT: Chen, Yu  
APPLICANT: Henderson, Daniel R.  
TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA  
TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,  
FILE REFERENCE: 348022001600  
CURRENT APPLICATION NUMBER: US/09/814,357  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 60/192,015  
PRIOR FILING DATE: 2000-03-24  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 341  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: 5' UTR region of HCV  
US-09-814-357-3

Query Match 100.0%; Score 20; DB 10; Length 341;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
DB 275 TTGGGACCCCAACTACTC 256

RESULT 139  
US-09-814-351-3/c  
Sequence 3, Application US/09814351  
Publication No. US20030148520A1  
GENERAL INFORMATION:  
APPLICANT: Yu, De-Chao  
APPLICANT: Li, Yuanhao  
APPLICANT: Henderson, Daniel R.  
TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS  
TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE  
FILE REFERENCE: 348022001700  
CURRENT APPLICATION NUMBER: US/09/814,351  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/192,156  
PRIOR FILING DATE: 2000-03-24  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 341  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: 5' UTR region of HCV  
US-09-814-351-3

OY 1 TTCCGACCCCAACTACTC 20  
|||  
Db 275 TTCCGACCCCAACTACTC 256

RESULT 140  
US-10-259-275-35/c  
; Sequence 35, Application US/10259275  
; Publication No. US20030125541A1  
; GENERAL INFORMATION:  
; APPLICANT: Lemov, Stanley M.  
; APPLICANT: Yi, Minkyung  
; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE  
; FILE REFERENCE: 265,0007 0120  
; CURRENT APPLICATION NUMBER: US/10/259,275  
; PRIOR FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: US 60/171,909  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: US 09/747,419  
; PRIOR FILING DATE: 2000-12-23  
; PRIOR APPLICATION NUMBER: US 60/325,236  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US 60/338,123  
; PRIOR FILING DATE: 2001-11-13  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35  
; LENGTH: 341  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL  
; FEATURE:  
; OTHER INFORMATION: nucleotide sequence of 5' NTR  
US-10-259-275-35

Query Match 100.0%; Score 20; DB 15; Length 341;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
|||  
Db 275 TTCCGACCCCAACTACTC 256

RESULT 141  
US-10-132-295-1/c  
; Sequence 1, Application US/10132295  
; Publication No. US20030124550A1  
; GENERAL INFORMATION:  
; APPLICANT: BML, Inc.  
; TITLE OF INVENTION: METHOD OF SCREENING DRUG FOR HEPATITIS C  
; FILE REFERENCE: 069614  
; CURRENT APPLICATION NUMBER: US/10/132,295  
; CURRENT FILING DATE: 2002-04-26  
; PRIOR APPLICATION NUMBER: JP 2001-329728  
; PRIOR FILING DATE: 2001-10-26  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 347  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-10-132-295-1

Query Match 100.0%; Score 20; DB 15; Length 347;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
|||  
Db 275 TTCCGACCCCAACTACTC 256

RESULT 142  
US-09-877-526A-48/c  
; Sequence 48, Application US/09877526A  
; Patent No. US20020102568A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc  
; APPLICANT: Usman, Nassim  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Zinnen, Shawn  
; APPLICANT: Seiwert, Scott  
; APPLICANT: Haebertli, Pete  
; APPLICANT: Chowli, Bharat  
; APPLICANT: Blatt, Larry  
; APPLICANT: Vaish, Narendra  
; TITLE OF INVENTION: A Process for the Detection of Nucleic Acid Using Nucleic Acid C

; FILE REFERENCE: MEH800-816-C (700/002)  
; CURRENT APPLICATION NUMBER: US/09/877,526A  
; CURRENT FILING DATE: 2001-03-06  
; PRIOR FILING DATE: 60/187,128  
; PRIOR APPLICATION NUMBER: 2000-03-06  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 48  
; LENGTH: 366  
; TYPE: RNA  
; ORGANISM: Hepatitis C virus  
US-09-877-526A-48

Query Match 100.0%; Score 20; DB 9; Length 366;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
|||  
Db 275 TTCCGACCCCAACTACTC 256

RESULT 143  
US-09-992-160-48/c  
; Sequence 48, Application US/09992160  
; Publication No. US2003008235A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc  
; APPLICANT: Usman, Nassim  
; APPLICANT: McSwigen, Jim  
; APPLICANT: Zinnen, Shawn  
; APPLICANT: Seiwert, Scott  
; APPLICANT: Haebertli, Pete  
; APPLICANT: Chowli, Bharat  
; APPLICANT: Blatt, Larry  
; TITLE OF INVENTION: Nucleic Acid Sensor Molecules  
; FILE REFERENCE: MEH800-816-D (700/004)  
; CURRENT APPLICATION NUMBER: US/09/992,160  
; CURRENT FILING DATE: 2001-11-05  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 48  
; LENGTH: 366  
; TYPE: RNA  
; ORGANISM: Hepatitis C virus  
US-09-992-160-48

Query Match 100.0%; Score 20; DB 10; Length 366;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
|||  
Db 275 TTCCGACCCCAACTACTC 256

RESULT 144  
US-09-740-332-9701/c

```
/ Sequence 9701, Application US/09740332
/ Publication No. US20030125270A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals Inc.
/ TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
/ FILE REFERENCE: RPI 400/003
/ CURRENT APPLICATION NUMBER: US/09/740,332
/ CURRENT FILING DATE: 2001-03-26
/ NUMBER OF SEQ ID NOS: 9704
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 9701
/ LENGTH: 366
/ TYPE: RNA
/ ORGANISM: artificial sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: HCV 5' UTR
US-09-740-332-9701

Query Match          100.0%; Score 20; DB 10; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 276 TTGGGACCCCAACTACTC 257

RESULT 145
US-09-817-879-9701/c
/ Sequence 9701, Application US/09817879
/ Publication No. US2003017131A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals Inc.
/ TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
/ FILE REFERENCE: RPI 400/003
/ CURRENT APPLICATION NUMBER: US/09/817,879
/ CURRENT FILING DATE: 2001-03-26
/ NUMBER OF SEQ ID NOS: 9703
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 9701
/ LENGTH: 366
/ TYPE: RNA
/ ORGANISM: artificial sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION:
/ OTHER INFORMATION: HCV 5' UTR
US-09-817-879-9701

Query Match          100.0%; Score 20; DB 10; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 276 TTGGGACCCCAACTACTC 257

RESULT 146
US-10-056-761-48/c
/ Sequence 48, Application US/10056761
/ Publication No. US20030065155A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc
/ APPLICANT: Usman, Nassim
/ APPLICANT: MGSWigen, Jim
/ APPLICANT: Zinnen, Shawn
/ APPLICANT: Selwert, Scott
/ APPLICANT: Haeblerli, Pete
```

```
/ APPLICANT: Chowrira, Bharat
/ APPLICANT: Blatt, Larry
/ TITLE OF INVENTION: Nucleic Acid Sensor Molecules
/ FILE REFERENCE: MBH00-816-E (700/005)
/ CURRENT APPLICATION NUMBER: US/10/056,761
/ CURRENT FILING DATE: 2002-01-23
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 48
/ LENGTH: 366
/ TYPE: RNA
/ ORGANISM: Hepatitis C Virus
US-10-056-761-48

Query Match          100.0%; Score 20; DB 14; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 275 TTGGGACCCCAACTACTC 256

RESULT 147
US-10-422-050-48/c
/ Sequence 48, Application US/10422050
/ Publication No. US20040009510A1
/ GENERAL INFORMATION:
/ APPLICANT: Sirna Therapeutics, Inc.
/ APPLICANT: Selwert, Scott
/ APPLICANT: Zinnen, Shawn
/ APPLICANT: Vaish, Narendra
/ APPLICANT: Jadhav, Vasant
/ APPLICANT: Kossen, Karl
/ TITLE OF INVENTION: Allosteric Nucleic Acid Sensor Molecules
/ FILE REFERENCE: 700/013 (MBH 00-816-M)
/ CURRENT APPLICATION NUMBER: US/10/422,050
/ CURRENT FILING DATE: 2003-04-23
/ PRIOR APPLICATION NUMBER: PCT/US 02/35529
/ PRIOR FILING DATE: 2002-11-05
/ PRIOR APPLICATION NUMBER: US 10/286,492
/ PRIOR FILING DATE: 2002-11-01
/ PRIOR APPLICATION NUMBER: US 10/283,858
/ PRIOR FILING DATE: 2002-10-30
/ PRIOR APPLICATION NUMBER: US 10/056,761
/ PRIOR FILING DATE: 2002-01-23
/ PRIOR APPLICATION NUMBER: US 09/992,160
/ PRIOR FILING DATE: 2002-11-05
/ PRIOR APPLICATION NUMBER: US 09/877,526
/ PRIOR FILING DATE: 2001-06-08
/ PRIOR APPLICATION NUMBER: US 09/800,594
/ PRIOR FILING DATE: 2001-03-06
/ PRIOR APPLICATION NUMBER: US 60/187,128
/ PRIOR FILING DATE: 2000-03-06
/ NUMBER OF SEQ ID NOS: 102
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 48
/ LENGTH: 366
/ TYPE: RNA
/ ORGANISM: Hepatitis C Virus
US-10-422-050-48

Query Match          100.0%; Score 20; DB 17; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20
Db 275 TTGGGACCCCAACTACTC 256

RESULT 148
US-10-669-841-16198/c
```

```
; Sequence 16198, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blact
; APPLICANT: Dennis, Macejak
; APPLICANT: James, MCSW199n
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; FILE REFERENCE: 400/04205 (MEHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16198
; LENGTH: 366
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: HCV 5' UTR
; US-10-669-841-16198

Query Match          100.0%; Score 20; DB 18; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  TTCCGACCCCACTACTC 20
Db      276 TTCCGACCCCACTACTC 257

RESULT 149
US-10-324-409B-32/c
; Sequence 32, Application US/10324409B
; Publication No. US20040086880A1
; GENERAL INFORMATION:
; APPLICANT: Sampson, et al.
; TITLE OF INVENTION: Method of Producing Nucleic Acid Molecules with Reduced
; FILE REFERENCE: 2003309-0028
; CURRENT APPLICATION NUMBER: US/10/324,409B
; CURRENT FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
```

```
; LENGTH: 374
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Nucleotides
; US-10-324-409B-32

Query Match          100.0%; Score 20; DB 17; Length 374;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  TTCCGACCCCACTACTC 20
Db      263 TTCCGACCCCACTACTC 244

RESULT 150
US-10-626-879-9/c
; Sequence 9, Application US/10626879
; Publication No. US20050058982A1
; GENERAL INFORMATION:
; APPLICANT: HAN, JANG
; APPLICANT: SEO, MI YOUNG
; APPLICANT: HOUGHTON, MICHAEL
; TITLE OF INVENTION: MODIFIED SMALL INTERFERING RNA MOLECULES AND METHODS OF USE
; FILE REFERENCE: 072121-0189-REG
; CURRENT APPLICATION NUMBER: US/10/626,879
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/470,230
; PRIOR FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: 60/461,838
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/398,605
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
; LENGTH: 383
; TYPE: RNA
; ORGANISM: Hepatitis C virus
; US-10-626-879-9

Query Match          100.0%; Score 20; DB 19; Length 383;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  TTCCGACCCCACTACTC 20
Db      275 TTCCGACCCCACTACTC 256

RESULT 151
US-10-332-626-1/c
; Sequence 1, Application US/10332626
; Publication No. US20040073880A1
; GENERAL INFORMATION:
; APPLICANT: Joseph D. Pugliesi
; TITLE OF INVENTION: Structural Targets of Hepatitis C Virus
; FILE REFERENCE: STAN-196
; CURRENT APPLICATION NUMBER: US/10/332,626
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: PCT/US01/21371
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,673
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 384
; TYPE: RNA
; ORGANISM: Hepatitis C virus
```

US-10-332-626-1

Query Match 100.0%; Score 20; DB 17; Length 384;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
|||||  
Db 276 TTGGGACCCCACTACTC 257

RESULT 152

US-09-940-925A-122/c

; Sequence 122, Application US/09940925A  
; Publication No. US20030054338A1  
; GENERAL INFORMATION:  
; APPLICANT: BROW, MARY ANN D.  
; LYAMICHEV, VICTOR I.  
; OLIVE, DAVID M.

; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
; PATHOGENS  
; NUMBER OF SEQUENCES: 165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL  
; STREET: 220 MONTGOMERY STREET, SUITE 2200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 94104

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/940,925A  
; FILING DATE: 10-Jun-2002  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: FORS-01756  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338

; INFORMATION FOR SEQ ID NO: 122:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 386 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 122:  
US-09-940-925A-122

Query Match 100.0%; Score 20; DB 10; Length 386;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
|||||  
Db 323 TTGGGACCCCACTACTC 304

RESULT 153

US-09-941-193A-122/c

; Sequence 122, Application US/09941193A  
; Publication No. US20030108873A1  
; GENERAL INFORMATION:  
; APPLICANT: BROW, MARY ANN D.  
; LYAMICHEV, VICTOR I.  
; OLIVE, DAVID M.

; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF

PATHOGENS

NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/941,193A  
; FILING DATE: 28-Aug-2001  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: FORS-01756  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338

; INFORMATION FOR SEQ ID NO: 122:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 386 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 122:  
US-09-941-193A-122

Query Match 100.0%; Score 20; DB 10; Length 386;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCACTACTC 20  
|||||  
Db 323 TTGGGACCCCACTACTC 304

RESULT 154

US-10-276-513-5/c

; Sequence 5, Application US/10276513  
; Publication No. US20030143528A1  
; GENERAL INFORMATION:  
; APPLICANT: KOHARA, MICHINORI  
; APPLICANT: MATSUZAKI, JUNICHI  
; APPLICANT: OKAMOTO, KOUICHI  
; APPLICANT: KATSUME, ASAO

; TITLE OF INVENTION: VECTOR FOR ANALYSING REPLICATION MECHANISM OF RNA VIRUS AND USE  
; FILE REFERENCE: 382.1038  
; CURRENT APPLICATION NUMBER: US/10/276,513  
; PRIOR FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: PCT/JP01/04033  
; PRIOR FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: JP 2000-142451  
; PRIOR FILING DATE: 2000-05-15

; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 393  
; TYPE: DNA  
; ORGANISM: Hepatitis C Virus

US-10-276-513-5

Query Match 100.0%; Score 20; DB 15; Length 393;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 287 TTGGGACCCCAACTACTC 268

## RESULT 155

US-10-276-513-4/C  
; Sequence 4, Application US/10276513  
; Publication No. US20030143528A1  
; GENERAL INFORMATION:  
; APPLICANT: KOHARA, MICHINORI  
; APPLICANT: MATSUZAKI, JUNICHI  
; APPLICANT: OKAMOTO, KOUICHI  
; APPLICANT: KATSUME, ASAO  
; TITLE OF INVENTION: VECTOR FOR ANALYSING REPLICATION MECHANISM OF RNA VIRUS AND USE T  
; FILE REFERENCE: 382.1038  
; CURRENT APPLICATION NUMBER: US/10/276,513  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: PCT/JP01/04033  
; PRIOR FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: JP 2000-142451  
; PRIOR FILING DATE: 2000-05-15  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 412  
; TYPE: DNA  
; ORGANISM: Hepatitis C Virus  
US-10-276-513-4

Query Match 100.0%; Score 20; DB 15; Length 412;  
Best Local Similarity 100.0%; Pred. No. 0.014;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 306 TTGGGACCCCAACTACTC 287

RESULT 156  
US-09-851-138-59/C  
; Sequence 59, Application US/09851138  
; Publication No. US20020183508A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT  
; APPLICANT: STUYVER, LIEVEN  
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES  
; AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC  
; AGENTS

NUMBER OF SEQUENCES: 207  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARNOLD, WHITE & DURKEE  
STREET: P.O. BOX 4433  
CITY: HOUSTON  
STATE: TEXAS  
COUNTRY: USA  
ZIP: 77210-4433

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Microsoft Word 6.0 / ASCII text output

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/851,138  
FILING DATE: 09-May-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/836,075  
FILING DATE: <Unknown>  
APPLICATION NUMBER: EP 94870166.9  
FILING DATE: 21 Oct 1994  
APPLICATION NUMBER: EP 95870076.7  
FILING DATE: 28 Jun 1995  
ATTORNEY/AGENT INFORMATION:

NAME: KAMMERER, PATRICIA A.  
REGISTRATION NUMBER: 29,775  
REFERENCE/DOCKET NUMBER: INNS-004  
INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:  
LENGTH: 652 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
US-09-851-138-59

Query Match 100.0%; Score 20; DB 9; Length 652;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 172 TTGGGACCCCAACTACTC 153

RESULT 157  
US-09-853-409-37/C  
; Sequence 37, Application US/09853409  
; Publication No. US20030171313A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Kevin P.  
; APPLICANT: Hanecek, Ronnie C.  
; APPLICANT: Dorr, F. Andrew  
; APPLICANT: Kwok, T. Jesse  
; TITLE OF INVENTION: Compositions and Methods for Treatment of Hepatitis C  
; FILE REFERENCE: ISPH-0569  
; CURRENT APPLICATION NUMBER: US/09/853,409  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 08/988,321  
; PRIOR FILING DATE: 1997-12-10  
; PRIOR APPLICATION NUMBER: 08/650,093  
; PRIOR FILING DATE: 1996-05-17  
; PRIOR APPLICATION NUMBER: 08/452,841  
; PRIOR FILING DATE: 1995-05-30  
; PRIOR APPLICATION NUMBER: 08/397,330  
; PRIOR FILING DATE: 1995-03-09  
; PRIOR APPLICATION NUMBER: 07/945,289  
; PRIOR FILING DATE: 1992-09-10  
; PRIOR APPLICATION NUMBER: 09/690,936  
; PRIOR FILING DATE: 2000-10-18  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 37  
; LENGTH: 685  
; TYPE: RNA  
; ORGANISM: Hepatitis C Virus  
US-09-853-409-37

Query Match 100.0%; Score 20; DB 10; Length 685;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 274 TTGGGACCCCAACTACTC 255

RESULT 158  
US-10-457-304-37/C  
; Sequence 37, Application US/10457304  
; Publication No. US20040033978A1  
; GENERAL INFORMATION:

APPLICANT: Anderson, Kevin P.  
APPLICANT: Hanecak, Ronnie C.  
APPLICANT: No. US20040033978A1aki, Chikateru  
APPLICANT: Dort, F. Andrew  
APPLICANT: Kwoh, T. Jesse  
TITLE OF INVENTION: Compositions and Methods for Treatment of Hepatitis C  
FILE REFERENCE: ISPH-0569  
CURRENT APPLICATION NUMBER: US/10/457,304  
CURRENT FILING DATE: 2003-06-09  
PRIOR APPLICATION NUMBER: US/09/853,409  
PRIOR FILING DATE: 2001-05-11  
PRIOR APPLICATION NUMBER: 08/988,321  
PRIOR FILING DATE: 1997-12-10  
PRIOR APPLICATION NUMBER: 08/650,093  
PRIOR FILING DATE: 1996-05-17  
PRIOR APPLICATION NUMBER: 08/452,841  
PRIOR FILING DATE: 1995-05-30  
PRIOR APPLICATION NUMBER: 08/397,330  
PRIOR FILING DATE: 1995-03-09  
PRIOR APPLICATION NUMBER: 07/945,289  
PRIOR FILING DATE: 1992-09-10  
PRIOR APPLICATION NUMBER: 09/690,936  
PRIOR FILING DATE: 2000-10-18  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn Ver. 2.1.  
SEQ ID NO 37  
LENGTH: 685  
TYPE: RNA  
ORGANISM: Hepatitis C virus  
US-10-457-304-37

Query Match 100.0%; Score 20; DB 17; Length 685;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
DB 274 TTGGGACCCCAACTACTC 255

RESULT 159  
US-10-454-293-37/c  
Sequence 37, Application US/10454293  
Publication No. US20040049021A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Kevin P.  
APPLICANT: Hanecak, Ronnie C.  
APPLICANT: No. US20040049021A1aki, Chikateru  
APPLICANT: Dort, F. Andrew  
APPLICANT: Kwoh, T. Jesse  
TITLE OF INVENTION: Compositions and Methods for Treatment of Hepatitis C  
FILE REFERENCE: ISPH-0743  
CURRENT APPLICATION NUMBER: US/10/454,293  
CURRENT FILING DATE: 2003-06-04  
PRIOR APPLICATION NUMBER: 09/853,409  
PRIOR FILING DATE: 2001-05-11  
PRIOR APPLICATION NUMBER: 08/988,321  
PRIOR FILING DATE: 1997-12-10  
PRIOR APPLICATION NUMBER: 08/650,093  
PRIOR FILING DATE: 1996-05-17  
PRIOR APPLICATION NUMBER: 08/452,841  
PRIOR FILING DATE: 1995-05-30  
PRIOR APPLICATION NUMBER: 08/397,330  
PRIOR FILING DATE: 1995-03-09  
PRIOR APPLICATION NUMBER: 07/945,289  
PRIOR FILING DATE: 1992-09-10  
PRIOR APPLICATION NUMBER: 09/690,936  
PRIOR FILING DATE: 2000-10-18  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn Ver. 2.1.  
SEQ ID NO 37

LENGTH: 685  
TYPE: RNA  
ORGANISM: Hepatitis C virus  
US-10-454-293-37

Query Match 100.0%; Score 20; DB 17; Length 685;  
Best Local Similarity 100.0%; Pred. No. 0.013;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
DB 274 TTGGGACCCCAACTACTC 255

RESULT 160  
US-10-066-130-20  
Sequence 20, Application US/10066130  
Publication No. US20030175663A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase  
FILE REFERENCE: PH-7171 NP  
CURRENT APPLICATION NUMBER: US/10/066,130  
CURRENT FILING DATE: 2002-01-31  
PRIOR APPLICATION NUMBER: US 60/265,437  
PRIOR FILING DATE: 2001-01-31  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 20  
LENGTH: 2327  
TYPE: DNA  
ORGANISM: viral  
US-10-066-130-20

Query Match 100.0%; Score 20; DB 16; Length 2327;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
DB 2053 TTGGGACCCCAACTACTC 2072

RESULT 161  
US-10-734-801-20  
Sequence 20, Application US/10734801  
Publication No. US20040126388A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase  
FILE REFERENCE: PH-7171-DIV  
CURRENT APPLICATION NUMBER: US/10/734,801  
CURRENT FILING DATE: 2003-12-12  
PRIOR APPLICATION NUMBER: US 60/265,437  
PRIOR FILING DATE: 2001-01-31  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 20  
LENGTH: 2327  
TYPE: DNA  
ORGANISM: viral  
US-10-734-801-20

Query Match 100.0%; Score 20; DB 18; Length 2327;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTGGGACCCCAACTACTC 20  
DB 2053 TTGGGACCCCAACTACTC 2072

```
RESULT 162
; US-10-066-130-19
; Sequence 19, Application US/10066130
; Publication No. US20030175683A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase
; FILE REFERENCE: PH-7171 NP
; CURRENT APPLICATION NUMBER: US/10/066,130
; CURRENT FILING DATE: 2002-01-31
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: viral
; US-10-066-130-19

Query Match          100.0%; Score 20; DB 16; Length 2674;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGAGCCCAACTACTC 20
Db 2400 TTGGGAGCCCAACTACTC 2419

RESULT 163
; US-10-734-801-19
; Sequence 19, Application US/10734801
; Publication No. US20040126388A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase
; FILE REFERENCE: PH-7171-DIV
; CURRENT APPLICATION NUMBER: US/10/734,801
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 60/265,437
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: viral
; US-10-734-801-19

Query Match          100.0%; Score 20; DB 18; Length 2674;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGAGCCCAACTACTC 20
Db 2400 TTGGGAGCCCAACTACTC 2419

RESULT 164
; US-10-066-130-18
; Sequence 18, Application US/10066130
; Publication No. US20030175683A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase
; FILE REFERENCE: PH-7171 NP
; CURRENT APPLICATION NUMBER: US/10/066,130
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/265,437
```

```
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 2771
; TYPE: DNA
; ORGANISM: viral
; US-10-066-130-18

Query Match          100.0%; Score 20; DB 16; Length 2771;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGAGCCCAACTACTC 20
Db 2400 TTGGGAGCCCAACTACTC 2419

RESULT 165
; US-10-734-801-18
; Sequence 18, Application US/10734801
; Publication No. US20040126388A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase
; FILE REFERENCE: PH-7171-DIV
; CURRENT APPLICATION NUMBER: US/10/734,801
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 60/265,437
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 2771
; TYPE: DNA
; ORGANISM: viral
; US-10-734-801-18

Query Match          100.0%; Score 20; DB 18; Length 2771;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGAGCCCAACTACTC 20
Db 2400 TTGGGAGCCCAACTACTC 2419

RESULT 166
; US-10-066-130-17
; Sequence 17, Application US/10066130
; Publication No. US20030175683A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase
; FILE REFERENCE: PH-7171 NP
; CURRENT APPLICATION NUMBER: US/10/066,130
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/265,437
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 5860
; TYPE: DNA
; ORGANISM: viral
; US-10-066-130-17

Query Match          100.0%; Score 20; DB 16; Length 5860;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```
Oy      1 TTGGGACCCCAACTACTC 20
|||
Db      2400 TTGGGACCCCAACTACTC 2419

RESULT 167
US-10-734-801-17
; Sequence 17, Application US/10734801
; Publication No. US20040126388A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: In Vitro System for Replication of RNA-Dependent RNA Polymerase
; FILE REFERENCE: PH-7171-DIV
; CURRENT FILING DATE: 2003-12-12
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 5860
; TYPE: DNA
; ORGANISM: Viral
US-10-734-801-17

Query Match      100.0%; Score 20; DB 18; Length 5860;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 TTGGGACCCCAACTACTC 20
|||
Db      2400 TTGGGACCCCAACTACTC 2419

RESULT 168
US-10-434-842-16/c
; Sequence 16, Application US/10434842
; Publication No. US20040005549A1
; GENERAL INFORMATION:
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE
; FILE REFERENCE: 0342/1H395US3
; CURRENT APPLICATION NUMBER: US/10/434,842
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 10/233,307
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/005,469
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FCA4 Replicon Sequence
US-10-434-842-16

Query Match      100.0%; Score 20; DB 17; Length 7989;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 TTGGGACCCCAACTACTC 20
|||
Db      275 TTGGGACCCCAACTACTC 256

RESULT 169
US-10-639-150-1/c
; Sequence 1, Application US/10639150
```

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```
; Publication No. US20040121975A1
; GENERAL INFORMATION:
; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
; TITLE OF INVENTION: HEPATITIS C VIRUS ASSAYS
; FILE REFERENCE: D0224 NP
; CURRENT APPLICATION NUMBER: US/10/639,150
; CURRENT FILING DATE: 2003-08-12
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: HCV Replicon
US-10-639-150-1

Query Match      100.0%; Score 20; DB 18; Length 7989;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 TTGGGACCCCAACTACTC 20
|||
Db      275 TTGGGACCCCAACTACTC 256

RESULT 170
US-10-897-648-17/c
; Sequence 17, Application US/10897648
; Publication No. US20050043266A1
; GENERAL INFORMATION:
; APPLICANT: Jayasena, Sumedha
; TITLE OF INVENTION: SHORT INTERFERING RNA AS AN ANTIVIRAL AGENT FOR HEPATITIS C
; FILE REFERENCE: A-835
; CURRENT APPLICATION NUMBER: US/10/897,648
; CURRENT FILING DATE: 2004-07-22
; PRIOR APPLICATION NUMBER: 60/490,204
; PRIOR FILING DATE: 2003-07-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 7989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-897-648-17

Query Match      100.0%; Score 20; DB 19; Length 7989;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 TTGGGACCCCAACTACTC 20
|||
Db      275 TTGGGACCCCAACTACTC 256

RESULT 171
US-10-005-469-1/c
; Sequence 1, Application US/10005469
; Publication No. US20020155133A1
; GENERAL INFORMATION:
; APPLICANT: AMADYS Pharmaceuticals, Inc.
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY R
; FILE REFERENCE: 0342/1H395US1
; CURRENT APPLICATION NUMBER: US/10/005,469
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
```

SEQ ID NO 1  
LENGTH: 7992  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HCV replicon I377/NS3-3'UTR  
US-10-005-469-1

Query Match 100.0%; Score 20; DB 13; Length 7992;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
|||||  
DB 275 TTCCGACCCCAACTACTC 256

RESULT 172  
US-10-005-469-2/c  
Sequence 2, Application US/10005469  
Publication No. US20020155133A1  
GENERAL INFORMATION:  
APPLICANT: ANADYS Pharmaceuticals, Inc.  
APPLICANT: Bichko, Vadim  
TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE  
FILE REFERENCE: 0342/1H395US1  
CURRENT APPLICATION NUMBER: US/10/005,469  
CURRENT FILING DATE: 2002-04-18  
PRIOR APPLICATION NUMBER: US 60/245,866  
PRIOR FILING DATE: 2000-11-07  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 7992  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HCV Replicon RNA from cell line HCVR2  
US-10-005-469-2

Query Match 100.0%; Score 20; DB 13; Length 7992;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
|||||  
DB 275 TTCCGACCCCAACTACTC 256

RESULT 173  
US-10-005-469-4/c  
Sequence 4, Application US/10005469  
Publication No. US20020155133A1  
GENERAL INFORMATION:  
APPLICANT: ANADYS Pharmaceuticals, Inc.  
APPLICANT: Bichko, Vadim  
TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE  
FILE REFERENCE: 0342/1H395US1  
CURRENT APPLICATION NUMBER: US/10/005,469  
CURRENT FILING DATE: 2002-04-18  
PRIOR APPLICATION NUMBER: US 60/245,866  
PRIOR FILING DATE: 2000-11-07  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 7992  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HCV Replicon RNA from cell line HCVR9  
US-10-005-469-4

Query Match 100.0%; Score 20; DB 13; Length 7992;

Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
|||||  
DB 275 TTCCGACCCCAACTACTC 256

RESULT 174  
US-10-005-469-5/c  
Sequence 5, Application US/10005469  
Publication No. US20020155133A1  
GENERAL INFORMATION:  
APPLICANT: ANADYS Pharmaceuticals, Inc.  
APPLICANT: Bichko, Vadim  
TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE  
FILE REFERENCE: 0342/1H395US1  
CURRENT APPLICATION NUMBER: US/10/005,469  
CURRENT FILING DATE: 2002-04-18  
PRIOR APPLICATION NUMBER: US 60/245,866  
PRIOR FILING DATE: 2000-11-07  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 7992  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HCV Replicon from cell line HCVR24  
US-10-005-469-5

Query Match 100.0%; Score 20; DB 13; Length 7992;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
|||||  
DB 275 TTCCGACCCCAACTACTC 256

RESULT 175  
US-10-005-469-6/c  
Sequence 6, Application US/10005469  
Publication No. US20020155133A1  
GENERAL INFORMATION:  
APPLICANT: ANADYS Pharmaceuticals, Inc.  
APPLICANT: Bichko, Vadim  
TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE  
FILE REFERENCE: 0342/1H395US1  
CURRENT APPLICATION NUMBER: US/10/005,469  
CURRENT FILING DATE: 2002-04-18  
PRIOR APPLICATION NUMBER: US 60/245,866  
PRIOR FILING DATE: 2000-11-07  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 7992  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HCV Replicon from cell line HCVR24  
US-10-005-469-6

Query Match 100.0%; Score 20; DB 13; Length 7992;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCCGACCCCAACTACTC 20  
|||||  
DB 275 TTCCGACCCCAACTACTC 256

RESULT 176

```
US-10-434-842-1/c
; Sequence 1, Application US/10434842
; Publication No. US20040005549A1
; GENERAL INFORMATION:
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY REF
; FILE REFERENCE: 0342/1H395US3
; CURRENT APPLICATION NUMBER: US/10/434,842
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 10/233,307
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/005,469
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 7992
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV1b-based chimeric replicon
US-10-434-842-1
Query Match      100.0%; Score 20; DB 17; Length 7992;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTCCGGACCCCAACTACTC 20
DB      275 TTCCGGACCCCAACTACTC 256

RESULT 177
US-10-434-842-2/c
; Sequence 2, Application US/10434842
; Publication No. US20040005549A1
; GENERAL INFORMATION:
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY REF
; FILE REFERENCE: 0342/1H395US3
; CURRENT APPLICATION NUMBER: US/10/434,842
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 10/233,307
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/005,469
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 7992
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCV2 subgenomic HCV replicon
US-10-434-842-2
Query Match      100.0%; Score 20; DB 17; Length 7992;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTCCGGACCCCAACTACTC 20
DB      275 TTCCGGACCCCAACTACTC 256

RESULT 178
US-10-434-842-4/c
; Sequence 4, Application US/10434842
; Publication No. US20040005549A1
; GENERAL INFORMATION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY REF
```

```
; GENERAL INFORMATION:
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY R
; FILE REFERENCE: 0342/1H395US3
; CURRENT APPLICATION NUMBER: US/10/434,842
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 10/233,307
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/005,469
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 7992
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCVR9 subgenomic HCV replicon
US-10-434-842-4
Query Match      100.0%; Score 20; DB 17; Length 7992;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTCCGGACCCCAACTACTC 20
DB      275 TTCCGGACCCCAACTACTC 256

RESULT 179
US-10-434-842-5/c
; Sequence 5, Application US/10434842
; Publication No. US20040005549A1
; GENERAL INFORMATION:
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY R
; FILE REFERENCE: 0342/1H395US3
; CURRENT APPLICATION NUMBER: US/10/434,842
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 10/233,307
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 10/005,469
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/245,866
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 7992
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HCVR2 subgenomic HCV replicon
US-10-434-842-5
Query Match      100.0%; Score 20; DB 17; Length 7992;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TTCCGGACCCCAACTACTC 20
DB      275 TTCCGGACCCCAACTACTC 256

RESULT 180
US-10-434-842-6/c
; Sequence 6, Application US/10434842
; Publication No. US20040005549A1
; GENERAL INFORMATION:
; APPLICANT: Bichko, Vadim
; TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY R
```

FILE REFERENCE: 0342/1H395US3  
CURRENT APPLICATION NUMBER: US/10/434,842  
CURRENT FILING DATE: 2003-05-09  
PRIOR APPLICATION NUMBER: US 10/233,307  
PRIOR FILING DATE: 2002-08-28  
PRIOR APPLICATION NUMBER: US 10/005,469  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: US 60/245,866  
PRIOR FILING DATE: 2000-11-07  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 7992  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HCV R24 subgenomic HCV replicon  
US-10-434-842-6

Query Match 100.0%; Score 20; DB 17; Length 7992;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 275 TTCCGACCCCAACTACTC 256

RESULT 181  
US-10-434-842-15/c  
Sequence 15, Application US/10434842  
Publication No. US20040005549A1  
GENERAL INFORMATION:  
APPLICANT: Bichko, Vadim  
TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE  
FILE REFERENCE: 0342/1H395US3  
CURRENT APPLICATION NUMBER: US/10/434,842  
CURRENT FILING DATE: 2003-05-09  
PRIOR APPLICATION NUMBER: US 10/233,307  
PRIOR FILING DATE: 2002-08-28  
PRIOR APPLICATION NUMBER: US 10/005,469  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: US 60/245,866  
PRIOR FILING DATE: 2000-11-07  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 15  
LENGTH: 7992  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: FCAL Replicon Sequence  
US-10-434-842-15

Query Match 100.0%; Score 20; DB 17; Length 7992;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 275 TTCCGACCCCAACTACTC 256

RESULT 182  
US-10-434-842-17/c  
Sequence 17, Application US/10434842  
Publication No. US20040005549A1  
GENERAL INFORMATION:  
APPLICANT: Bichko, Vadim  
TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE  
FILE REFERENCE: 0342/1H395US3  
CURRENT APPLICATION NUMBER: US/10/434,842  
CURRENT FILING DATE: 2003-05-09

PRIOR APPLICATION NUMBER: US 10/233,307  
PRIOR FILING DATE: 2002-08-28  
PRIOR APPLICATION NUMBER: US 10/005,469  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: US 60/245,866  
PRIOR FILING DATE: 2000-11-07  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 17  
LENGTH: 7992  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: FCA22 Replicon Sequence  
US-10-434-842-17

Query Match 100.0%; Score 20; DB 17; Length 7992;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 275 TTCCGACCCCAACTACTC 256

RESULT 183  
US-10-005-469-3/c  
Sequence 3, Application US/10005469  
Publication No. US2002015513A1  
GENERAL INFORMATION:  
APPLICANT: ANADYS Pharmaceuticals, Inc.  
TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY R  
FILE REFERENCE: 0342/1H395US1  
CURRENT APPLICATION NUMBER: US/10/005,469  
CURRENT FILING DATE: 2002-04-18  
PRIOR APPLICATION NUMBER: US 60/245,866  
PRIOR FILING DATE: 2000-11-07  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 7995  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HCV Replicon RNA from cell line HCV R  
US-10-005-469-3

Query Match 100.0%; Score 20; DB 13; Length 7995;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTCCGACCCCAACTACTC 20  
|||||  
Db 275 TTCCGACCCCAACTACTC 256

RESULT 184  
US-10-434-842-3/c  
Sequence 3, Application US/10434842  
Publication No. US20040005549A1  
GENERAL INFORMATION:  
APPLICANT: Bichko, Vadim  
TITLE OF INVENTION: HEPATITIS C VIRUS CONSTRUCTS CHARACTERIZED BY HIGH EFFICIENCY RE  
FILE REFERENCE: 0342/1H395US3  
CURRENT APPLICATION NUMBER: US/10/434,842  
CURRENT FILING DATE: 2003-05-09  
PRIOR APPLICATION NUMBER: US 10/233,307  
PRIOR FILING DATE: 2002-08-28  
PRIOR APPLICATION NUMBER: US 10/005,469  
PRIOR FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: US 60/245,866  
PRIOR FILING DATE: 2000-11-07

NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 3  
LENGTH: 7995  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HCVr8 subgenomic HCV replicon  
US-10-434-842-3

Query Match 100.0%; Score 20; DB 17; Length 7995;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 275 TTGGGACCCCAACTACTC 256

## RESULT 185

US-10-475-989-3/c  
Sequence 3, Application US/10475989  
Publication No. US20040142320A1  
GENERAL INFORMATION:  
APPLICANT: CNRS  
TITLE OF INVENTION: PROCESS FOR THE REPLICATION OF THE HEPATITIS C VIRUS  
FILE REFERENCE: MOB 01 AA CNR GENO  
CURRENT APPLICATION NUMBER: US/10/475,989  
CURRENT FILING DATE: 2003-10-27  
PRIOR APPLICATION NUMBER: FR 01/05732  
PRIOR FILING DATE: 2001-04-27  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 3  
LENGTH: 8451  
TYPE: DNA  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: replicon obtained by fusion of a hygromycin B  
OTHER INFORMATION: resistance gene with sequence SEQ ID NO: 1  
US-10-475-989-3

Query Match 100.0%; Score 20; DB 18; Length 8451;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 275 TTGGGACCCCAACTACTC 256

## RESULT 186

US-10-029-907-6/c  
Sequence 6, Application US/10029907  
Publication No. US20020142350A1  
GENERAL INFORMATION:  
APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
FILE REFERENCE: 13/083  
CURRENT APPLICATION NUMBER: US/10/029,907  
CURRENT FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 60/257,857  
PRIOR FILING DATE: 2000-12-22  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 8638  
TYPE: DNA  
ORGANISM: HCV  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1802)...(8407)

Qy 1 TTGGGACCCCAACTACTC 20  
Db 275 TTGGGACCCCAACTACTC 256

US-10-029-907-6

Query Match 100.0%; Score 20; DB 13; Length 8638;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 275 TTGGGACCCCAACTACTC 256

## RESULT 187

US-10-029-907-7/c  
Sequence 7, Application US/10029907  
Publication No. US20020142350A1  
GENERAL INFORMATION:  
APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
FILE REFERENCE: 13/083  
CURRENT APPLICATION NUMBER: US/10/029,907  
CURRENT FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 60/257,857  
PRIOR FILING DATE: 2000-12-22  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 8638  
TYPE: DNA  
ORGANISM: HCV  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1802)...(8407)  
US-10-029-907-7

Query Match 100.0%; Score 20; DB 13; Length 8638;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20  
Db 275 TTGGGACCCCAACTACTC 256

## RESULT 188

US-10-029-907-24/c  
Sequence 24, Application US/10029907  
Publication No. US20020142350A1  
GENERAL INFORMATION:  
APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
FILE REFERENCE: 13/083  
CURRENT APPLICATION NUMBER: US/10/029,907  
CURRENT FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 60/257,857  
PRIOR FILING DATE: 2000-12-22  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 24  
LENGTH: 8638  
TYPE: DNA  
ORGANISM: HCV  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1802)...(8407)  
US-10-029-907-24

Query Match 100.0%; Score 20; DB 13; Length 8638;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGGACCCCAACTACTC 20

Db 275 TTGCGACCCCAACTACTC 256

RESULT 189  
US-10-029-907-25/c  
; Sequence 25, Application US/10029907  
; Publication No. US20020142350A1  
; GENERAL INFORMATION:  
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
; FILE REFERENCE: 13/083  
; CURRENT APPLICATION NUMBER: US/10/029,907  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,857  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 8638  
; TYPE: DNA  
; ORGANISM: HCV  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1802)...(8407)  
US-10-029-907-25

Query Match 100.0%; Score 20; DB 13; Length 8638;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCAACTACTC 20  
Db 275 TTGCGACCCCAACTACTC 256

RESULT 190  
US-10-309-561-6/c  
; Sequence 6, Application US/10309561  
; Publication No. US20030148348A1  
; GENERAL INFORMATION:  
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
; FILE REFERENCE: 13/083  
; CURRENT APPLICATION NUMBER: US/10/309,561  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: US/10/029,907  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,857  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 8638  
; TYPE: DNA  
; ORGANISM: HCV  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1802)...(8407)  
US-10-309-561-6

Query Match 100.0%; Score 20; DB 15; Length 8638;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCAACTACTC 20  
Db 275 TTGCGACCCCAACTACTC 256

RESULT 191

US-10-309-561-7/c  
; Sequence 7, Application US/10309561  
; Publication No. US20030148348A1  
; GENERAL INFORMATION:  
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
; FILE REFERENCE: 13/083  
; CURRENT APPLICATION NUMBER: US/10/309,561  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: US/10/029,907  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,857  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 8638  
; TYPE: DNA  
; ORGANISM: HCV  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1802)...(8407)  
US-10-309-561-7

Query Match 100.0%; Score 20; DB 15; Length 8638;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCAACTACTC 20  
Db 275 TTGCGACCCCAACTACTC 256

RESULT 192  
US-10-309-561-24/c  
; Sequence 24, Application US/10309561  
; Publication No. US20030148348A1  
; GENERAL INFORMATION:  
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.  
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM  
; FILE REFERENCE: 13/083  
; CURRENT APPLICATION NUMBER: US/10/309,561  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: US/10/029,907  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/257,857  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 8638  
; TYPE: DNA  
; ORGANISM: HCV  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1802)...(8407)  
US-10-309-561-24

Query Match 100.0%; Score 20; DB 15; Length 8638;  
Best Local Similarity 100.0%; Pred. No. 0.011;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGCGACCCCAACTACTC 20  
Db 275 TTGCGACCCCAACTACTC 256

RESULT 193  
US-10-309-561-25/c  
; Sequence 25, Application US/10309561  
; Publication No. US20030148348A1

```

; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
;   TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/309,561
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US/10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-309-561-25

Query Match          100.0%; Score 20; DB 15; Length 8638;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 275 TTGGGACCCCAACTACTC 256

RESULT 194
US-10-789-355-6/c
; Sequence 6, Application US/10789355
; Publication No. US20040180333A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
;   TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/789,355
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-789-355-6

Query Match          100.0%; Score 20; DB 18; Length 8638;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 275 TTGGGACCCCAACTACTC 256

RESULT 195
US-10-789-355-7/c
; Sequence 7, Application US/10789355
; Publication No. US20040180333A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
```

```

;   TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/789,355
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-789-355-7

Query Match          100.0%; Score 20; DB 18; Length 8638;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 275 TTGGGACCCCAACTACTC 256

RESULT 196
US-10-789-355-24/c
; Sequence 24, Application US/10789355
; Publication No. US20040180333A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
;   TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/789,355
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-789-355-24

Query Match          100.0%; Score 20; DB 18; Length 8638;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGGGACCCCAACTACTC 20
DB 275 TTGGGACCCCAACTACTC 256

RESULT 197
US-10-789-355-25/c
; Sequence 25, Application US/10789355
; Publication No. US20040180333A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
;   TITLE OF INVENTION: HEPATITIS C VIRUS
; FILE REFERENCE: 13/083
; CURRENT APPLICATION NUMBER: US/10/789,355
```

```
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-686-835-25
```

```
Query Match      100.0%; Score 20; DB 18; Length 8638;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGGGAGCCCAACTACTC 20
        |||||
Db      275 TTGGGAGCCCAACTACTC 256
```

```
RESULT 198
US-10-686-835-6/c
; Sequence 6, Application US/10686835
; Publication No. US20040203020A1
; GENERAL INFORMATION:
; APPLICANT: Kukulj, George and Pause, Armin
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083-2-C1
; CURRENT APPLICATION NUMBER: US/10/686,835
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US 10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-686-835-6
```

```
Query Match      100.0%; Score 20; DB 18; Length 8638;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGGGAGCCCAACTACTC 20
        |||||
Db      275 TTGGGAGCCCAACTACTC 256
```

```
RESULT 199
US-10-686-835-7/c
; Sequence 7, Application US/10686835
; Publication No. US20040203020A1
; GENERAL INFORMATION:
; APPLICANT: Kukulj, George and Pause, Armin
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083-2-C1
; CURRENT APPLICATION NUMBER: US/10/686,835
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US 10/029,907
; PRIOR FILING DATE: 2001-12-21
```

```
; PRIOR APPLICATION NUMBER: US 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-686-835-7
```

```
Query Match      100.0%; Score 20; DB 18; Length 8638;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGGGAGCCCAACTACTC 20
        |||||
Db      275 TTGGGAGCCCAACTACTC 256
```

```
RESULT 200
US-10-686-835-24/c
; Sequence 24, Application US/10686835
; Publication No. US20040203020A1
; GENERAL INFORMATION:
; APPLICANT: Kukulj, George and Pause, Armin
; TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
; FILE REFERENCE: 13/083-2-C1
; CURRENT APPLICATION NUMBER: US/10/686,835
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US 10/029,907
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/257,857
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 8638
; TYPE: DNA
; ORGANISM: HCV
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1802)...(8407)
US-10-686-835-24
```

```
Query Match      100.0%; Score 20; DB 18; Length 8638;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TTGGGAGCCCAACTACTC 20
        |||||
Db      275 TTGGGAGCCCAACTACTC 256
```

```
Search completed: April 25, 2005, 16:27:21
Job time : 300.526 secs
```



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 25, 2005, 13:09:42 ; Search time 779.211 Seconds  
(without alignments)  
1119.330 Million cell updates/sec

Title: US-08-887-505B-38

Perfect score: 18

Sequence: 1 GGGGUCCTCGAGANNNNNN 18

Scoring table: OLIGO NUC

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:\*  
1: gb\_ha:\*  
2: gb\_hgt:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	6 AX803675	AX803675 Sequence
2	18	100.0	24	6 AX803704	AX803704 Sequence
3	16	88.9	65130	2 AC026845	AC026845 Homo sapi
4	16	88.9	132013	2 CR354556	CR354556 Homo sapi
5	16	88.9	132597	2 AC074014	AC074014 Homo sapi
6	16	88.9	155605	2 BX927307	BX927307 Homo sapi
7	16	88.9	162408	2 CR752651	CR752651 Homo sapi
8	16	88.9	166622	2 CR774197	CR774197 Homo sapi
9	16	88.9	172578	2 CR812468	CR812468 Homo sapi
10	16	88.9	177849	2 BX927353	BX927353 Homo sapi
11	16	88.9	178025	2 CR752654	CR752654 Homo sapi
12	16	88.9	184628	2 AC133391	AC133391 Homo sapi
13	16	88.9	189909	2 CR735108	CR735108 Homo sapi
14	16	88.9	198047	2 CR376763	CR376763 Homo sapi
15	16	88.9	213402	2 BX901895	BX901895 Homo sapi
16	16	88.9	215185	2 BX927073	BX927073 Homo sapi
17	16	88.9	221924	2 CR388047	CR388047 Homo sapi
18	16	88.9	222876	2 AC068379	AC068379 Homo sapi
19	16	88.9	228022	2 BX927188	BX927188 Homo sapi

20	C	88.9	256581	2	CR394526	CR394526 Danio rer
21	16	83.3	29	6	AX528761	AX528761 Sequence
22	C	83.3	29	6	AX528762	AX528762 Sequence
23	15	83.3	62373	2	AC129972	AC129972 Felis cat
24	15	83.3	72483	2	AC101265	AC101265 Mus muscu
25	15	83.3	84720	2	AC115635	AC115635 Mus muscu
26	15	83.3	110000	2	AC097780	AC097780 Rattus no
27	15	83.3	150670	2	AC143037	AC143037 Macaca mu
28	C	83.3	151787	2	AC105679	AC105679 Rattus no
29	15	83.3	211680	2	CR385082	CR385082 Danio rer
30	15	83.3	222685	2	AC130029	AC130029 Rattus no
31	15	83.3	235173	2	AC112325	AC112325 Rattus no
32	14	77.8	27	6	AX037200	AX037200 Sequence
33	14	77.8	27	6	AX037201	AX037201 Sequence
34	14	77.8	27	6	AX037202	AX037202 Sequence
35	14	77.8	27	6	AX037203	AX037203 Sequence
36	14	77.8	27	6	AX037204	AX037204 Sequence
37	14	77.8	27	6	AX037205	AX037205 Sequence
38	14	77.8	27	6	AX037206	AX037206 Sequence
39	14	77.8	27	6	AX037207	AX037207 Sequence
40	14	77.8	27	6	AX037208	AX037208 Sequence
41	14	77.8	27	6	AX037209	AX037209 Sequence
42	14	77.8	27	6	AX037210	AX037210 Sequence
43	14	77.8	27	6	AX037211	AX037211 Sequence
44	14	77.8	27	6	AX037212	AX037212 Sequence
45	14	77.8	27	6	AX037213	AX037213 Sequence
46	14	77.8	27	6	AX037214	AX037214 Sequence
47	14	77.8	27	6	AX037215	AX037215 Sequence
48	14	77.8	49799	2	AC100909	AC100909 Mus muscu
49	14	77.8	55662	2	AC100333	AC100333 Mus muscu
50	14	77.8	59918	2	AC100339	AC100339 Mus muscu
51	14	77.8	62676	2	AC125441	AC125441 Mus muscu
52	14	77.8	64345	2	AC062003	AC062003 Homo sapi
53	14	77.8	65174	2	AC025214	AC025214 Homo sapi
54	14	77.8	66795	2	AC100485	AC100485 Mus muscu
55	14	77.8	67822	2	AC027792	AC027792 Homo sapi
56	14	77.8	73882	2	AC102023	AC102023 Mus muscu
57	14	77.8	81233	2	AC021390	AC021390 Homo sapi
58	14	77.8	83547	2	AC022890	AC022890 Homo sapi
59	14	77.8	85440	2	AC034264	AC034264 Mus muscu
60	14	77.8	88940	2	AC138602	AC138602 Mus muscu
61	14	77.8	110000	2	AC095920	AC095920 03
62	14	77.8	110000	2	AC096315	AC096315 3
63	14	77.8	110000	2	AC112872	AC112872 0
64	14	77.8	133614	2	AC025433	AC025433 Homo sapi
65	14	77.8	150695	2	AC023576	AC023576 Homo sapi
66	14	77.8	151097	2	AC142149	AC142149 Rattus no
67	14	77.8	151448	2	AC074261	AC074261 Homo sapi
68	14	77.8	152420	2	BX927200	BX927200 Danio rer
69	14	77.8	154474	2	AC117546	AC117546 Mus muscu
70	14	77.8	154696	2	AC025626	AC025626 Homo sapi
71	14	77.8	158981	2	AC144021	AC144021 Macaca mu
72	14	77.8	159732	2	AC027535	AC027535 Rattus no
73	14	77.8	161829	2	AC027535	AC027535 Homo sapi
74	14	77.8	163732	2	BX908804	BX908804 Danio rer
75	14	77.8	173423	2	AC026082	AC026082 Homo sapi
76	14	77.8	173705	2	CR335046	CR335046 Danio rer
77	14	77.8	175056	2	AP002368	AP002368 Homo sapi
78	14	77.8	176565	2	AC144311	AC144311 Macaca mu
79	14	77.8	177380	2	AC151062	AC151062 Bos tauru
80	14	77.8	178472	2	AC125597	AC125597 Rattus no
81	14	77.8	180506	2	BX927248	BX927248 Danio rer
82	14	77.8	184869	2	AC015622	AC015622 Homo sapi
83	14	77.8	184748	2	BX927379	BX927379 Danio rer
84	14	77.8	188931	2	AC113158	AC113158 Mus muscu
85	14	77.8	189756	2	CR356244	CR356244 Danio rer
86	14	77.8	189787	2	CR293534	CR293534 Homo sapi
87	14	77.8	191502	2	AC068920	AC068920 Homo sapi
88	14	77.8	194513	2	CR524482	CR524482 Danio rer
89	14	77.8	202456	2	AC150020	AC150020 Papio anu
90	14	77.8	210310	2	CR749177	CR749177 Danio rer
91	14	77.8	210481	2	CR376743	CR376743 Danio rer
92	14	77.8	213181	2	AC122949	AC122949 Rattus no

93	14	77.8	215479	2	AC125694	Rattus no	AC125694	Rattus no	166	13	72.2	71396	2	AC100674	Mus muscu	AC100674	Mus muscu	166	13	72.2	71396	2	AC100674	Mus muscu	AC100674	Mus muscu
94	14	77.8	215604	2	CR376804	Danio rer	CR376804	Danio rer	167	13	72.2	72369	2	AC026581	Homo sapi	AC026581	Homo sapi	167	13	72.2	72369	2	AC026581	Homo sapi	AC026581	Homo sapi
95	14	77.8	216013	2	BX927238	Danio rer	BX927238	Danio rer	168	13	72.2	73173	2	AC025146	Homo sapi	AC025146	Homo sapi	168	13	72.2	73173	2	AC025146	Homo sapi	AC025146	Homo sapi
96	14	77.8	217309	2	BX901905	Danio rer	BX901905	Danio rer	169	13	72.2	75974	2	AC090991	Homo sapi	AC090991	Homo sapi	169	13	72.2	75974	2	AC090991	Homo sapi	AC090991	Homo sapi
97	14	77.8	222632	2	AC106115	Rattus no	AC106115	Rattus no	170	13	72.2	76113	2	AC023453	Homo sapi	AC023453	Homo sapi	170	13	72.2	76113	2	AC023453	Homo sapi	AC023453	Homo sapi
98	14	77.8	223961	2	CR382363	Danio rer	CR382363	Danio rer	171	13	72.2	76856	2	AC021526	Homo sapi	AC021526	Homo sapi	171	13	72.2	76856	2	AC021526	Homo sapi	AC021526	Homo sapi
99	14	77.8	224370	2	AC097049	Rattus no	AC097049	Rattus no	172	13	72.2	76856	2	AC015735	Homo sapi	AC015735	Homo sapi	172	13	72.2	76856	2	AC015735	Homo sapi	AC015735	Homo sapi
100	14	77.8	228022	2	BX927188	Danio rer	BX927188	Danio rer	173	13	72.2	87463	2	AC140498	Homo sapi	AC140498	Homo sapi	173	13	72.2	87463	2	AC140498	Homo sapi	AC140498	Homo sapi
101	14	77.8	232460	2	AC107590	Rattus no	AC107590	Rattus no	174	13	72.2	90108	2	AC021611	Homo sapi	AC021611	Homo sapi	174	13	72.2	90108	2	AC021611	Homo sapi	AC021611	Homo sapi
102	14	77.8	239166	2	BX950179	Danio rer	BX950179	Danio rer	175	13	72.2	92726	6	AC695818	Sequence	AC695818	Sequence	175	13	72.2	92726	6	AC695818	Sequence	AC695818	Sequence
103	14	77.8	241934	2	AC110826	Rattus no	AC110826	Rattus no	176	13	72.2	99591	2	AC013392	Homo sapi	AC013392	Homo sapi	176	13	72.2	99591	2	AC013392	Homo sapi	AC013392	Homo sapi
104	14	77.8	243490	2	AC131536	Rattus no	AC131536	Rattus no	177	13	72.2	99630	2	AC142060	Rattus no	AC142060	Rattus no	177	13	72.2	99630	2	AC142060	Rattus no	AC142060	Rattus no
105	14	77.8	245358	2	AC112977	Rattus no	AC112977	Rattus no	178	13	72.2	110000	2	AC091367	Continuation (3 of	AC091367	Continuation (3 of	178	13	72.2	110000	2	AC091367	Continuation (3 of	AC091367	Continuation (3 of
106	14	77.8	247436	2	CR812481	Danio rer	CR812481	Danio rer	179	13	72.2	110000	2	AC107093	Continuation (2 of	AC107093	Continuation (2 of	179	13	72.2	110000	2	AC107093	Continuation (2 of	AC107093	Continuation (2 of
107	14	77.8	248358	2	AC122944	Rattus no	AC122944	Rattus no	180	13	72.2	110000	2	AC130665	Continuation (2 of	AC130665	Continuation (2 of	180	13	72.2	110000	2	AC130665	Continuation (2 of	AC130665	Continuation (2 of
108	14	77.8	250161	2	AC127927	Rattus no	AC127927	Rattus no	181	13	72.2	110000	2	AC145127	Continuation (2 of	AC145127	Continuation (2 of	181	13	72.2	110000	2	AC145127	Continuation (2 of	AC145127	Continuation (2 of
109	14	77.8	256409	2	AC111204	Rattus no	AC111204	Rattus no	182	13	72.2	110000	2	AC055726	Continuation (2 of	AC055726	Continuation (2 of	182	13	72.2	11000					

C 239	13	72.2 211251	2	AC121029	312	12	66.7	18	6	AX803689	AX803689 Sequence
240	13	72.2 212116	2	AC079973	313	12	66.7	18	6	AX803690	AX803690 Sequence
241	13	72.2 214434	2	AC125695	314	12	66.7	18	6	AX803691	AX803691 Sequence
242	13	72.2 214508	2	AC103532	C 315	12	66.7	20	6	A52659	A52659 Sequence 4
243	13	72.2 215373	2	AC128023	C 316	12	66.7	20	6	AR031224	AR031224 Sequence
C 244	13	72.2 216566	2	AC108254	C 317	12	66.7	20	6	AR145040	AR145040 Sequence
245	13	72.2 216915	2	AC125580	318	12	66.7	20	6	AR167022	AR167022 Sequence
246	13	72.2 220006	2	AC084068	319	12	66.7	20	6	AR167022	AR167022 Sequence
C 247	13	72.2 220103	2	AC073781	320	12	66.7	20	6	AR167023	AR167023 Sequence
248	13	72.2 226190	2	AC095562	321	12	66.7	20	6	AR167024	AR167024 Sequence
C 249	13	72.2 227164	2	AC103418	322	12	66.7	20	6	AR167024	AR167024 Sequence
250	13	72.2 229438	2	AC107408	323	12	66.7	20	6	E08298	E08298 Sequence
C 251	13	72.2 229604	2	AC130102	324	12	66.7	20	6	E08299	E08299 Sequence
C 252	13	72.2 230760	2	AC073714	325	12	66.7	20	6	E08300	E08300 Sequence
253	13	72.2 233796	2	AC130568	326	12	66.7	20	6	E08301	E08301 Sequence
254	13	72.2 234079	2	AC099074	327	12	66.7	20	6	E44258	E44258 Oligo-DNA s
C 255	13	72.2 235182	2	AC099082	328	12	66.7	20	6	E44259	E44259 Oligo-DNA s
C 256	13	72.2 235888	2	AC096391	329	12	66.7	20	6	E44260	E44260 Oligo-DNA s
257	13	72.2 237346	2	AC120688	330	12	66.7	20	6	AR210676	AR210676 Sequence
258	13	72.2 237855	2	AC136663	331	12	66.7	20	6	AR210677	AR210677 Sequence
259	13	72.2 238135	2	AC102968	332	12	66.7	20	6	AR210678	AR210678 Sequence
260	13	72.2 238976	2	AC106187	333	12	66.7	20	6	AR210679	AR210679 Sequence
261	13	72.2 240200	2	AC116206	C 334	12	66.7	20	6	AR210682	AR210682 Sequence
C 262	13	72.2 240783	2	AC025587	C 335	12	66.7	20	6	AR349613	AR349613 Sequence
263	13	72.2 241909	2	AC127399	C 336	12	66.7	20	6	AX555049	AX555049 Sequence
C 264	13	72.2 243122	2	AC134020	C 337	12	66.7	20	6	AX803656	AX803656 Sequence
C 265	13	72.2 243686	2	AC096430	338	12	66.7	20	6	AX803657	AX803657 Sequence
C 266	13	72.2 244105	2	AC098897	C 339	12	66.7	21	6	AX037298	AX037298 Sequence
C 267	13	72.2 246625	2	AC094293	C 340	12	66.7	21	6	AX037299	AX037299 Sequence
268	13	72.2 247141	2	AC129710	C 341	12	66.7	21	6	AX037300	AX037300 Sequence
C 269	13	72.2 247654	2	AC122658	C 342	12	66.7	21	6	AX037301	AX037301 Sequence
C 270	13	72.2 248880	2	AC111302	C 343	12	66.7	22	6	CQ827605	CQ827605 Sequence
271	13	72.2 249811	2	AC094988	C 344	12	66.7	22	6	KR349602	KR349602 Sequence
272	13	72.2 249967	2	AC128272	C 345	12	66.7	22	6	AX370745	AX370745 Sequence
C 273	13	72.2 250169	2	AC126583	C 346	12	66.7	22	6	AX556786	AX556786 Sequence
C 274	13	72.2 251856	2	AC146256	347	12	66.7	24	6	AR061891	AR061891 Sequence
C 275	13	72.2 253525	2	AC107349	348	12	66.7	24	6	AX803685	AX803685 Sequence
276	13	72.2 253746	2	AC135747	349	12	66.7	24	6	AX803692	AX803692 Sequence
C 277	13	72.2 254280	2	AC131372	350	12	66.7	24	6	AX803693	AX803693 Sequence
278	13	72.2 254839	2	AC103176	351	12	66.7	24	6	AX803694	AX803694 Sequence
279	13	72.2 255447	2	AC096032	352	12	66.7	24	6	AX803695	AX803695 Sequence
280	13	72.2 255598	2	AC107340	353	12	66.7	24	6	AX803696	AX803696 Sequence
C 281	13	72.2 256059	2	AC098893	354	12	66.7	24	6	AX803697	AX803697 Sequence
282	13	72.2 259921	2	AC114206	355	12	66.7	24	6	AX803698	AX803698 Sequence
283	13	72.2 264110	2	AC122626	356	12	66.7	24	6	AX803699	AX803699 Sequence
284	13	72.2 265566	2	AC123187	357	12	66.7	24	6	AX803700	AX803700 Sequence
C 285	13	72.2 266609	2	AC116237	358	12	66.7	24	6	AX803701	AX803701 Sequence
286	13	72.2 268694	2	AC095697	359	12	66.7	24	6	AX803702	AX803702 Sequence
287	13	72.2 270962	2	AC149067	360	12	66.7	24	6	AX803703	AX803703 Sequence
C 288	13	72.2 283789	2	AC110840	C 361	12	66.7	25	6	AR349603	AR349603 Sequence
289	13	72.2 292715	2	AC098382	C 362	12	66.7	25	6	AR349611	AR349611 Sequence
290	13	72.2 295057	2	AC106987	C 363	12	66.7	26	6	AR167081	AR167081 Sequence
291	13	72.2 336873	2	AC073666	364	12	66.7	26	6	BD135777	BD135777 Method of
292	13	72.2 346597	2	AC134498	C 365	12	66.7	26	6	E08297	E08297 s' noncodin
C 293	12	66.7 12	6	BD194958	C 366	12	66.7	26	6	AR210736	AR210736 Sequence
C 294	12	66.7 12	6	AR349607	367	12	66.7	27	6	AX037234	AX037234 Sequence
C 295	12	66.7 12	6	AX003945	368	12	66.7	27	6	AX037235	AX037235 Sequence
C 296	12	66.7 12	6	AX021569	369	12	66.7	27	6	AX037236	AX037236 Sequence
C 297	12	66.7 12	6	AX803684	370	12	66.7	27	6	AX037237	AX037237 Sequence
C 298	12	66.7 14	6	E08296	371	12	66.7	27	6	AX037238	AX037238 Sequence
C 299	12	66.7 14	6	AR210735	372	12	66.7	27	6	AX037239	AX037239 Sequence
300	12	66.7 16	6	AR234385	373	12	66.7	27	6	AX037240	AX037240 Sequence
301	12	66.7 18	6	AX803676	374	12	66.7	27	6	AX037241	AX037241 Sequence
302	12	66.7 18	6	AX803677	375	12	66.7	27	6	AX037242	AX037242 Sequence
303	12	66.7 18	6	AX803678	376	12	66.7	27	6	AX037243	AX037243 Sequence
304	12	66.7 18	6	AX803679	377	12	66.7	27	6	AX037244	AX037244 Sequence
305	12	66.7 18	6	AX803680	378	12	66.7	27	6	AX037245	AX037245 Sequence
306	12	66.7 18	6	AX803681	379	12	66.7	27	6	AX037246	AX037246 Sequence
307	12	66.7 18	6	AX803682	380	12	66.7	27	6	AX037247	AX037247 Sequence
308	12	66.7 18	6	AX803683	381	12	66.7	27	6	AX037248	AX037248 Sequence
309	12	66.7 18	6	AX803684	382	12	66.7	27	6	AX037249	AX037249 Sequence
310	12	66.7 18	6	AX803687	383	12	66.7	27	6	AX037250	AX037250 Sequence
311	12	66.7 18	6	AX803688	384	12	66.7	27	6	AX037251	AX037251 Sequence

385	12	66.7	27	6	AX037252	Sequence	458	12	66.7	61	6	AX979339	Sequence
386	12	66.7	27	6	AX037253	Sequence	459	12	66.7	61	6	BD114198	BD114198 EST and e
387	12	66.7	27	6	AX037254	Sequence	460	12	66.7	110	14	AY690640	AY690640 Hepatitis
388	12	66.7	27	6	AX037255	Sequence	461	12	66.7	110	14	AY690641	AY690641 Hepatitis
389	12	66.7	27	6	AX037256	Sequence	462	12	66.7	110	14	AY690642	AY690642 Hepatitis
390	12	66.7	27	6	AX037257	Sequence	463	12	66.7	110	14	AY690643	AY690643 Hepatitis
391	12	66.7	27	6	AX037258	Sequence	464	12	66.7	110	14	AY690644	AY690644 Hepatitis
392	12	66.7	27	6	AX037259	Sequence	465	12	66.7	110	14	AY690645	AY690645 Hepatitis
393	12	66.7	27	6	AX037260	Sequence	466	12	66.7	110	14	AY690646	AY690646 Hepatitis
394	12	66.7	27	6	AX037261	Sequence	467	12	66.7	110	14	AY690647	AY690647 Hepatitis
395	12	66.7	27	6	AX037262	Sequence	468	12	66.7	110	14	AY690648	AY690648 Hepatitis
396	12	66.7	27	6	AX037263	Sequence	469	12	66.7	110	14	AY690649	AY690649 Hepatitis
397	12	66.7	27	6	AX037264	Sequence	470	12	66.7	110	14	AY690650	AY690650 Hepatitis
398	12	66.7	27	6	AX037265	Sequence	471	12	66.7	110	14	AY690651	AY690651 Hepatitis
399	12	66.7	27	6	AX037266	Sequence	472	12	66.7	110	14	AY690652	AY690652 Hepatitis
400	12	66.7	27	6	AX037267	Sequence	473	12	66.7	110	14	AY690653	AY690653 Hepatitis
401	12	66.7	27	6	AX037268	Sequence	474	12	66.7	110	14	AY690654	AY690654 Hepatitis
402	12	66.7	27	6	AX037269	Sequence	475	12	66.7	110	14	AY690655	AY690655 Hepatitis
403	12	66.7	27	6	AX037270	Sequence	476	12	66.7	116	14	HPCCHA12	M74254 Hepatitis
404	12	66.7	27	6	AX037271	Sequence	477	12	66.7	121	11	G31188	G31188 UC-66 Human
405	12	66.7	27	6	AX037272	Sequence	478	12	66.7	123	14	HPCCHA13	M74255 Hepatitis
406	12	66.7	27	6	AX037273	Sequence	479	12	66.7	125	14	HPCCHA14	M74256 Hepatitis
407	12	66.7	27	6	AX037274	Sequence	480	12	66.7	128	14	AY336151	M74257 Hepatitis
408	12	66.7	27	6	AX037275	Sequence	481	12	66.7	137	14	AY336151	M74258 Hepatitis
409	12	66.7	27	6	AX037276	Sequence	482	12	66.7	138	6	E10300	E10300 Anti-sense
410	12	66.7	27	6	AX037277	Sequence	483	12	66.7	140	6	E10301	E10301 Anti-sense
411	12	66.7	27	6	AX037278	Sequence	484	12	66.7	142	14	S72378	S72378 (5' region
412	12	66.7	27	6	AX037279	Sequence	485	12	66.7	149	14	HPCCB13	D10120 Hepatitis
413	12	66.7	27	6	AX037280	Sequence	486	12	66.7	149	14	HPCCB16	D10121 Hepatitis
414	12	66.7	27	6	AX037281	Sequence	487	12	66.7	149	14	HPCCB18	D10122 Hepatitis
415	12	66.7	27	6	AX037282	Sequence	488	12	66.7	149	14	HPCCB2	D10113 Hepatitis
416	12	66.7	27	6	AX037283	Sequence	489	12	66.7	149	14	HPCCB2	D10113 Hepatitis
417	12	66.7	27	6	AX037284	Sequence	490	12	66.7	151	14	AY145960	AY145960 Hepatitis
418	12	66.7	27	6	AX037285	Sequence	491	12</					

C 531	12	66.7	159	14	AF506625	AF506625 Hepatitis	C 604	12	66.7	176	14	AY145904	AY145904 Hepatitis
C 532	12	66.7	160	14	AY145915	AY145915 Hepatitis	C 605	12	66.7	176	14	AY145905	AY145905 Hepatitis
C 533	12	66.7	160	14	AY146043	AY146043 Hepatitis	C 606	12	66.7	176	14	AY145925	AY145925 Hepatitis
C 534	12	66.7	161	10	S45855	S45855 macrophage	C 607	12	66.7	176	14	AY145947	AY145947 Hepatitis
C 535	12	66.7	161	14	AY145979	AY145979 Hepatitis	C 608	12	66.7	176	14	HCV6329	HCV6329 Hepatitis
C 536	12	66.7	161	14	AY145995	AY145995 Hepatitis	C 609	12	66.7	176	14	HPC58CRAC	HPC58CRAC Hepatitis
C 537	12	66.7	161	14	AY146018	AY146018 Hepatitis	C 610	12	66.7	176	14	HPCUT34CTLN	HPCUT34CTLN Hepatitis
C 538	12	66.7	162	14	AY145983	AY145983 Hepatitis	C 611	12	66.7	176	14	HPCUT42CTLN	HPCUT42CTLN Hepatitis
C 539	12	66.7	162	14	AY145985	AY145985 Hepatitis	C 612	12	66.7	176	14	HPCUTCTLN1	HPCUTCTLN1 Hepatitis
C 540	12	66.7	162	14	AY145989	AY145989 Hepatitis	C 613	12	66.7	177	6	A39089	A39089 Sequence 61
C 541	12	66.7	163	14	AF506690	AF506690 Hepatitis	C 614	12	66.7	177	6	A39095	A39095 Sequence 67
C 542	12	66.7	163	14	AY145986	AY145986 Hepatitis	C 615	12	66.7	177	6	A39096	A39096 Sequence 68
C 543	12	66.7	163	14	AY145991	AY145991 Hepatitis	C 616	12	66.7	177	6	A39097	A39097 Sequence 69
C 544	12	66.7	163	14	AY146016	AY146016 Hepatitis	C 617	12	66.7	177	6	A39098	A39098 Sequence 70
C 545	12	66.7	163	14	HPCUT8CTLN	HPCUT8CTLN	C 618	12	66.7	177	6	A39100	A39100 Sequence 72
C 546	12	66.7	164	14	AY145908	AY145908 Hepatitis	C 619	12	66.7	177	6	A39101	A39101 Sequence 73
C 547	12	66.7	165	14	AY145918	AY145918 Hepatitis	C 620	12	66.7	177	6	A39102	A39102 Sequence 74
C 548	12	66.7	165	14	AY145929	AY145929 Hepatitis	C 621	12	66.7	177	6	A39103	A39103 Sequence 75
C 549	12	66.7	165	14	AY145954	AY145954 Hepatitis	C 622	12	66.7	177	6	A39104	A39104 Sequence 76
C 550	12	66.7	165	14	AY145961	AY145961 Hepatitis	C 623	12	66.7	177	6	A39105	A39105 Sequence 77
C 551	12	66.7	165	14	AY146002	AY146002 Hepatitis	C 624	12	66.7	177	6	A39106	A39106 Sequence 78
C 552	12	66.7	165	14	AY146035	AY146035 Hepatitis	C 625	12	66.7	177	6	A39107	A39107 Sequence 79
C 553	12	66.7	165	14	AY146036	AY146036 Hepatitis	C 626	12	66.7	177	6	A39108	A39108 Sequence 80
C 554	12	66.7	165	14	AY146039	AY146039 Hepatitis	C 627	12	66.7	177	6	AR063423	AR063423 Sequence
C 555	12	66.7	166	14	AY146029	AY146029 Hepatitis	C 628	12	66.7	177	6	AR063429	AR063429 Sequence
C 556	12	66.7	166	14	AY146048	AY146048 Hepatitis	C 629	12	66.7	177	6	AR063430	AR063430 Sequence
C 557	12	66.7	167	14	AY145942	AY145942 Hepatitis	C 630	12	66.7	177	6	AR063431	AR063431 Sequence
C 558	12	66.7	167	14	AY146017	AY146017 Hepatitis	C 631	12	66.7	177	6	AR063432	AR063432 Sequence
C 559	12	66.7	167	14	AY146065	AY146065 Hepatitis	C 632	12	66.7	177	6	AR063434	AR063434 Sequence
C 560	12	66.7	167	14	AY146066	AY146066 Hepatitis	C 633	12	66.7	177	6	AR063435	AR063435 Sequence
C 561	12	66.7	169	14	AY145988	AY145988 Hepatitis	C 634	12	66.7	177	6	AR063436	AR063436 Sequence
C 562	12	66.7	169	14	AY146013	AY146013 Hepatitis	C 635	12	66.7	177	6	AR063437	AR063437 Sequence
C 563	12	66.7	169	14	AY146033	AY146033 Hepatitis	C 636	12	66.7	177	6	AR063438	AR063438 Sequence
C 564	12	66.7	170	14	AY145910	AY145910 Hepatitis	C 637	12	66.7	177	6	AR063439	AR063439 Sequence
C 565	12	66.7	170	14	AY145952	AY145952 Hepatitis	C 638	12	66.7	177	6	AR063440	AR063440 Sequence
C 566	12	66.7	170	14	AY146041	AY146041 Hepatitis	C 639	12	66.7	177	6	AR063441	AR063441 Sequence
C 567	12	66.7	170	14	AY146044	AY146044 Hepatitis	C 640	12	66.7	177	6	AR063442	AR063442 Sequence
C 568	12	66.7	171	14	AF506640	AF506640 Hepatitis	C 641	12	66.7	177	6	AR123614	AR123614 Sequence
C 569	12	66.7	171	14	AF506646	AF506646 Hepatitis	C 642	12	66.7	177	6	AR123620	AR123620 Sequence
C 570	12	66.7	171	14	AF506650	AF506650 Hepatitis	C 643	12	66.7	177	6	AR123621	AR123621 Sequence
C 571	12	66.7	171	14	AF506665	AF506665 Hepatitis	C 644	12	66.7	177	6	AR123622	AR123622 Sequence
C 572	12	66.7	171	14	AF506668	AF506668 Hepatitis	C 645	12	66.7	177	6	AR123623	AR123623 Sequence
C 573	12	66.7	171	14	AF506675	AF506675 Hepatitis	C 646	12	66.7	177	6	AR123625	AR123625 Sequence
C 574	12	66.7	171	14	AF506691	AF506691 Hepatitis	C 647	12	66.7	177	6	AR123626	AR123626 Sequence
C 575	12	66.7	171	14	AY145919	AY145919 Hepatitis	C 648	12	66.7	177	6	AR123627	AR123627 Sequence
C 576	12	66.7	171	14	AY145921	AY145921 Hepatitis	C 649	12	66.7	177	6	AR123628	AR123628 Sequence
C 577	12	66.7	171	14	AY145923	AY145923 Hepatitis	C 650	12	66.7	177	6	AR123629	AR123629 Sequence
C 578	12	66.7	171	14	AY145941	AY145941 Hepatitis	C 651	12	66.7	177	6	AR123630	AR123630 Sequence
C 579	12	66.7	171	14	AY146063	AY146063 Hepatitis	C 652	12	66.7	177	6	AR123631	AR123631 Sequence
C 580	12	66.7	172	14	AF506660	AF506660 Hepatitis	C 653	12	66.7	177	6	AR123632	AR123632 Sequence
C 581	12	66.7	172	14	AY146019	AY146019 Hepatitis	C 654	12	66.7	177	6	AR123633	AR123633 Sequence
C 582	12	66.7	172	14	AY146020	AY146020 Hepatitis	C 655	12	66.7	177	6	AR267355	AR267355 Sequence
C 583	12	66.7	172	14	AY146023	AY146023 Hepatitis	C 656	12	66.7	177	6	AR267361	AR267361 Sequence
C 584	12	66.7	172	14	AY146032	AY146032 Hepatitis	C 657	12	66.7	177	6	AR267362	AR267362 Sequence
C 585	12	66.7	172	14	AY146034	AY146034 Hepatitis	C 658	12	66.7	177	6	AR267363	AR267363 Sequence
C 586	12	66.7	173	14	AF506676	AF506676 Hepatitis	C 659	12	66.7	177	6	AR267364	AR267364 Sequence
C 587	12	66.7	173	14	AY145949	AY145949 Hepatitis	C 660	12	66.7	177	6	AR267366	AR267366 Sequence
C 588	12	66.7	174	14	AF506673	AF506673 Hepatitis	C 661	12	66.7	177	6	AR267367	AR267367 Sequence
C 589	12	66.7	174	14	AF506685	AF506685 Hepatitis	C 662	12	66.7	177	6	AR267368	AR267368 Sequence
C 590	12	66.7	174	14	AF506692	AF506692 Hepatitis	C 663	12	66.7	177	6	AR267369	AR267369 Sequence
C 591	12	66.7	174	14	AF506693	AF506693 Hepatitis	C 664	12	66.7	177	6	AR267370	AR267370 Sequence
C 592	12	66.7	174	14	AY145917	AY145917 Hepatitis	C 665	12	66.7	177	6	AR267371	AR267371 Sequence
C 593	12	66.7	174	14	AY145946	AY145946 Hepatitis	C 666	12	66.7	177	6	AR267372	AR267372 Sequence
C 594	12	66.7	174	14	AY146047	AY146047 Hepatitis	C 667	12	66.7	177	6	AR267374	AR267374 Sequence
C 595	12	66.7	174	14	AY146061	AY146061 Hepatitis	C 668	12	66.7	177	6	AR267374	AR267374 Sequence
C 596	12	66.7	175	14	AF506661	AF506661 Hepatitis	C 669	12	66.7	177	6	AR305765	AR305765 Sequence
C 597	12	66.7	175	14	AY146055	AY146055 Hepatitis	C 670	12	66.7	177	6	AR305771	AR305771 Sequence
C 598	12	66.7	175	14	AY146057	AY146057 Hepatitis	C 671	12	66.7	177	6	AR305772	AR305772 Sequence
C 599	12	66.7	175	14	HPC58CRAC	HPC58CRAC	C 672	12	66.7	177	6	AR305773	AR305773 Sequence
C 600	12	66.7	176	3	SLMRDNL10	SLMRDNL10	C 673	12	66.7	177	6	AR305774	AR305774 Sequence
C 601	12	66.7	176	14	AF506645	AF506645 Hepatitis	C 674	12	66.7	177	6	AR305776	AR305776 Sequence
C 602	12	66.7	176	14	AF506658	AF506658 Hepatitis	C 675	12	66.7	177	6	AR305777	AR305777 Sequence
C 603	12	66.7	176	14	AF506694	AF506694 Hepatitis	C 676	12	66.7	177	6	AR305778	AR305778 Sequence

C 677	12	66.7	177	6	AR305779	Sequence	C 750	12	66.7	178	6	AR305775	Sequence	AR305775	Sequence
C 678	12	66.7	177	6	AR305780	Sequence	C 751	12	66.7	178	6	AR305781	Sequence	AR305781	Sequence
C 679	12	66.7	177	6	AR305781	Sequence	C 752	12	66.7	178	6	AR305782	Sequence	AR305782	Sequence
C 680	12	66.7	177	6	AR305782	Sequence	C 753	12	66.7	178	6	AR305783	Sequence	AR305783	Sequence
C 681	12	66.7	177	6	AR305783	Sequence	C 754	12	66.7	178	6	AR305784	Sequence	AR305784	Sequence
C 682	12	66.7	177	6	AR305784	Sequence	C 755	12	66.7	178	6	AR305785	Sequence	AR305785	Sequence
C 683	12	66.7	177	6	AR305785	Sequence	C 756	12	66.7	178	6	AR305786	Sequence	AR305786	Sequence
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C 686	12	66.7	177	6	AR305788	Sequence	C 759	12	66.7	178	6	AR305789	Sequence	AR305789	Sequence
C 687	12	66.7	177	6	AR305789	Sequence	C 760	12	66.7	178	6	AR305790	Sequence	AR305790	Sequence
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C 693	12	66.7	177	6	AR305795	Sequence	C 766	12	66.7	178	6	AR305796	Sequence	AR305796	Sequence
C 694	12	66.7	177	6	AR305796	Sequence	C 767	12	66.7	178	6	AR305797	Sequence	AR305797	Sequence
C 695	12	66.7	177	6	AR305797	Sequence	C 768	12	66.7	178	6	AR305798	Sequence	AR305798	Sequence
C 696	12	66.7	177	6	AR305798	Sequence	C 769	12	66.7	178	6	AR305799	Sequence	AR305799	Sequence
C 697	12	66.7	177	6	AR305799	Sequence	C 770	12	66.7	178	6	AR305800	Sequence	AR305800	Sequence
C 698	12	66.7	177	6	AR305800	Sequence	C 771	12	66.7	178	6	AR305801	Sequence	AR305801	Sequence
C 699	12	66.7	177	6	AR305801	Sequence	C 772	12	66.7	178	6	AR305802	Sequence	AR305802	Sequence
C 700	12	66.7	177	6	AR305802	Sequence	C 773	12	66.7	178	6	AR305803	Sequence	AR305803	Sequence
C 701	12	66.7	177	6	AR305803	Sequence	C 774	12	66.7	178	6	AR305804	Sequence	AR305804	Sequence
C 702	12	66.7	177	6	AR305804	Sequence	C 775	12	66.7	178	6	AR305805	Sequence	AR305805	Sequence
C 703	12	66.7	177	6	AR305805	Sequence	C 776	12	66.7	178	6	AR305806	Sequence	AR305806	Sequence
C 704	12	66.7	177	6	AR305806	Sequence	C 777	12	66.7	178	6	AR305807	Sequence	AR305807	Sequence
C 705	12	66.7	177	6	AR305807	Sequence	C 778	12	66.7	178	6	AR305808	Sequence	AR305808	Sequence
C 706	12	66.7	177	6	AR305808	Sequence	C 779	12	66.7	178	6	AR305809	Sequence	AR305809	Sequence
C 707	12	66.7	177	6	AR305809	Sequence	C 780	12	66.7	178	6	AR305810	Sequence	AR305810	Sequence
C 708	12	66.7	177	6	AR305810	Sequence	C 781	12	66.7	178	6	AR305811	Sequence	AR305811	Sequence
C 709	12	66.7	177	6	AR305811	Sequence	C 782	12	66.7	178	6	AR305812	Sequence	AR305812	Sequence
C 710	12	66.7	177	6	AR305812	Sequence	C 783	12	66.7	178	6	AR305813	Sequence	AR305813	Sequence
C 711	12	66.7	177	6	AR305813	Sequence	C 784	12	66.7	178	6	AR305814	Sequence	AR305814	Sequence
C 712	12	66.7	177	6	AR305814	Sequence	C 785	12	66.7	178	6	AR305815	Sequence	AR305815	Sequence
C 713	12	66.7	177	6	AR305815	Sequence	C 786	12	66.7	178	6	AR305816	Sequence	AR305816	Sequence
C 714	12	66.7	177	6	AR305816	Sequence	C 787	12	66.7	178	6	AR305817	Sequence	AR305817	Sequence
C 715	12	66.7	177	6	AR305817	Sequence	C 788	12	66.7	178	6	AR305818	Sequence	AR305818	Sequence
C 716	12	66.7	177	6	AR305818	Sequence	C 789	12	66.7	178	6	AR305819	Sequence	AR305819	Sequence
C 717	12	66.7	177	6	AR305819	Sequence	C 790	12	66.7	178	6	AR305820	Sequence	AR305820	Sequence
C 718	12	66.7	177	6	AR305820	Sequence	C 791	12	66.7	178	6	AR305821	Sequence	AR305821	Sequence
C 719	12	66.7	177	6	AR305821	Sequence	C 792	12	66.7	178	6	AR305822	Sequence	AR305822	Sequence
C 720	12	66.7	177	6	AR305822	Sequence	C 793	12	66.7	178	6	AR305823	Sequence	AR305823	Sequence
C 721	12	66.7	177	6	AR305823	Sequence	C 794	12	66.7	178	6	AR305824	Sequence	AR305824	Sequence
C 722	12	66.7	177	6	AR305824	Sequence	C 795	12	66.7	178	6	AR305825	Sequence	AR305825	Sequence
C 723	12	66.7	177	6	AR305825	Sequence	C 796	12	66.7	178	6	AR305826	Sequence	AR305826	Sequence
C 724	12	66.7	177	6	AR305826	Sequence	C 797	12	66.7	178	6	AR305827	Sequence	AR305827	Sequence
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C 727	12	66.7	177	6	AR305829	Sequence	C 800	12	66.7	178	6	AR305830	Sequence	AR305830	Sequence
C 728	12	66.7	177	6	AR305830	Sequence	C 801	12	66.7	178	6	AR305831	Sequence	AR305831	Sequence
C 729	12	66.7	177	6	AR305831	Sequence	C 802	12	66.7	178	6	AR305832	Sequence	AR305832	Sequence
C 730	12	66.7	177	6	AR305832	Sequence	C 803	12	66.7	178	6	AR305833	Sequence	AR305833	Sequence
C 731	12	66.7	177	6	AR305833	Sequence	C 804	12	66.7	178	6	AR305834	Sequence	AR305834	Sequence
C 732	12	66.7	177	6	AR305834	Sequence	C 805	12	66.7	178	6	AR305835	Sequence	AR305835	Sequence
C 733	12	66.7	177	6	AR305835	Sequence	C 806	12	66.7	178	6	AR305836	Sequence	AR305836	Sequence
C 734	12	66.7	177	6	AR305836	Sequence	C 807	12	66.7	178	6	AR305837	Sequence	AR305837	Sequence
C 735	12	66.7	177	6	AR305837	Sequence	C 808	12	66.7	178	6	AR305838	Sequence	AR305838	Sequence
C 736	12	66.7	177	6	AR305838	Sequence	C 809	12	66.7	178	6	AR305839	Sequence	AR305839	Sequence
C 737	12	66.7	177	6	AR305839	Sequence	C 810	12	66.7	178	6	AR305840	Sequence	AR305840	Sequence
C 738	12	66.7	177	6	AR305840	Sequence	C 811	12	66.7	178	6	AR305841	Sequence	AR305841	Sequence
C 739	12	66.7	177	6	AR305841	Sequence	C 812	12	66.7	178	6	AR305842	Sequence	AR305842	Sequence
C 740	12	66.7	177	6	AR305842	Sequence	C 813	12	66.7	178	6	AR305843	Sequence	AR305843	Sequence
C 741	12	66.7	177	6	AR305843	Sequence	C 814	12	66.7	178	6	AR305844	Sequence	AR305844	Sequence
C 742	12	66.7	177	6	AR305844	Sequence	C 815	12	66.7	178	6	AR305845	Sequence	AR305845	Sequence
C 743	12	66.7	177	6	AR305845	Sequence	C 816	12	66.7	178	6	AR305846	Sequence	AR305846	Sequence
C 744	12	66.7	177	6	AR305846	Sequence	C 817	12	66.7	178	6	AR305847	Sequence	AR305847	Sequence
C 745	12	66.7	177	6	AR305847	Sequence	C 818	12	66.7	178	6	AR305848	Sequence	AR305848	Sequence
C 746	12	66.7	177	6	AR305848	Sequence	C 819	12	66.7	178	6	AR305849	Sequence	AR305849	Sequence
C 747	12	66.7	177	6	AR305849	Sequence	C 820	12	66.7	178	6	AR305850	Sequence	AR305850	Sequence
C 748	12	66.7	177	6	AR305850	Sequence	C 821	12	66.7	178	6	AR305851	Sequence	AR305851	Sequence
C 749	12	66.7	177	6	AR305851	Sequence	C 822	12	66.7	178	6	AR305852	Sequence	AR305852	Sequence

C 823	12	66.7	181	14	AF158608	Hepatitis	C 896	12	66.7	182	14	AY190380	AY190380	Hepatitis
C 824	12	66.7	181	14	AF158609	Hepatitis	C 897	12	66.7	182	14	AY190399	AY190399	Hepatitis
C 825	12	66.7	181	14	AF158610	Hepatitis	C 898	12	66.7	182	14	AY190403	AY190403	Hepatitis
C 826	12	66.7	181	14	AF158611	Hepatitis	C 899	12	66.7	182	14	AY190419	AY190419	Hepatitis
C 827	12	66.7	181	14	AF158612	Hepatitis	C 900	12	66.7	182	14	AY190442	AY190442	Hepatitis
C 828	12	66.7	181	14	AF158617	Hepatitis	C 901	12	66.7	183	14	AF245282	AF245282	Hepatitis
C 829	12	66.7	181	14	AF1590379	Hepatitis	C 902	12	66.7	183	14	AF245283	AF245283	Hepatitis
C 830	12	66.7	181	14	AF1590381	Hepatitis	C 903	12	66.7	183	14	AF245284	AF245284	Hepatitis
C 831	12	66.7	181	14	AF1590382	Hepatitis	C 904	12	66.7	183	14	AF245285	AF245285	Hepatitis
C 832	12	66.7	181	14	AF1590385	Hepatitis	C 905	12	66.7	183	14	AF245287	AF245287	Hepatitis
C 833	12	66.7	181	14	AF1590388	Hepatitis	C 906	12	66.7	183	14	AF245290	AF245290	Hepatitis
C 834	12	66.7	181	14	AF1590389	Hepatitis	C 907	12	66.7	185	14	HPCBU74B	HPCBU74B	Hepatitis C
C 835	12	66.7	181	14	AF1590392	Hepatitis	C 908	12	66.7	187	14	AY306255	AY306255	Hepatitis
C 836	12	66.7	181	14	AF1590393	Hepatitis	C 909	12	66.7	187	14	AY306296	AY306296	Hepatitis
C 837	12	66.7	181	14	AF1590396	Hepatitis	C 910	12	66.7	187	14	AY306297	AY306297	Hepatitis
C 838	12	66.7	181	14	AF1590398	Hepatitis	C 911	12	66.7	187	14	AY311048	AY311048	Hepatitis
C 839	12	66.7	181	14	AF1590401	Hepatitis	C 912	12	66.7	188	14	AY145964	AY145964	Hepatitis
C 840	12	66.7	181	14	AF1590406	Hepatitis	C 913	12	66.7	188	14	AY146042	AY146042	Hepatitis
C 841	12	66.7	181	14	AF1590411	Hepatitis	C 914	12	66.7	188	14	AY306229	AY306229	Hepatitis
C 842	12	66.7	181	14	AF1590414	Hepatitis	C 915	12	66.7	188	14	AY306230	AY306230	Hepatitis
C 843	12	66.7	181	14	AF1590415	Hepatitis	C 916	12	66.7	188	14	AY306231	AY306231	Hepatitis
C 844	12	66.7	181	14	AF1590418	Hepatitis	C 917	12	66.7	188	14	AY306232	AY306232	Hepatitis
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KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1  
Frank, B. L., Goodchild, J., Hamlin, H. A., Kulkarni, R. E.,  
Roberts, P. C., Roberts, N. A., Walther, D. M. and Wolfe, J. L.  
Oligonucleotides specific for Hepatitis C Virus  
Patent: EP 1331267-A 38 30-JUL-2003;  
HYBRIDON, INC. (US)  
location/Qualifiers  
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DEFINITION Sequence 67 from Patent EP1331267.

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ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1  
Frank, B. L., Goodchild, J., Hamlin, H. A., Kulkarni, R. E.,  
Roberts, P. C., Roberts, N. A., Walther, D. M. and Wolfe, J. L.  
Oligonucleotides specific for Hepatitis C Virus  
Patent: EP 1331267-A 67 30-JUL-2003;  
HYBRIDON, INC. (US)  
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SEQUENCE SAMPLING.  
ACCESSION AC026845  
VERSION AC026845.3 GI:7677910  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

1 (bases 1 to 65130)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abrahams, H., Allen, N.,  
Anderson, S., Baldwin, J., Barna, N., Bassten, V., Beda, F.,  
Boguslavsky, L., Bouckhagalter, E., Brown, A., Burkett, G.,  
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Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Testaye, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J.,  
Vasiliiev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,  
Young, G., Zainoun, J., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (24-MAR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On May 2, 2000 this sequence version replaced gi:7549706.  
All repeats were identified using RepeatMasker:  
Smit, A. F. A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLE  
JOURNAL  
COMMENT



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----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIPR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L8785
Center clone name: 338_I_9

* NOTE: This record contains 76 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
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AUTHORS     McLay, K.
TITLES      Direct Submission
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              On Mar 24, 2004 this sequence version replaced gi:45581026.
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              Web site: http://www.sanger.ac.uk
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              Coverage: 9.02x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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Best Local Similarity 87.5%  Pred. NO. 5.1;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3  GGUCCTGGAGGNNNNNN 18
Db      27694  GGTCCTGGAGNNNNNN 27679

RESULT 5
LOCUS      AC074014      132597 bp      DNA      linear      HTG 10-JUL-2000
DEFINITION  Homo sapiens chromosome 10 clone RP11-113N2, *** SEQUENCING IN
ACCESSION  AC074014
VERSION     AC074014.1  GI:8990970
KEYWORDS    HTG; HTGS_PHASE1.

```

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS 1 (bases 1 to 132597)  
TITLE Waterston,R.H.  
JOURNAL The sequence of Homo sapiens clone  
REFERENCE Unpublished  
AUTHORS 2 (bases 1 to 132597)  
TITLE Waterston,R.H.  
JOURNAL Direct Submission  
Submitted (10-JUL-2000) Genome Sequencing Center, Washington  
University School of Medicine, 444 Forest Park Parkway, St. Louis,  
MO 63108, USA

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu/gsc/index.shtml  
----- Project Information -----  
Center project name: H\_NH0113N02

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 49 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1005: contig of 1005 bp in length  
1106 1105: contig of 1460 bp in length  
2665 2665: gap of unknown length  
4049 4049: contig of 1384 bp in length  
4149 4149: gap of unknown length  
5338 5338: contig of 1189 bp in length  
5439 5439: gap of unknown length  
6956 6956: contig of 1518 bp in length  
7056 7056: gap of unknown length  
8352 8352: contig of 1295 bp in length  
8451 8451: gap of unknown length  
10097 10097: contig of 1646 bp in length  
10198 10198: gap of unknown length  
11921 11921: contig of 1724 bp in length  
12021 12021: gap of unknown length  
13539 13539: contig of 1518 bp in length  
13639 13639: gap of unknown length  
15191 15191: contig of 1552 bp in length  
15291 15291: gap of unknown length  
16374 16374: contig of 1083 bp in length  
16474 16474: gap of unknown length  
17665 17665: contig of 1191 bp in length  
17765 17765: gap of unknown length  
19279 19279: contig of 1514 bp in length  
19379 19379: gap of unknown length  
21165 21165: contig of 1786 bp in length  
21265 21265: gap of unknown length  
23667 23667: contig of 2402 bp in length  
23767 23767: gap of unknown length  
25010 25010: contig of 1243 bp in length  
25110 25110: gap of unknown length  
26546 26546: contig of 1436 bp in length  
26646 26646: gap of unknown length  
28807 28807: contig of 2161 bp in length  
28907 28907: gap of unknown length  
30678 30678: contig of 1771 bp in length  
30778 30778: gap of unknown length  
32558 32558: contig of 1780 bp in length  
32659 32659: gap of unknown length  
35293 35293: contig of 2635 bp in length  
35294 35294: gap of unknown length  
37213 37213: contig of 1820 bp in length

37214 37313: gap of unknown length  
3852 3852: contig of 1539 bp in length  
38853 38853: gap of unknown length  
38953 38953: gap of unknown length  
40925 40925: contig of 1973 bp in length  
41025 41025: gap of unknown length  
43907 43907: contig of 2882 bp in length  
43908 43908: gap of unknown length  
44008 44008: contig of 1752 bp in length  
45760 45760: gap of unknown length  
45859 45859: gap of unknown length  
48247 48247: contig of 2388 bp in length  
48248 48248: gap of unknown length  
50917 50917: contig of 2570 bp in length  
50918 50918: gap of unknown length  
51018 51018: contig of 3587 bp in length  
54605 54605: gap of unknown length  
54705 54705: contig of 2387 bp in length  
57092 57092: gap of unknown length  
57192 57192: contig of 2398 bp in length  
59589 59589: gap of unknown length  
59680 59680: contig of 2730 bp in length  
62420 62420: gap of unknown length  
62519 62519: contig of 1315 bp in length  
63835 63835: gap of unknown length  
63935 63935: contig of 1893 bp in length  
65827 65827: gap of unknown length  
65927 65927: contig of 2053 bp in length  
67980 67980: gap of unknown length  
68080 68080: contig of 2055 bp in length  
68081 68081: gap of unknown length  
70135 70135: contig of 2055 bp in length  
70235 70235: gap of unknown length  
70336 70336: contig of 3524 bp in length  
73759 73759: gap of unknown length  
73760 73760: contig of 3501 bp in length  
73760 73760: gap of unknown length  
77361 77361: gap of unknown length  
77461 77461: contig of 2780 bp in length  
80241 80241: gap of unknown length  
80341 80341: contig of 3640 bp in length  
83980 83980: gap of unknown length  
83981 83981: contig of 4856 bp in length  
88936 88936: gap of unknown length  
88937 88937: gap of unknown length  
89037 89037: contig of 4929 bp in length  
93965 93965: gap of unknown length  
93966 93966: contig of 4996 bp in length  
94066 94066: gap of unknown length  
99061 99061: contig of 4031 bp in length  
99062 99062: gap of unknown length  
99161 99161: contig of 4031 bp in length  
103193 103193: gap of unknown length  
103282 103282: contig of 5290 bp in length  
108583 108583: gap of unknown length  
108682 108682: contig of 5329 bp in length  
114011 114011: gap of unknown length  
114012 114012: gap of unknown length  
114112 114112: contig of 5825 bp in length  
119936 119936: gap of unknown length  
119937 119937: contig of 5825 bp in length  
120037 120037: gap of unknown length  
126622 126622: contig of 5876 bp in length  
126722 126722: gap of unknown length  
126722 126722: contig of 5876 bp in length.

FEATURES  
source location/Qualifiers  
1..132597  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="10"  
/clone="RP11-113N2"

ORIGIN  
Query Match 88.9%; Score 16; DB 2; Length 132597;  
Best local Similarity 87.5%; Pred. No. 5.1;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGUCUGGAGNNNNN 18  
||:|||||  
Db 10207 GGTCCTGAGNNNNN 10192

RESULT 6

```

BX927307/c      BX927307      155605 bp   DNA       linear    HTG 29-JAN-2004
LOCUS           Dario reio clone DKEX-93M12, *** SEQUENCING IN PROGRESS ***, 8
DEFINITION     unordered pieces.
ACCESSION      BX927307
VERSION        BX927307.1 GI:41392964
KEYWORDS       HTG; HTGS PHASE1.
SOURCE         Dario reio (zebrafish)
ORGANISM       Dario reio
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
               Actinopterygii; Neopterygii; Teleostei; Osteichthys;
               Cypriniformes; Cyprinidae; Danio.
               1 (bases 1 to 155605)
REFERENCE      McRay, K.
AUTHORS        Direct Submission
TITLE          Submitted (28-JUN-2004) Wellcome Trust Sanger Institute, Hinxton,
JOURNAL        Cambridgehire, CB10 1SA, UK. E-mail enquiries:
               zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT        ----- Genome Center
               Center: Wellcome Trust Sanger Institute
               Center code: SC
               Web site: http://www.sanger.ac.uk
               Contact: zfish-help@sanger.ac.uk
               Project information
               -----
               Summary Statistics
               Assembly program: XGAP4; version 4.5
               Chemistry: Dye-terminator; 100% of reads
               Consensus quality: 152630 bases at least Q40
               Consensus quality: 153155 bases at least Q30
               Consensus quality: 153593 bases at least Q20
               Insert size: 154905; sum-of-contigs
               Insert size: 175125; 3.3% error; agarose-fp
               Quality coverage: 11.48x in Q20 bases; sum-of-contigs Quality
               coverage: 10.25x in Q20 bases; agarose-fp
               -----
               * NOTE: This is a 'working draft' sequence. It currently
               * consists of 8 contigs. The true order of the pieces
               * is not known and their order in this sequence record is
               * arbitrary. Gaps between the contigs are represented as
               * runs of N, but the exact sizes of the gaps are unknown.
               * This record will be updated with the finished sequence
               * as soon as it is available and the accession number will
               * be preserved
               *
               1      36395: contig of 36395 bp in length
               *
               1      36396: gap of 100 bp
               *
               36496  45440: contig of 8945 bp in length
               *
               45441  45540: gap of 100 bp
               *
               45541  73268: contig of 27728 bp in length
               *
               73269  73369: gap of 100 bp
               *
               73369  78367: contig of 4999 bp in length
               *
               78368  78467: gap of 100 bp
               *
               78468  95723: contig of 17256 bp in length
               *
               95724  95823: gap of 100 bp
               *
               95824  98390: contig of 2567 bp in length
               *
               98391  98490: gap of 100 bp
               *
               98491  104560: contig of 6070 bp in length
               *
               104561  104660: gap of 100 bp
               *
               104661  155605: contig of 50945 bp in length.
               Location/Qualifiers
                   1..155605
                       /organism="Dario reio"
                       /mol_type="genomic DNA"
                       /db_xref="taxon:7955"
                       /clone="DKEX-93M12"
                       /clone_id="DanioKey"
                   1..36395
                       /note="assembly fragment: 01036
                           fragment chain: 1"
                   36496..45440
                       /note="assembly fragment: 00150
                           fragment chain: 1"
                   45541..73268

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```

misc_feature      /note="assembly_fragment:00527
                  fragment_chain:1"
                  73369..78367
                  /note="assembly_fragment:00037
                  fragment_chain:1"
                  78468..95723
                  /note="assembly_fragment:00309
                  fragment_chain:1"
                  95824..98390
misc_feature      /note="assembly_fragment:00024"
                  98491..104560
                  /note="assembly_fragment:00082.0"
                  104661..155605
                  /note="assembly_fragment:01671"
ORIGIN
Query Match      88.9%; Score 16; DB 2; Length 155605;
Best Local Similarity 87.5%; Pred. No. 5.1;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Oy               3 GGUCCUGGAGGNNNNNN 18
                  |||:|||||
Db               45550 GGTCTGTGAGNNNNNN 45535

RESULT 7
LOCUS             CR752651                162408 bp    DNA       linear   HTG 26-AUG-2004
DEFINITION        Danio rerio clone CH211-167J6, WORKING DRAFT SEQUENCE, 11 unordered
ACCESSION         CR752651
VERSION           CR752651.2 GI:51571682
KEYWORDS          HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE            Danio rerio (zebrafish)
ORGANISM          Danio rerio
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                  Cypriniformes; Cyprinidae; Danio.
                  1 (bases 1 to 162408)
                  Burton, J.
                  Direct Submission
                  Submitted (24-AUG-2004) Wellcome Trust Sanger Institute, Hinxton,
                  Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                  zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
                  On Aug 26, 2004 this sequence version replaced gi:51534192.
COMMENT
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: ZC167J6
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 158163 bases at least Q40
Consensus quality: 159103 bases at least Q30
Consensus quality: 159748 bases at least Q20
Insert size: 161308; sum-of-contigs
Insert size: 160976; 2.4% error; agarose-fp
Quality coverage: 6.33x in Q20 bases; sum-of-contigs Quality
coverage: 7.91x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 20585: contig of 20585 bp in length
* 20586 20685: gap of 100 bp

```

\* 20686 34543: contig of 13858 bp in length  
\* 34544 34643: gap of 100 bp  
\* 34644 62759: contig of 2816 bp in length  
\* 62760 62859: gap of 100 bp  
\* 62860 126982: contig of 64123 bp in length  
\* 126983 127083: gap of 100 bp  
\* 127083 130122: contig of 3040 bp in length  
\* 130123 130222: gap of 100 bp  
\* 130223 132710: contig of 2488 bp in length  
\* 132711 132893: gap of 183 bp  
\* 132894 132897: contig of 4 bp in length  
\* 132898 149121: contig of 16124 bp in length  
\* 149122 149231: gap of 100 bp  
\* 149232 151297: contig of 2076 bp in length  
\* 151298 151397: gap of 100 bp  
\* 151398 155131: contig of 3734 bp in length  
\* 155132 155231: gap of 100 bp  
\* 155232 162408: contig of 7177 bp in length.  
\* 155232 Location/Qualifiers

FEATURES  
Source 1.162408  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="CH211-16706"  
/clone\_lib="CHORI-211"  
1.20565  
/note="assembly\_fragment:00681  
fragment\_chain:1"  
20686.34543  
/note="assembly\_fragment:00297  
fragment\_chain:1"  
clone\_end:77  
vector\_side:left"  
34644.62759  
/note="assembly\_fragment:00951  
fragment\_chain:1"  
62860.126982  
/note="assembly\_fragment:01369  
fragment\_chain:1"  
127083.130122  
/note="assembly\_fragment:00187  
fragment\_chain:1"  
130223.132897  
/note="assembly\_fragment:00173  
fragment\_chain:1"  
13298.149121  
/note="assembly\_fragment:00485  
fragment\_chain:1"  
clone\_end:86  
vector\_side:right"  
149222.151297  
/note="assembly\_fragment:00130"  
151398.155131  
/note="assembly\_fragment:00162"  
155232.162408  
/note="assembly\_fragment:00210"  
ORIGIN  
Query Match 88.9%; Score 16; DB 2; Length 162408;  
Best Local Similarity 87.5%; Pred. No. 5.1;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 3 GGUCGAGAGNNNNNN 18  
Db 130113 GGTCCTGAGAGNNNNNN 130128  
RESULT 8  
CR774197/c 166622 bp DNA linear HTG 16-SEP-2004  
LOCUS Danio rerio clone DKEX-279J3, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 5  
DEFINITION unordered pieces.

ACCESSION CR774197  
VERSION CR774197.1 GI:52213982  
KEYWORDS HTG; HTGS\_PHASE1.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 166622)  
REFERENCE  
AUTHORS McClay, K.  
TITLE Direct Submission  
JOURNAL Submitted (15-SEP-2004) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
zf1sh-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: zf1sh-help@sanger.ac.uk  
----- Project Information  
Center project name: ZK279J3  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 100% of reads  
Consensus quality: 164818 bases at least Q40  
Consensus quality: 165177 bases at least Q40  
Consensus quality: 165623 bases at least Q20  
Insert size: 166222; sum-of-contigs  
Insert size: 169536; 2.7% error; agarose-fp  
Quality coverage: 7.81x in Q20 bases; sum-of-contigs Quality  
coverage: 7.73x in Q20 bases; agarose-fp

\*\*\*\*\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 5 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 13522: contig of 13522 bp in length  
\* 13523 13622: gap of 100 bp  
\* 13623 90740: contig of 77118 bp in length  
\* 90741 90840: gap of 100 bp  
\* 90841 132601: contig of 41761 bp in length  
\* 132602 132701: gap of 100 bp  
\* 132702 139994: contig of 7293 bp in length  
\* 139995 140094: gap of 100 bp  
\* 140095 166622: contig of 26528 bp in length.  
\* Location/Qualifiers  
Source 1.166622  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKEX-279J3"  
/clone\_lib="DanioKey"  
1.13522  
/note="assembly\_fragment:00072  
fragment\_chain:1"  
13623.90740  
/note="assembly\_fragment:00972  
fragment\_chain:1"  
90841.132601  
/note="assembly\_fragment:00561  
fragment\_chain:1"  
132702.139994  
/note="assembly\_fragment:00019"  
140095.166622  
/note="assembly\_fragment:00207.0"  
ORIGIN  
Query Match 88.9%; Score 16; DB 2; Length 166622;  
Best Local Similarity 87.5%; Pred. No. 5.1;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGUCGAGAGNNNNN 18  
 ||:|||||  
 Db 90850 GGTCCTGAGAGNNNNN 90835

RESULT 9  
 CR812468/c 172578 bp DNA linear HTG 27-SEP-2004  
 LOCUS Danio rerio clone CH211-252P18, WORKING DRAFT SEQUENCE, 9 unordered  
 DEFINITION pieces.  
 CR812468  
 ACCESSION CR812468.2 GI:57748667  
 VERSION HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
 KEYWORDS Danio rerio (zebrafish)  
 SOURCE Danio rerio  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 172578)  
 REFERENCE Burton, J.  
 AUTHORS Direct Submission  
 TITLE Submitted (26-SEP-2004) Wellcome Trust Sanger Institute, Hinxton,  
 JOURNAL Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
 On Sep 27, 2004 this sequence version replaced gi:52694424.  
 COMMENT ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: zfish-help@sanger.ac.uk  
 ----- Project Information  
 Center project name: zc252P18  
 ----- Summary Statistics  
 Assembly program: XGAP; version 4.5  
 Chemistry: Dye-terminator; 10% of reads  
 Consensus quality: 169202 bases at least Q40  
 Consensus quality: 169775 bases at least Q30  
 Consensus quality: 170291 bases at least Q20  
 Insert size: 171778; sum-of-coverage  
 Insert size: 177356; 3.4% error; agarose-gel  
 Quality coverage: 7.52x in Q20 bases; sum-of-coverage  
 coverage: 7.28x in Q20 bases; agarose-gel

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 9 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1  
 3746 3745: contig of 3745 bp in length  
 3846 3845: gap of 100 bp  
 7409 7408: contig of 3563 bp in length  
 7509 7508: gap of 100 bp  
 16761 16760: contig of 9252 bp in length  
 16861 16860: gap of 100 bp  
 34628 34627: contig of 1767 bp in length  
 34728 34727: gap of 100 bp  
 58287 58286: contig of 23560 bp in length  
 58388 58387: gap of 100 bp  
 87381 87380: contig of 28994 bp in length  
 87481 87480: gap of 100 bp  
 108999 108998: contig of 21418 bp in length  
 109000 109000: gap of 100 bp  
 160081 160080: contig of 51061 bp in length  
 160181 160180: gap of 100 bp  
 160181 172578: contig of 12398 bp in length.  
 Location/Qualifiers  
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 /organism="Danio rerio"

/mol\_type="genomic DNA"  
 /db\_xref="taxon:7955"  
 /clone="CH211-252P18"  
 /clone\_1b="CHORI-211"  
 1..3745  
 /note="assembly\_fragment:00055  
 clone\_end:SP6  
 vector\_side:left"  
 3846..7408  
 /note="assembly\_fragment:00024  
 fragment\_chain:1"  
 7509..16760  
 /note="assembly\_fragment:00091  
 fragment\_chain:1"  
 16861..34627  
 /note="assembly\_fragment:00369  
 fragment\_chain:1"  
 34728..58287  
 /note="assembly\_fragment:00801  
 fragment\_chain:1"  
 58388..87381  
 /note="assembly\_fragment:01078  
 fragment\_chain:1"  
 87482..108999  
 /note="assembly\_fragment:00562  
 fragment\_chain:1"  
 109000..160080  
 /note="assembly\_fragment:01434  
 fragment\_chain:1"  
 160181..172578  
 /note="assembly\_fragment:00188  
 fragment\_chain:1  
 clone\_end:77  
 vector\_side:right"

ORIGIN

Query Match 88.9%; Score 16; DB 2; Length 172578;  
 Best Local Similarity 87.5%; Pred. No. 5.1;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGUCGAGAGNNNNN 18  
 ||:|||||  
 Db 160190 GGTCCTGAGAGNNNNN 160175.

RESULT 10  
 BX927353/c 177849 bp DNA linear HTG 30-MAR-2004  
 LOCUS Danio rerio clone CH211-83P14, \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 DEFINITION unordered pieces.  
 BX927353  
 ACCESSION BX927353.3 GI:46016460  
 VERSION HTG; HTGS\_PHASE1.  
 KEYWORDS Danio rerio (zebrafish)  
 SOURCE Danio rerio  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 177849)  
 REFERENCE Sims, S.  
 AUTHORS Direct Submission  
 TITLE Submitted (29-MAR-2004) Wellcome Trust Sanger Institute, Hinxton,  
 JOURNAL Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
 On Apr 1, 2004 this sequence version replaced gi:45822741.  
 COMMENT ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: zfish-help@sanger.ac.uk  
 ----- Project Information  
 Center project name: zc83P14  
 ----- Summary Statistics

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 14 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of 'N', but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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source
1. 177849
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-83F14"
/clone_lib="CHORI-211"
1. 12893

misc_feature
/note="assembly fragment:00524"
fragment_chain:1
clone_end:56
vector_side:left"
12994..23124
/note="assembly fragment:00395"
fragment_chain:1"
2325..30967

misc_feature
/note="assembly fragment:00295"
fragment_chain:1"
31068..47374
/note="assembly fragment:00699"
fragment_chain:2"
47375..69050
/note="assembly fragment:00947"
fragment_chain:2"
69151..71771
/note="assembly fragment:00121"
fragment_chain:2"
71872..113609

misc_feature
/note="assembly fragment:00524"
fragment_chain:1
clone_end:56
vector_side:left"
12994..23124
/note="assembly fragment:00395"
fragment_chain:1"
2325..30967

misc_feature
/note="assembly fragment:00295"
fragment_chain:1"
31068..47374
/note="assembly fragment:00699"
fragment_chain:2"
47375..69050
/note="assembly fragment:00947"
fragment_chain:2"
69151..71771
/note="assembly fragment:00121"
fragment_chain:2"
71872..113609
```

Query Match	88.9%	Score 16;	DB 2;	Length 177849;
Best Local Similarity	87.5%;	Pred. No. 5.1;		
Matches 14;	Conservative 2;	Mismatches 0;	Indels 0	

RESULT	11
LOCUS	CR752654
DEFINITION	CR752654 178025 bp DNA linear HTG 26-AUG-2004 Danio rerio clone DKEX-168C17, WORKING DRAFT SEQUENCE, 17 unordered

Cypriniformes; Cyprinidae; Danio  
1 (bases 1 to 178025)

**TITLE** Direct Submission  
**JOURNAL** Submitted (24-JUG-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
**COMMENT** On Aug 26, 2004 this sequence version replaced gi:151534195.

```

Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
Project Information
Center project name: ZK168C17
----- Summary Statistics -----
Assembly program: XGAP4, version 4.5
Chemistry: dye-terminator, 100% of reads
Consensus quality: 172534 bases at least Q40
Consensus quality: 173763 bases at least Q30
Consensus quality: 174582 bases at least Q20
Insert size: 176425, sum-of-contigs
Insert size: 154806, 2.0% error, agarose-fp
Quality coverage: 4,54x in Q20 bases, sum-of-contigs
Quality coverage: 5,33x in Q20 bases, agarose-fp
-----

```





Center code: NISC  
 Web site: <http://www.nisc.nih.gov>  
 Contact: [nisc\\_zoo@nhgri.nih.gov](mailto:nisc_zoo@nhgri.nih.gov)  
 Project Information  
 Center project name: dkg  
 Center clone name: 034G07

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

#### ----- Summary Statistics -----

Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 183467 bases at least Q40  
 Consensus quality: 183739 bases at least Q30  
 Consensus quality: 183840 bases at least Q20  
 Insert size: 14400; agarose-fp  
 Insert size: 183928; sum-of-contigs  
 Quality coverage: 16.21x in Q20 bases; agarose-fp  
 Quality coverage: 12.69x in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

\* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1  
 11239 11238: contig of 11238 bp in length  
 11339 70156: contig of 58818 bp in length  
 70157 70256: gap of unknown length  
 70257 79761: contig of 9505 bp in length  
 79762 79861: gap of unknown length  
 79862 90719: contig of 10858 bp in length  
 90720 90819: gap of unknown length  
 90820 115756: contig of 24937 bp in length  
 115757 115856: gap of unknown length  
 115857 161819: contig of 45963 bp in length  
 161820 161919: gap of unknown length  
 161920 164501: contig of 2582 bp in length  
 164502 164601: gap of unknown length  
 164602 184628: contig of 20027 bp in length.

#### FEATURES

source  
 1. 184628  
 /organism="Danio rerio"  
 /mol\_type="genomic DNA"  
 /strain="Tue"  
 /db\_xref="taxon:7955"  
 /clone="CH211-34G7"  
 /clone\_id="CH211"  
 1. 11238  
 /note="assembly\_fragment  
 clone\_end:SP6  
 vector\_side:left"  
 11339..70156  
 /note="assembly\_fragment"  
 70257..79761  
 /note="assembly\_fragment"  
 79862..90719  
 /note="assembly\_fragment"  
 misc\_feature  
 misc\_feature  
 misc\_feature  
 misc\_feature

misc\_feature 90820..115756  
 /note="assembly\_fragment"  
 misc\_feature 115857..161819  
 /note="assembly\_fragment"  
 misc\_feature 161920..164501  
 /note="assembly\_fragment"  
 misc\_feature 164602..184628  
 /note="assembly\_fragment  
 clone\_end:F7  
 vector\_side:right"

#### ORIGIN

Query Match 88.9%; Score 16; DB 2; Length 184628;  
 Best Local Similarity 87.5%; Pred. No. 5;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

3 GGUCCUGAGAGNNNNN 18  
 ||:|||||  
 Db 79871 GGTCTTGAGNNNNN 79856

#### RESULT 13

CR735108 189909 bp DNA linear HTG 19-AUG-2004  
 LOCUS  
 DEFINITION Danio rerio clone DKEY-262A18, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 10  
 unorderd pieces.  
 CR735108  
 VERSION CR735108.2 GI:51476924  
 HTG; HTGS PHASE1.  
 KEYWORDS  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 189909)  
 McIay, K.  
 Direct Submission  
 Submitted (16-AUG-2004) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
 On Aug 20, 2004 this sequence version replaced gi:51241605.

#### REFERENCE

AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: [zfish-help@sanger.ac.uk](mailto:zfish-help@sanger.ac.uk)  
 Project Information  
 Center project name: ZK262A18

----- Summary Statistics -----  
 Assembly program: XGAP4; version 4.5  
 Chemistry: Dye-terminator; 100% of reads  
 Consensus quality: 186842 bases at least Q40  
 Consensus quality: 187400 bases at least Q30  
 Consensus quality: 187753 bases at least Q20  
 Insert size: 18909; sum-of-contigs  
 Insert size: 193430; 5.3% error; agarose-fp  
 Quality coverage: 9.12x in Q20 bases; sum-of-contigs Quality  
 coverage: 9.21x in Q20 bases; agarose-fp

\* NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 14842: contig of 14842 bp in length  
 14843 14942: gap of 100 bp  
 14943 22644: contig of 7702 bp in length  
 22645 22744: gap of 100 bp  
 22745 32691: contig of 9947 bp in length  
 32692 32791: gap of 100 bp

```

* 32792 57260: contig of 24469 bp in length
* 57261 57360: gap of 100 bp
* 57361 63085: contig of 5725 bp in length
* 63086 63185: gap of 100 bp
* 63186 137034: contig of 73849 bp in length
* 137035 137134: gap of 100 bp
* 137135 164138: contig of 27004 bp in length
* 164139 164238: gap of 100 bp
* 164239 170118: contig of 5880 bp in length
* 170119 170218: gap of 100 bp
* 170219 177353: contig of 7135 bp in length
* 177354 177454: gap of 100 bp
* 177455 189909: contig of 12456 bp in length.

```

# FEATURES

```

source
  1..189909
    /organism="Danio rerio"
    /mol_type="genomic DNA"
    /db_xref="taxon:7955"
    /clone="DKEX-262A18"
    /clone_id="DanioKey"
  1..14842
    /note="assembly_fragment:00491"
    /fragment_chain="1"
  14943..22644
    /note="assembly_fragment:00108"
    /fragment_chain="1"
  22745..32691
    /note="assembly_fragment:00675"
    /fragment_chain="1"
  32792..57260
    /note="assembly_fragment:01254"
    /fragment_chain="1"
  57361..63085
    /note="assembly_fragment:00187"
    /fragment_chain="2"
  63186..137034
    /note="assembly_fragment:01656"
    /fragment_chain="2"
  137135..164138
    /note="assembly_fragment:00868"
    /fragment_chain="2"
  164239..170118
    /note="assembly_fragment:00064"
    /fragment_chain="2"
  170219..177353
    /note="assembly_fragment:00268.0"
    /fragment_chain="2"
  177454..189909
    /note="assembly_fragment:00351"

```

```

ORIGIN
Query Match      88.9%; Score 16; DB 2; Length 189909;
Best Local Similarity 87.5%; Pred. No. 5;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY      3 GGUCCUGAGANNNNNN 18
Db      14833 GGTCTGAGANNNNNN 14848

```

```

RESULT 14
LOCUS CR376763 198047 bp DNA linear HTG 03-APR-2004
DEFINITION Danio rerio clone CH211-10L22, *** SEQUENCING IN PROGRESS ***, 14
unordered pieces.
ACCESSION CR376763
VERSION CR376763.4 GI:46194657
KEYWORDS HTG; HTGS; PHASE1.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 198047)
AUTHORS McIay,K.

```

## TITLE

### JOURNAL

### COMMENT

Direct Submission  
Submitted (01-APR-2004) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
zf1sh-help@sanger.ac.uk Clone request: clonerequest@sanger.ac.uk  
On Apr 3, 2004 this sequence version replaced gi:46019467.

----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: zf1sh-help@sanger.ac.uk  
----- Project Information  
Center project name: zc10L22

----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 100% of reads  
Consensus quality: 192805 bases at least Q40  
Consensus quality: 193672 bases at least Q30  
Consensus quality: 194568 bases at least Q20  
Insert size: 196747; sum-of-contigs  
Insert size: 201230; 9.6% error; agarose-fp  
Quality coverage: 7.13x in Q20 bases; sum-of-contigs Quality  
coverage: 7.02x in Q20 bases; agarose-fp

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 14 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

```

1 3382: contig of 3382 bp in length
3383 3482: gap of 100 bp
3483 21388: contig of 17906 bp in length
21389 21488: gap of 100 bp
21489 37498: contig of 16010 bp in length
37499 37598: gap of 100 bp
37599 67786: contig of 30188 bp in length
67787 67886: gap of 100 bp
67887 71536: contig of 3650 bp in length
71537 71636: gap of 100 bp
71637 80081: contig of 8445 bp in length
80082 80181: gap of 100 bp
80182 82322: contig of 2141 bp in length
82323 82422: gap of 100 bp
82423 106063: contig of 23641 bp in length
106064 106163: gap of 100 bp
106164 109599: contig of 3436 bp in length
109600 109699: gap of 100 bp
109700 113444: contig of 3745 bp in length
113445 113544: gap of 100 bp
113545 143985: contig of 30441 bp in length
143986 144085: gap of 100 bp
144086 164108: contig of 20023 bp in length
164109 164208: gap of 100 bp
164209 169935: contig of 5727 bp in length
169936 170035: gap of 100 bp
170036 198047: contig of 28012 bp in length.

```

## FEATURES

```

source
  1..198047
    /organism="Danio rerio"
    /mol_type="genomic DNA"
    /db_xref="taxon:7955"
    /clone="CH211-10L22"
    /clone_id="CHOR1-211"
  1..3382
    /note="assembly_fragment:00160"
    /fragment_chain="1"
  3483..21388
    /note="assembly_fragment:00723"
    /fragment_chain="1"
  21489..37498
    /note="assembly_fragment:00356"

```

```
misc_feature      37589..67786      fragment chain:1"
                    /note="assembly_fragment:01223
                    fragment_chain:1"
misc_feature      67887..71536      /note="assembly_fragment:00093
                    fragment_chain:2"
misc_feature      71637..80081      /note="assembly_fragment:00261
                    fragment_chain:2"
misc_feature      80182..82322      /note="assembly_fragment:00022"
                    fragment_chain:3"
misc_feature      82423..106063     /note="assembly_fragment:00965"
                    /note="assembly_fragment:00040
                    fragment_chain:3"
misc_feature      106164..109599     /note="assembly_fragment:00040
                    fragment_chain:3"
misc_feature      109700..113444     /note="assembly_fragment:00123
                    fragment_chain:3"
misc_feature      113545..143985     /note="assembly_fragment:01882
                    fragment_chain:3"
misc_feature      144086..164108     /note="assembly_fragment:00528
                    fragment_chain:3"
misc_feature      164209..169935     /note="assembly_fragment:00200
                    /note="assembly_fragment:01525
                    fragment_chain:3"
misc_feature      170036..198047     /note="assembly_fragment:01525
                    fragment_chain:3"
                    clone_end:77
                    vector_side:right"
```

```
ORIGIN
Query Match      88.9%: Score 16; DB 2; Length 198047;
Best Local Similarity 87.5%: Pred. No. 5;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      3 GGUCCUGAGAGNNNNNN 18
      |||:|||||
Db      3492 GGTCTGTGAGNNNNNN 3477
```

```
RESULT 15
BX901895/c
LOCUS      BX901895      213402 bp      DNA      linear      HTG 31-JAN-2004
DEFINITION      Danio rerio clone CH211-218C11, WORKING DRAFT SEQUENCE, 15
ACCESSION      BX901895
VERSION      BX901895.4 GI:41529663
KEYWORDS      HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULUTOP.
SOURCE      Danio rerio (zebrafish)
ORGANISM      Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE      Submitted (30-JAN-2004) Wellcome Trust Sanger Institute, Hinxton,
AUTHORS      Cambridgehire, CB10 1SA, UK. E-mail enquiries:
            zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
TITLE      On Jan 31, 2004 this sequence version replaced gi:41411281.
JOURNAL      ----- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: zfish-help@sanger.ac.uk
            Project Information
            Center project name: zC218C11
            ----- Summary Statistics
```

```
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 207066 bases at least Q40
Consensus quality: 208069 bases at least Q30
Consensus quality: 209254 bases at least Q20
Insert size: 212002; sum-of-contigs
Insert size: 217067; 3.2% error; aggrorse-fp
Quality coverage: 11.46x in Q20 bases; sum-of-contigs Quality
coverage: 11.33x in Q20 bases; aggrorse-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1      56095: contig of 56095 bp in length
*      56096: gap of 100 bp
*      56196: contig of 35682 bp in length
*      91877: gap of 100 bp
*      91878: gap of 100 bp
*      91978: contig of 28616 bp in length
*      120594: contig of 28616 bp in length
*      120594: gap of 100 bp
*      120694: contig of 6658 bp in length
*      127352: gap of 100 bp
*      127452: contig of 6257 bp in length
*      133708: gap of 100 bp
*      133809: contig of 3467 bp in length
*      133809: gap of 100 bp
*      133726: contig of 6161 bp in length
*      133736: contig of 6161 bp in length
*      143636: gap of 100 bp
*      143637: contig of 5543 bp in length
*      149179: gap of 100 bp
*      149280: contig of 4246 bp in length
*      149280: gap of 100 bp
*      153625: gap of 100 bp
*      153626: gap of 100 bp
*      175190: contig of 21565 bp in length
*      175191: gap of 100 bp
*      175290: gap of 100 bp
*      175291: contig of 11293 bp in length
*      186583: gap of 100 bp
*      186584: gap of 100 bp
*      186684: contig of 5727 bp in length
*      192411: contig of 5727 bp in length
*      192411: gap of 100 bp
*      192511: contig of 3497 bp in length
*      196007: contig of 3497 bp in length
*      196107: gap of 100 bp
*      209446: contig of 13339 bp in length
*      196108: gap of 100 bp
*      209447: gap of 100 bp
*      209447: contig of 3856 bp in length.
*
Location/Qualifiers
1..213402
  /organism="Danio rerio"
  /mol_type="genomic DNA"
  /db_xref="taxon:7955"
  /clone="CH211-218C11"
  /clone_1bp="CHORI-211"
1..56095
  /note="assembly_fragment:03265
  fragment_chain:1"
56196..91877
  /note="assembly_fragment:02468
  fragment_chain:1"
91978..120593
  /note="assembly_fragment:01885
  fragment_chain:1"
120694..127351
  /note="assembly_fragment:00484
  fragment_chain:1"
127452..133708
  /note="assembly_fragment:00625
  fragment_chain:1"
133809..137275
  /note="assembly_fragment:00001"
137376..143536
  /note="assembly_fragment:00376"
```

```
misc_feature 143637..149179
/note="assembly_fragment:00977"
misc_feature 149280..153525
/note="assembly_fragment:00193
fragment_chain:2"
misc_feature 153626..175190
/note="assembly_fragment:01442
fragment_chain:2"
misc_feature 175291..186593
/note="assembly_fragment:00773
fragment_chain:2"
misc_feature 186684..192410
/note="assembly_fragment:00279
fragment_chain:2"
misc_feature 192511..196007
/note="assembly_fragment:00046
fragment_chain:2"
misc_feature 196108..209446
/note="assembly_fragment:01162
fragment_chain:2"
misc_feature 209547..213402
/note="assembly_fragment:00115
fragment_chain:2
clone_end:SP6
vector_side:right"

ORIGIN
Query Match 88.9%; Score 16; DB 2; Length 213402;
Best Local Similarity 87.5%; Pred. No. 5;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGUCGAGAGNNNNNN 18
Db 127461 GGTCTCGAGNNNNNN 127446

RESULT 16
BX927073 215185 bp DNA linear HTG 18-FEB-2004
LOCUS Danio rerio clone DKEYP-78C2, *** SEQUENCING IN PROGRESS ***, 7
DEFINITION unoriented pieces.
ACCESSION BX927073
VERSION BX927073.3 GI:42592534
KEYWORDS HTG; HTGS PHASE1.
SOURCE Danio rerio (zebrafish)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 215185)
McLay, K.
Direct Submission
Submitted (16-FEB-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Feb 17, 2004 this sequence version replaced gi:41016204.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: zK078C2
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 211838 bases at least Q40
Consensus quality: 212487 bases at least Q30
Consensus quality: 213129 bases at least Q20
Insert size: 214585; sum-of-contigs
Insert size: 219324; 2.6% error; agarose-fp
Quality coverage: 8.00x in Q20 bases; sum-of-contigs Quality
coverage: 7.92x in Q20 bases; agarose-fp
```

```
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 3729: contig of 3729 bp in length
* 3730 3829: gap of 100 bp
* 3830 26383: contig of 22554 bp in length
* 26384 26483: gap of 100 bp
* 26484 33119: contig of 6636 bp in length
* 33120 33219: gap of 100 bp
* 33220 110818: contig of 77599 bp in length
* 110819 110918: gap of 100 bp
* 110919 127149: contig of 16231 bp in length
* 127150 127249: gap of 100 bp
* 127250 154645: contig of 27396 bp in length
* 154646 154745: gap of 100 bp
* 154746 215185: contig of 60440 bp in length.
Location/Qualifiers
source 1..215185
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEYP-78C2"
/clone_1b="DanioKeyplot"
1..3729
/note="assembly_fragment:00023
fragment_chain:1"
misc_feature 3830..26383
/note="assembly_fragment:00331
fragment_chain:1"
misc_feature 26484..33119
/note="assembly_fragment:00064
fragment_chain:2"
misc_feature 33220..110818
/note="assembly_fragment:01713
fragment_chain:2"
misc_feature 110919..127149
/note="assembly_fragment:00146"
misc_feature 127250..154645
/note="assembly_fragment:00622.0"
misc_feature 154746..215185
/note="assembly_fragment:00949"

ORIGIN
Query Match 88.9%; Score 16; DB 2; Length 215185;
Best Local Similarity 87.5%; Pred. No. 5;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGUCGAGAGNNNNNN 18
Db 3720 GGTCTCGAGNNNNNN 3735

RESULT 17
CR388047 221924 bp DNA linear HTG 20-AUG-2004
LOCUS Danio rerio clone DKEY-244D13, WORKING DRAFT SEQUENCE, 13 unordered
DEFINITION pieces.
ACCESSION CR388047
VERSION CR388047.4 GI:51491001
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.
SOURCE Danio rerio (zebrafish)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 221924)
Sims, S.
```

TITLE  
JOURNAL

Direct Submission  
Submitted (18-AUG-2004) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
On Aug 20, 2004 this sequence version replaced gi:51470662.

## COMMENT

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: zfish-help@sanger.ac.uk

Project Information

Center project name: zK244D13

Summary Statistics

Assembly program: XGAP4; version 4.5

Chemistry: Dye-terminator; 100% of reads

Consensus quality: 217655 bases at least Q40

Consensus quality: 218961 bases at least Q30

Consensus quality: 219692 bases at least Q20

Insert size: 220724; sum-of-contigs

Quality coverage: 6.50x in Q20 bases; sum-of-contigs Quality

coverage: 6.61x in Q20 bases; agarose-fp

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 13 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 8096: contig of 8096 bp in length  
8097 8196: gap of 100 bp  
8197 12272: contig of 4076 bp in length  
12273 12372: gap of 100 bp  
12373 25914: contig of 13542 bp in length  
25915 26014: gap of 100 bp  
26015 34581: contig of 8567 bp in length  
34582 34681: gap of 100 bp  
34682 41378: contig of 6697 bp in length  
41379 41478: gap of 100 bp  
41479 70308: contig of 28830 bp in length  
70309 70408: gap of 100 bp  
70409 78606: contig of 8198 bp in length  
78607 78706: gap of 100 bp  
78707 91797: contig of 13091 bp in length  
91798 91897: gap of 100 bp  
91898 97614: contig of 5717 bp in length  
97615 97714: gap of 100 bp  
97715 107223: contig of 9509 bp in length  
107224 107323: gap of 100 bp  
107324 124557: contig of 17234 bp in length  
124558 124657: gap of 100 bp  
124658 148614: contig of 23957 bp in length  
148615 148714: gap of 100 bp  
148715 221924: contig of 73210 bp in length.

## FEATURES

## Source

1. 221924

/organism="Danio rerio"

/mol\_type="genomic DNA"

/db\_xref="taxon:7955"

/clone="DKFZ-244D13"

/clone\_idb="PantloKey"

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## ORIGIN

Query Match 88.9%; Score 16; DB 2; Length 221924;  
Best Local Similarity 87.5%; Pred. No. 5;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGUCGCGAGNNNNNN 18

Db 97605 GGTCTCGAGNNNNNN 97620

## RESULT 18

## AC068379

## LOCUS

AC068379 Homo sapiens chromosome 3 clone RP11-537116 map 3, LOW-PASS

## DEFINITION

SEQUENCE SAMPLING.

AC068379.4 GI:10945763

HTG; HTGS PHASE0.

KEYWORDS

## SOURCE

## ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 222876)

Homo sapiens chromosome 3, clone RP11-537116

## REFERENCE

## JOURNAL

## TITLE

## AUTHORS

Unpublished

2 (bases 1 to 222876)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

Anderson,S., Baldwin,J., Barna,N., Baerlein,V., Beda,F.,

Boguslavskiy,L., Bouckgalter,B., Brown,A., Burkett,G.,

Campione,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,

Collamore,A., Cooke,P., DeRellano,K., Dewar,K., Diaz,J.S.,

Dodge,S., Domingo,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,

Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,

Grand-Pierre,N., Grant,G., Hagos,B., Heatford,A., Horton,L.,

Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatae,A.,

Klein,J., LaRoque,K., Lamazara,R., Lander,E., Lebecky,J.,

Levine,R., Lieu,C., Liu,G., Locke,K., MacDonald,P., Margulis,N.,

McCarthy,M., McEwan,P., McGuirk,A., McKernan,K., McPherson,R.,

Meldrum,J., Menon,L., Mihova,T., Miranda,C., Miura,V., Morrow,J.,

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O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,

Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,

Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,

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fragment chain:4"

148715. 221924

/note="assembly fragment:01540.0"

TITLE  
JOURNAL  
COMMENT

Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,U.,  
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,D.,  
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
Young,G., Zainoun,U., Zimmer,A. and Zody,M.  
Submitted (02-MAY-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Oct 22, 2000 this sequence version replaced gi:10305231.  
All repeats were identified using RepeatMasker:  
Smit,A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WtBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
Project Information  
Center project name: L10217  
Center clone name: 537\_I\_16

NOTE: This record contains 278 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 728: contig of 728 bp in length  
\* 729 828: gap of 100 bp  
\* 829 1559: contig of 731 bp in length  
\* 1560 2382: gap of 100 bp  
\* 1660 2382: contig of 723 bp in length  
\* 2383 2482: gap of 100 bp  
\* 2483 3231: contig of 749 bp in length  
\* 3232 3331: gap of 100 bp  
\* 3332 4056: contig of 725 bp in length  
\* 4057 4156: gap of 100 bp  
\* 4157 4881: contig of 725 bp in length  
\* 4882 4981: gap of 100 bp  
\* 4982 5714: contig of 733 bp in length  
\* 5715 5814: gap of 100 bp  
\* 5815 6526: contig of 712 bp in length  
\* 6527 7343: gap of 100 bp  
\* 7344 7443: contig of 717 bp in length  
\* 7444 8173: contig of 730 bp in length  
\* 8174 8273: gap of 100 bp  
\* 8274 8980: contig of 707 bp in length  
\* 8981 9080: gap of 100 bp  
\* 9081 9788: contig of 708 bp in length  
\* 9789 9888: gap of 100 bp  
\* 9889 10620: contig of 732 bp in length  
\* 10621 10720: gap of 100 bp  
\* 10721 11471: contig of 751 bp in length  
\* 11472 11571: gap of 100 bp  
\* 11572 12317: contig of 746 bp in length  
\* 12318 12417: gap of 100 bp  
\* 12419 13148: contig of 731 bp in length  
\* 13149 13248: gap of 100 bp  
\* 13249 13973: contig of 725 bp in length  
\* 13974 14073: gap of 100 bp  
\* 14074 14812: contig of 735 bp in length  
\* 14813 14912: gap of 100 bp  
\* 14913 15633: contig of 721 bp in length  
\* 15634 15733: gap of 100 bp  
\* 15734 16475: contig of 742 bp in length  
\* 16476 16575: gap of 100 bp  
\* 16576 17284: contig of 703 bp in length  
\* 17285 17384: gap of 100 bp

17385 18078: contig of 694 bp in length  
\* 18079 18178: gap of 100 bp  
\* 18179 18888: contig of 710 bp in length  
\* 18889 18988: gap of 100 bp  
\* 18989 19732: contig of 744 bp in length  
\* 19733 19832: gap of 100 bp  
\* 19833 20559: contig of 727 bp in length  
\* 20560 20659: gap of 100 bp  
\* 20660 21391: contig of 732 bp in length  
\* 21392 21491: gap of 100 bp  
\* 21492 22218: contig of 727 bp in length  
\* 22219 23037: gap of 100 bp  
\* 23038 23137: gap of 100 bp  
\* 23138 23846: contig of 709 bp in length  
\* 23847 23946: gap of 100 bp  
\* 23947 24668: contig of 722 bp in length  
\* 24669 24768: gap of 100 bp  
\* 24769 25500: contig of 732 bp in length  
\* 25501 25600: gap of 100 bp  
\* 25601 26321: contig of 721 bp in length  
\* 26322 26421: gap of 100 bp  
\* 26422 27131: contig of 710 bp in length  
\* 27132 27231: gap of 100 bp  
\* 27232 27952: contig of 721 bp in length  
\* 27953 28052: gap of 100 bp  
\* 28053 28736: contig of 684 bp in length  
\* 28737 28836: gap of 100 bp  
\* 28837 29582: contig of 746 bp in length  
\* 29583 29682: gap of 100 bp  
\* 29683 30397: contig of 715 bp in length  
\* 30398 30497: gap of 100 bp  
\* 30498 31242: contig of 745 bp in length  
\* 31243 31342: gap of 100 bp  
\* 31343 32069: contig of 727 bp in length  
\* 32070 32169: gap of 100 bp  
\* 32170 32889: contig of 720 bp in length  
\* 32890 32989: gap of 100 bp  
\* 32990 33723: contig of 733 bp in length  
\* 33724 33823: gap of 100 bp  
\* 33824 34523: contig of 700 bp in length  
\* 34524 34623: gap of 100 bp  
\* 34624 35342: contig of 719 bp in length  
\* 35343 35442: gap of 100 bp  
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\* 36173 36272: gap of 100 bp  
\* 36273 36988: contig of 716 bp in length  
\* 36989 37088: gap of 100 bp  
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\* 41175 41907: contig of 733 bp in length  
\* 41908 42007: gap of 100 bp  
\* 42009 42726: contig of 719 bp in length  
\* 42727 42827: gap of 100 bp  
\* 42828 43579: contig of 753 bp in length  
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\* 43680 44374: contig of 635 bp in length  
\* 44375 44474: gap of 100 bp  
\* 44475 45180: contig of 706 bp in length  
\* 45181 45280: gap of 100 bp  
\* 45281 45979: contig of 699 bp in length  
\* 45980 46079: gap of 100 bp  
\* 46080 46821: contig of 742 bp in length  
\* 46822 46921: gap of 100 bp  
\* 46922 47645: contig of 724 bp in length

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* 47646 47745: gap of 100 bp
* 47746 48465: contig of 720 bp in length
* 48466 48565: gap of 100 bp
* 48566 49289: contig of 724 bp in length
* 49289 49389: gap of 100 bp
* 49389 50107: contig of 718 bp in length
* 50108 50207: gap of 100 bp
* 50208 50925: contig of 718 bp in length
* 50926 51025: gap of 100 bp
* 51026 51736: contig of 711 bp in length
* 51737 51836: gap of 100 bp
* 51837 52543: contig of 707 bp in length
* 52544 52643: gap of 100 bp
* 52644 53346: contig of 703 bp in length
* 53347 53446: gap of 100 bp
* 53447 54192: contig of 746 bp in length
* 54193 54292: gap of 100 bp
* 54293 55014: contig of 722 bp in length
* 55015 55114: gap of 100 bp
* 55115 55824: contig of 710 bp in length
* 55825 55924: gap of 100 bp
* 55925 56551: contig of 727 bp in length

Query Match      88.9%; Score 16; DB 2; Length 222876;
Best Local Similarity 87.5%; Pred. No. 5;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 GGUCCTGGAGNNNNNN 18
Db      61571 GGTCCTGGAGNNNNNN 61586

RESULT 19
LOCUS    BX927188      228022 bp      DNA      linear      HTG 10-OCT-2004
DEFINITION Danio rerio clone DKEX-264N13, WORKING DRAFT SEQUENCE, 9 unordered
            pieces.
ACCESSION BX927188.4 GI:41630180
VERSION   HTG_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS  Danio rerio (zebrafish)
SOURCE    Danio rerio
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
            1 (bases 1 to 228022)
            McLaren, S.
REFERENCE Direct Submission
            Submitted (08-OCT-2004) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
            On Feb 2, 2004 this sequence version replaced gi:41322817.
            ----- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: zfish-help@sanger.ac.uk
            ----- Project Information
            Center project name: ZK264N13
            ----- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Chemistry: dye-terminator; 100% of reads
            Consensus quality: 225138 bases at least Q40
            Consensus quality: 225502 bases at least Q30
            Consensus quality: 225841 bases at least Q20
            Insert size: 227222; sum-of-contigs
            Insert size: 221727; 4.7% error; agarose-fp
            Quality coverage: 8.04x in Q20 bases; sum-of-contigs Quality
            coverage: 8.28x in Q20 bases; agarose-fp
            -----
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 9 contigs. The true order of the pieces
            * is not known and their order in this sequence record is

```

```

* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 16758: contig of 16758 bp in length
* 16759 16858: gap of 100 bp
* 16859 20882: contig of 4024 bp in length
* 20883 20982: gap of 100 bp
* 20983 75976: contig of 54994 bp in length
* 75977 76076: gap of 100 bp
* 76077 82135: contig of 6059 bp in length
* 82136 82235: gap of 100 bp
* 82236 88535: contig of 7301 bp in length
* 88537 89637: gap of 100 bp
* 89637 101310: contig of 11674 bp in length
* 101311 101410: gap of 100 bp
* 101411 120443: contig of 19033 bp in length
* 120444 120543: gap of 100 bp
* 120544 168465: contig of 47923 bp in length
* 168467 168566: gap of 100 bp
* 168567 228022: contig of 59456 bp in length.
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ORIGIN
Query Match      88.9%; Score 16; DB 2; Length 228022;
Best Local Similarity 87.5%; Pred. No. 5;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 GGUCCTGGAGNNNNNN 18
Db      168457 GGTCCTGGAGNNNNNN 168472

RESULT 20
LOCUS    CR394526      256581 bp      DNA      linear      HTG 23-SEP-2004
DEFINITION Danio rerio clone DKEX-161J15, *** SEQUENCING IN PROGRESS ***
ACCESSION CR394526
VERSION   CR394526.3 GI:52626694
KEYWORDS  HTG; HTGS_PHASE1.

```

SOURCE  
ORGANISM Danio rerio (zebrafish)

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Actinopterygii; Neopterygii; Teleostei; Osteichthys;  
JOURNAL Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 256581)  
Sims, S.  
Direct Submission  
Submitted (22-SEP-2004) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
zf1sh-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
On Sep 23, 2004 this sequence version replaced gi:52546046.  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: zf1sh-help@sanger.ac.uk  
----- Project Information  
Center project name: XK161J15  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 100% of reads  
Consensus quality: 247852 bases at least Q40  
Consensus quality: 249576 bases at least Q30  
Consensus quality: 250950 bases at least Q20  
Insert size: 253981; sum-of-contigs  
Insert coverage: 254707; 1.2% error; agarose-fp  
Quality coverage: 6.48x in Q20 bases; sum-of-contigs Quality  
coverage: 7.43x in Q20 bases; agarose-fp  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 27 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of 'N', but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 3691: contig of 3691 bp in length  
\* 3692 3791: gap of 100 bp  
\* 3792 7092: contig of 3301 bp in length  
\* 7093 7192: gap of 100 bp  
\* 7193 9583: contig of 2391 bp in length  
\* 9584 9684: gap of 100 bp  
\* 9684 34302: contig of 24619 bp in length  
\* 34303 34402: gap of 100 bp  
\* 34403 50724: contig of 16322 bp in length  
\* 50725 50824: gap of 100 bp  
\* 50825 60657: contig of 9833 bp in length  
\* 60658 60757: gap of 100 bp  
\* 60758 78706: contig of 17949 bp in length  
\* 78707 78806: gap of 100 bp  
\* 78807 85343: contig of 6536 bp in length  
\* 85343 85443: gap of 100 bp  
\* 85443 88417: contig of 2975 bp in length  
\* 88418 88517: gap of 100 bp  
\* 88518 110986: contig of 22469 bp in length  
\* 110987 111086: gap of 100 bp  
\* 111087 153766: contig of 42680 bp in length  
\* 153767 153866: gap of 100 bp  
\* 153867 157321: contig of 3455 bp in length  
\* 157322 157421: gap of 100 bp  
\* 157422 162377: contig of 4956 bp in length  
\* 162378 162477: gap of 100 bp  
\* 162478 177129: contig of 14652 bp in length  
\* 177130 177229: gap of 100 bp  
\* 177230 180400: contig of 3171 bp in length  
\* 180401 180500: gap of 100 bp  
\* 180501 182753: contig of 2253 bp in length  
\* 182754 182853: gap of 100 bp  
\* 182854 187045: contig of 4192 bp in length  
\* 187046 187145: gap of 100 bp  
\* 187146 189392: contig of 2247 bp in length

FEATURES  
Source

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\* 189493 198638: contig of 9146 bp in length  
\* 198639 198738: gap of 100 bp  
\* 198739 209790: contig of 11052 bp in length  
\* 209791 209890: gap of 100 bp  
\* 209891 212263: contig of 2373 bp in length  
\* 212264 212363: gap of 100 bp  
\* 212364 214381: contig of 2018 bp in length  
\* 214382 214481: gap of 100 bp  
\* 214482 216967: contig of 2486 bp in length  
\* 216968 217067: gap of 100 bp  
\* 217068 219235: contig of 2168 bp in length  
\* 219236 219335: gap of 100 bp  
\* 219336 222890: contig of 3555 bp in length  
\* 222891 222990: gap of 100 bp  
\* 222991 238467: contig of 15477 bp in length  
\* 238468 238567: gap of 100 bp  
\* 238568 256581: contig of 18014 bp in length.  
Location/Qualifiers

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/clone\_id="DKX-161J15"  
/clone\_lib="DanioKey"  
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fragment\_chain:1"  
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7193. 9583  
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ORGANISM synthetic construct  
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1 Pedersen,M.L.  
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DEFINITION Sequence 11 from Patent WO2059357.  
ACCESSION AX528762

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KEYWORDS  
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ORGANISM synthetic construct  
REFERENCE  
1 Pedersen,M.L.  
Assay and kit for analyzing gene expression  
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DEFINITION Felis catus clone RP86-320J5, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC129972  
VERSION AC129972.1 GI:22267645  
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Birren,B., Nusbaum,C. and Lander,E.  
Felis catus, clone RP86-320J5  
Unpublished  
2 (bases 1 to 62373)  
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,  
Barra,N., Bastien,V., Bloom,T., Boguslavsky,L., Bouhglalter,B.,  
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Testaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,  
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,  
Zembek,L., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (16-AUG-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit,A.F.A. & Green,P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L24474

Center clone name: 320\_J\_5

NOTE: This record contains 77 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

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3128 3227: gap of 100 bp  
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6413 6512: gap of 100 bp  
6513 7215: contig of 703 bp in length  
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8024 8123: gap of 100 bp  
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9656 9755: gap of 100 bp  
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15317 15416: gap of 100 bp  
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AC101265.1 GI:17060040  
HTG: HTGS PHASE0.  
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1 (bases 1 to 72483)  
Birten, B., Linton, L., Nusbaum, C. and Lander, E.  
Mus musculus, clone RP23-101A12  
Unpublished  
2 (bases 1 to 72483)  
Birten, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,  
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Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,  
Zainoun, J., Zemek, L., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A. P. A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
Project Information  
Center project name: L1635  
Center clone name: 101\_A\_12

\* NOTE: This record contains 87 individual

\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allow  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
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* 36762 37490: contig of 729 bp in length
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Query Match
Best Local Similarity 83.3%; Score 15; DB 2; Length 72483;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GUCCUGAGAGNNNNNN 18
Db 16635 GTCCTGAGAGNNNNNN 16649

RESULT 25
AC115635.4
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Sequence split into 5 fragments
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AC115635.0 1 110000
AC115635.1 100001 210000
AC115635.2 200001 310000
AC115635.3 300001 410000
AC115635.4 400001 484720
Continuation (5 of 5) of AC115635 from base 400001 (AC115635 Rattus norvegicus clone CH2)

Query Match
Best Local Similarity 86.7%; Score 15; DB 2; Length 84720;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GUCCUGAGAGNNNNNN 18
Db 24354 GTCCTGAGAGNNNNNN 24368

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RESULT 26
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Fragment Name Begin End
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AC097780.1 100001 210000
AC097780.2 200001 310000
AC097780.3 300001 362708
LOCUS AC097780 362708 bp DNA linear HTG 26-SRP-2002
DEFINITION Rattus norvegicus clone CH230-39A11, *** SEQUENCING IN PROGRESS ***
ACCESSION AC097780
VERSION AC097780.5 GI:23322019
KEYWORDS HTG; HTGS PHASE1.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 362708)
REFERENCE
1 Muzny, D., Marie, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Albrooks, S., Amin, A., Angiano, D.,
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Hernandez, R., Hines, S., Hladun, S., L., Hodgson, A., Hughes, M.,

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Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowals, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenz, H., Louisa, L., Louisa, H., Lozada, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangun, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mchinery, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundaasa, M., Murphy, M., Nair, L., Nakevish, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwackemeh, O., Okwunonu, G., Olarunpasegun, A., Pal, S., Parke, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C.D., Smaje, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steime, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseca, D., Waldron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wiczysk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Unpublished  
2 (bases 1 to 362708)  
Worley, K.C.

Direct Submission  
Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 362708)  
Rat Genome Sequencing Consortium.

Direct Submission  
Submitted (26-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Sep 26, 2002 this sequence version replaced gi:21723602. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu

----- Project Information  
Center project name: GPEK  
Center clone name: CH230-39A11

----- Summary Statistics  
Assembly program: Phrap, version 0.990129  
Consensus quality: 288667 bases at least Q40  
Consensus quality: 300638 bases at least Q30  
Consensus quality: 307068 bases at least Q20  
Estimated insert size: 494733; sum-of-contigs estimation  
Quality coverage: 2x in Q20 bases; sum-of-contigs estimation

----- NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html))  
\* NOTE: This sequence may represent more than one clone.  
\* NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces

is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 38758: contig of 38758 bp in length  
38759: gap of unknown length  
38859: contig of 11836 bp in length  
38859: gap of unknown length  
50695: contig of 77416 bp in length  
50795: 128210: contig of 19432 bp in length  
128311: 147742: gap of unknown length  
147743: gap of unknown length  
147843: gap of unknown length  
147843: contig of 14044 bp in length  
161887: gap of unknown length  
161887: gap of unknown length  
173563: contig of 11577 bp in length  
173564: gap of unknown length  
173664: contig of 7042 bp in length  
180705: gap of unknown length  
180706: gap of unknown length  
180806: contig of 125597 bp in length  
306403: gap of unknown length  
306503: gap of unknown length  
317764: contig of 11261 bp in length  
317863: gap of unknown length  
317864: contig of 1625 bp in length  
319489: gap of unknown length  
319588: gap of unknown length  
319589: contig of 1618 bp in length  
321207: gap of unknown length  
321306: gap of unknown length  
322705: contig of 1399 bp in length  
322706: gap of unknown length  
322805: gap of unknown length  
325171: contig of 2366 bp in length  
325172: gap of unknown length  
325272: gap of unknown length  
326695: contig of 1424 bp in length  
326795: gap of unknown length  
328719: contig of 1924 bp in length  
328720: gap of unknown length  
328820: gap of unknown length  
334149: contig of 5330 bp in length  
334150: gap of unknown length  
334249: gap of unknown length  
337024: contig of 2775 bp in length  
337025: gap of unknown length  
337124: gap of unknown length  
337125: contig of 3858 bp in length  
340982: gap of unknown length  
340983: gap of unknown length  
341082: gap of unknown length  
341083: contig of 3437 bp in length  
344519: gap of unknown length  
344619: gap of unknown length  
344620: gap of unknown length  
353148: contig of 8529 bp in length  
353149: gap of unknown length  
353249: contig of 9460 bp in length.

Location/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-39A11"  
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38859. 40544  
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46606. 50694  
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128311. 130030  
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135593. 139818  
/note="wgs contig"  
145468. 147742  
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147843. 150010  
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150061. 153563  
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159654. 161886  
/note="wgs contig"  
161887. 164399  
/note="wgs contig"



OY 4 GUCCUGAGNNNNN 18  
 Db 128508 GTCTGAGAGNNNNN 128522  
 RESULT 28  
 AC105679/c  
 LOCUS  
 DEFINITION  
 Rattus norvegicus clone CH230-266N24, \*\*\* SEQUENCING IN PROGRESS  
 \*\*\* 4 unordered pieces.  
 AC105679  
 AC105679.3 GI:23603083  
 HTG: HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.  
 Rattus norvegicus (Norway rat)  
 SOURCE  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 161787)  
 REFERENCE  
 AUTHORS  
 Marzly,D,Marle, Metzker,M, Lee, Abramzon,S., Adams,C., Alder,J.,  
 Allen,C., Allen,H., Albrooke,S., Amin,A., Angiano,D.,  
 Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,  
 Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,  
 Blawato,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,  
 Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,  
 Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,  
 Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,  
 Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,  
 Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,  
 Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,  
 Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,  
 Egan,A., Ercotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,  
 Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,  
 Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,  
 Gbureggis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guvarva,W.,  
 Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,  
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 Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,  
 Lorenzowa,L., Louissege,H., Lozada,R.J., Lu,X., Ma,J.,  
 Maheswari,M., Mahindartne,M., Mahmood,M., Malloy,K., Mangum,A.,  
 Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,  
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 Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,  
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 Nankervis,C., Neal,D., Newton,G., Olarpunagoon,A., Pal,S., Parks,K.,  
 Pastenak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C.,  
 Plopper,F., Polidexter,A., Popovic,C., Primus,B., Pu,L.,  
 Pizzo,M., Quiroz,J., Rachin,E., Reeves,K., Regier,M.A., Reigh,R.,  
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 Rives,C., Rodkey,T., Rojase,A., Rose,M., Rose,R., Ruiz,S.J.,  
 Sanders,W., Savary,G., Scheier,S., Scott,G., Shaesman,S., Shen,H.,  
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 Valas,R., Vera,V., Villaseña,D., Waldron,L., Walker,B., Wang,D.,  
 Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,  
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 Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,  
 Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Zhou,D., von  
 Niederhausen,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,  
 Weinstock,G., and Gibbs,R.A.  
 TITLE  
 JOURNAL  
 2 (bases 1 to 161787)  
 REFERENCE  
 AUTHORS  
 Worley,K.C.

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Submitted (09-JAN-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 161787)  
 Rat Genome Sequencing Consortium.  
 Direct Submission  
 Submitted (11-OCT-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Oct 9, 2002 this sequence version replaced gi:21736578.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (http://www.hgsc.bcm.tmc.edu/projects/rac/). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented. The sequence  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
 table.

----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: http://www.hgsc.bcm.tmc.edu/  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: GNM0  
 Center clone name: CH230-266N24  
 ----- Summary Statistics  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 135243 bases at least Q40  
 Consensus quality: 138805 bases at least Q30  
 Consensus quality: 141344 bases at least Q20  
 Estimated insert size: 147765; sum-of-contigs estimation  
 Quality coverage: 5x in Q20 bases; sum-of-contigs estimation  
 -----  
 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 4 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preentered.  
 \* 1 153976: contig of 153976 bp in length  
 \* 153977 154076: gap of unknown length  
 \* 154077 156006: contig of 1930 bp in length  
 \* 156007 156106: gap of unknown length  
 \* 156107 158905: contig of 2799 bp in length  
 \* 158906 159005: gap of unknown length  
 \* 159006 161787: contig of 2782 bp in length.  
 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10116"  
 /clone="CH230-266N24"  
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 /note="wgs\_end\_extension  
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 clone\_end:Sp6  
 site:Indel  
 end\_sequence:RXAEH84TV"  
 ORIGIN  
 Query Match 83.3%; Score 15; DB 2; Length 161787;





TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Unpublished  
Direct Submission  
Submitted (08-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 222685)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Nov 20, 2002 this sequence version replaced gi:23267477.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly ('a' config-scaffold). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center -----  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information -----  
Project name: KBZU  
Center clone name: CH230-163G18  
----- Summary Statistics -----  
Assembly program: Phrap; version 0.990329  
Consensus quality: 186066 bases at least Q40  
Consensus quality: 190065 bases at least Q30  
Consensus quality: 192829 bases at least Q20  
Estimated insert size: 195607; sum-of-contigs estimation

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Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* See http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a "working draft" sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
*   1      124266: contig of 124266 bp in length
* *    124267     124366: gap of unknown length
* *    124367     146780: contig of 22414 bp in length
* *    146781     146880: gap of unknown length
* *    146881     222685: contig of 75805 bp in length.
*       Location/Qualifiers
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ORIGIN
Query Match           83.3%; Score 15; DB 2; Length 222685;
Bseq Local Similarity 86.7%; Pred. No. 22;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Oy         4 GUCCUGAGANNNNN 18
|::|||:|||
Db        180084 GTCTGTGAGNNNNN 180098
RESULT 31
ACLI2325
LOCUS              235173 bp      DNA               linear   HTG 15-NOV-2002
DEFINITION Rattus norvegicus clone CH230-119B23, *** SEQUENCING IN PROGRESS
ACCI2325
ACCESSION ACI12325
VERSION ACI12325.4 GI:25006559
KEYWORDS HTG; HTGS PHASE; HTGS DRAFT; HTGS_ENRICHD.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 235173)
Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Angiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
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Delgado,O., Benson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Bayes,K.,
Egan,A., Escoto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,

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Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebreyes, E., Geer, K., Gill, R., Grady, W., Guerra, M., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howell, S., Huliyil, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Kapachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovat, C., Kowals, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenz, H., Louie, L., Louie, H., Lozano, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmood, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Mlosojevic, A., Miner, G., Mirza, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nsamenang, O., Okunolu, G., Olariu, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Pioppe, F., Polidexter, A., Popovic, D., Pritts, E., Pu, L., Plazo, M., Quiroz, J., Rachin, B., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., J., Sanders, W., Saverly, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C.D., Smajls, D., Speed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tinney, A., Trejos, D., Umanli, K., Valas, R., Vera, V., Villanueva, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczek, R., Woodson, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstein, G., and Gibbs, R.A.

## TITLE

## JOURNAL

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## JOURNAL

## REFERENCE

## AUTHORS

## COMMENT

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Nov 15, 2002 this sequence version replaced gi:23267822.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

## ----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information

Center project name: GONS

Center clone name: CH230-119B23

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 196107 bases at least Q40

Consensus quality: 201820 bases at least Q30  
Consensus quality: 205011 bases at least Q20  
Estimated insert size: 193547; sum-of-contigs estimation  
Quality coverage: 5x in 920 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_drat\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_drat_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 5 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 224145: contig of 224145 bp in length  
\* 224146 224245: gap of unknown length  
\* 224246 228440: contig of 4195 bp in length  
\* 228441 228540: gap of unknown length  
\* 228541 230920: contig of 2380 bp in length  
\* 230921 231020: gap of unknown length  
\* 231021 232289: contig of 1269 bp in length  
\* 232290 232389: gap of unknown length  
\* 232390 235173: contig of 2784 bp in length.

## FEATURES

## source

1. 235173  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-119B23"  
12474. 13929  
/note="wgs\_contig"  
165157. 167210  
/note="wgs\_contig"  
184533. 185625  
/note="wgs\_contig"  
224246. 225932  
/note="wgs\_contig"

## ORIGIN

Query Match 83.3%; Score 15; DB 2; Length 235173;  
Best local Similarity 86.7%; Pred. No. 22;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

4 GUCCTGAGAGNNNNN 18

Db 173271 GTCTGTGAGNNNNN 173285

## RESULT 32

AX037200 27 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 112 from Patent WO0056923.  
AX037200

VERSION AX037200.1 GI:11226625

## KEYWORDS

## SOURCE

synthetic construct

other sequences; artificial sequences.

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## ACCESSION

## PATENT

## SIBSON

## ROSS

## GB

## CLATTERIDGE

## CANCER

## RES

## TRUST

## (GB)

## LOCATION/Qualifiers

## 1. 27

## /organism="synthetic construct"

## /mol\_type="unassigned DNA"

## /db\_xref="taxon:32630"

## /note="replacement plasmid sequence"

## ORIGIN

## Query Match

77.8%; Score 14; DB 6; Length 27;

Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGAGNNNNN 18  
:|||||  
Db 4 TCCTGAGAGNNNNN 17

## RESULT 33

AX037201 27 bp DNA linear PAT 16-NOV-2000  
LOCUS Sequence 113 from Patent WO056923.  
DEFINITION AX037201  
ACCESSION AX037201  
VERSION AX037201.1 GI:11226626  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE 1  
AUTHORS Sibson, R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 113 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source 1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

## ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 UCCUGAGAGNNNNN 18  
:|||||  
Db 4 TCCTGAGAGNNNNN 17

## RESULT 34

AX037202 27 bp DNA linear PAT 16-NOV-2000  
LOCUS Sequence 114 from Patent WO056923.  
DEFINITION AX037202  
ACCESSION AX037202  
VERSION AX037202.1 GI:11226627  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE 1  
AUTHORS Sibson, R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 114 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source 1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

## ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 UCCUGAGAGNNNNN 18  
:|||||  
Db -4 TCCTGAGAGNNNNN 17

## RESULT 35

AX037203 27 bp DNA linear PAT 16-NOV-2000  
LOCUS Sequence 115 from Patent WO056923.  
DEFINITION AX037203  
ACCESSION AX037203  
VERSION AX037203.1 GI:11226628  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE 1  
AUTHORS Sibson, R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 115 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source 1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

## ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 UCCUGAGAGNNNNN 18  
:|||||  
Db 4 TCCTGAGAGNNNNN 17

## RESULT 36

AX037204 27 bp DNA linear PAT 16-NOV-2000  
LOCUS Sequence 116 from Patent WO056923.  
DEFINITION AX037204  
ACCESSION AX037204  
VERSION AX037204.1 GI:11226629  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE 1  
AUTHORS Sibson, R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 116 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source 1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

## ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 UCCUGAGAGNNNNN 18  
:|||||  
Db 4 TCCTGAGAGNNNNN 17

## RESULT 37

AX037205 27 bp DNA linear PAT 16-NOV-2000  
LOCUS Sequence 117 from Patent WO056923.  
DEFINITION AX037205  
ACCESSION AX037205  
VERSION AX037205.1 GI:11226630  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE 1  
AUTHORS Sibson, R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 117 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source 1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 117 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source 1..27  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"  
ORIGIN  
Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 5 UCCUGAGAGNNNNNN 18  
:|||||  
4 TCCTGAGAGNNNNNN 17  
Db  
RESULT 38  
AX037206 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 118 from Patent WO0056923.  
ACCESSION AX037206  
VERSION AX037206.1 GI:11226631  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 118 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source 1..27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"  
ORIGIN  
Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 5 UCCUGAGAGNNNNNN 18  
:|||||  
4 TCCTGAGAGNNNNNN 17  
Db  
RESULT 39  
AX037207 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 119 from Patent WO0056923.  
ACCESSION AX037207  
VERSION AX037207.1 GI:11226632  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 119 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source 1..27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/note="replacement plasmid sequence"

ORIGIN  
Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 5 UCCUGAGAGNNNNNN 18  
:|||||  
4 TCCTGAGAGNNNNNN 17  
Db  
RESULT 40  
AX037208 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 120 from Patent WO0056923.  
ACCESSION AX037208  
VERSION AX037208.1 GI:11226633  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 120 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source 1..27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"  
ORIGIN  
Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 5 UCCUGAGAGNNNNNN 18  
:|||||  
4 TCCTGAGAGNNNNNN 17  
Db  
RESULT 41  
AX037209 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 121 from Patent WO0056923.  
ACCESSION AX037209  
VERSION AX037209.1 GI:11226634  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 121 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source 1..27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"  
ORIGIN  
Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 5 UCCUGAGAGNNNNNN 18

Db 4 TCCTGGAGNNNNNN 17

RESULT 42  
LOCUS AX037210 27 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 122 from Patent WO0056923.  
ACCESSION AX037210  
VERSION AX037210.1 GI:11226635  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1. .27  
/organism="synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
1. .27  
/mol\_type="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Gaps 0; Indels 0;

Qy 5 UCCUGAGNNNNNN 18  
Db 4 TCCTGGAGNNNNNN 17

RESULT 43  
LOCUS AX037211 27 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 123 from Patent WO0056923.  
ACCESSION AX037211  
VERSION AX037211.1 GI:11226636  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1. .27  
/organism="synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
SIBSON R. Genetic analysis  
Patent: WO 0056923-A 123 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Gaps 0; Indels 0;

Qy 5 UCCUGAGNNNNNN 18  
Db 4 TCCTGGAGNNNNNN 17

RESULT 44  
LOCUS AX037212 27 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 124 from Patent WO0056923.  
ACCESSION AX037212

VERSION AX037212.1 GI:11226637  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1. .27  
/organism="synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
SIBSON R. Genetic analysis  
Patent: WO 0056923-A 124 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Gaps 0; Indels 0;

Qy 5 UCCUGAGNNNNNN 18  
Db 4 TCCTGGAGNNNNNN 17

RESULT 45  
LOCUS AX037213 27 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 125 from Patent WO0056923.  
ACCESSION AX037213  
VERSION AX037213.1 GI:11226638  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1. .27  
/organism="synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
SIBSON R. Genetic analysis  
Patent: WO 0056923-A 125 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 27;  
Best Local Similarity 85.7%; Pred. No. 1.3e+02;  
Matches 12; Conservative 2; Mismatches 0; Gaps 0; Indels 0;

Qy 5 UCCUGAGNNNNNN 18  
Db 4 TCCTGGAGNNNNNN 17

RESULT 46  
LOCUS AX037214 27 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 126 from Patent WO0056923.  
ACCESSION AX037214  
VERSION AX037214.1 GI:11226639  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
1. .27  
/organism="synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
SIBSON R. Genetic analysis  
Patent: WO 0056923-A 126 28-SEP-2000;

FEATURES SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
 source Location/Qualifiers  
 1. 27  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="replacement plasmid sequence"

ORIGIN  
 Query Match 77.8% Score 14; DB 6; Length 27;  
 Best Local Similarity 85.7% Pred. No. 1.3e+02;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGANNNNNN 18  
 Db 4 TCCTGGAGANNNNNN 17

RESULT 47  
 AX037215 27 bp DNA linear PAT 16-NOV-2000  
 LOCUS Sequence 127 from Patent WO0056923.  
 AX037215  
 VERSION AX037215.1 GI:11226640  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM other sequences; artificial sequences.

REFERENCE 1  
 Sibson,R.  
 TITLE Genetic analysis  
 JOURNAL Patent: WO 0056923-A 127 28-SEP-2000;  
 SIBSON,ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
 FEATURES  
 source Location/Qualifiers  
 1. 27  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="replacement plasmid sequence"

ORIGIN  
 Query Match 77.8% Score 14; DB 6; Length 27;  
 Best Local Similarity 85.7% Pred. No. 1.3e+02;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGANNNNNN 18  
 Db 4 TCCTGGAGANNNNNN 17

RESULT 48  
 AC100909 49799 bp DNA linear HTG 23-NOV-2001  
 LOCUS Mus musculus clone RP23-70124, LOW-PASS SEQUENCE SAMPLING.  
 AC100909  
 VERSION AC100909.1 GI:17059683  
 KEYWORDS HTG: HTGS PHASE0.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 49799)  
 Birren,B., Linton,L., Nuebaum,C. and Lander,E.  
 Mus musculus, clone RP23-70124  
 Unpublished  
 2 (bases 1 to 49799)  
 Birren,B., Linton,L., Nuebaum,C., Lander,E., Ali,A., Allen,N.,  
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Bouhgalter,B.,  
 Brown,A., Camarata,J., Campolino,A., Chang,J., Chazaro,B.,  
 Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,  
 Cooke,P., Dearellano,K., Dewar,K., Diaz,U.S., Dodge,S., Fero,S.,  
 Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gaidyna,S.,  
 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,

TITLE  
 JOURNAL  
 COMMENT  
 Hagos,B., Headford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,  
 Jones,C., Kamat,A., Karatas,A., Kells,C., Labocque,K.,  
 Iamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,  
 MacLennan,C., Macdonald,P., Major,J., Margulis,N., Matthews,C.,  
 McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrum,J.,  
 Meneses,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,  
 Nordu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,  
 Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,  
 Raymond,C., Rella,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,  
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schnupack,R.,  
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
 Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,  
 Topham,K., Travers,M., Travis,N., Triggillo,D., Vassiliev,H.,  
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 All repeats were identified using RepeatMasker:  
 Smit,A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RW/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: MIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L14550  
 Center clone name: 70\_1\_24  
 -----  
 \* NOTE: This record contains 61 individual  
 \* sequencing reads that have not been assembled into  
 \* contigs. Runs of N are used to separate the reads  
 \* and the order in which they appear is completely  
 \* arbitrary. Low-pass sequence sampling is useful for  
 \* identifying clones that may be gene-rich and allows  
 \* overlap relationships among clones to be deduced.  
 \* However, it should not be assumed that this clone  
 \* will be sequenced to completion. In the event that  
 \* the record is updated, the accession number will  
 \* be preserved.  
 \* 1  
 \* 673 772: contig of 672 bp in length  
 \* 773 772: gap of 100 bp  
 \* 1484 772: contig of 712 bp in length  
 \* 1485 772: gap of 100 bp  
 \* 1585 772: contig of 707 bp in length  
 \* 2291 772: contig of 707 bp in length  
 \* 2392 772: gap of 100 bp  
 \* 3095 772: contig of 704 bp in length  
 \* 3096 772: gap of 100 bp  
 \* 3196 772: contig of 707 bp in length  
 \* 3902 772: contig of 707 bp in length  
 \* 3903 772: gap of 100 bp  
 \* 4003 772: contig of 730 bp in length  
 \* 4733 772: gap of 100 bp  
 \* 4833 772: contig of 728 bp in length  
 \* 5561 772: gap of 100 bp  
 \* 5661 772: contig of 697 bp in length  
 \* 6358 772: gap of 100 bp  
 \* 6457 772: contig of 714 bp in length  
 \* 6458 772: gap of 100 bp  
 \* 7171 772: contig of 714 bp in length  
 \* 7172 772: gap of 100 bp  
 \* 8003 772: contig of 732 bp in length  
 \* 8004 772: gap of 100 bp  
 \* 8104 772: contig of 714 bp in length  
 \* 8106 772: gap of 100 bp  
 \* 8817 772: contig of 726 bp in length  
 \* 8818 772: gap of 100 bp  
 \* 8918 772: contig of 725 bp in length  
 \* 9643 772: gap of 100 bp  
 \* 9743 772: contig of 725 bp in length  
 \* 10468 772: gap of 100 bp  
 \* 10568 772: contig of 726 bp in length  
 \* 11294 772: gap of 100 bp  
 \* 11394 772: contig of 728 bp in length  
 \* 12122 772: gap of 100 bp  
 \* 12222 772: contig of 690 bp in length  
 \* 12912 772: gap of 100 bp

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* 13012 13704: contig of 693 bp in length
* 13705 13804: gap of 100 bp
* 13805 14518: contig of 714 bp in length
* 14519 14618: gap of 100 bp
* 14619 15315: contig of 697 bp in length
* 15316 15415: gap of 100 bp
* 15416 16136: contig of 721 bp in length
* 16137 16236: gap of 100 bp
* 16237 16953: contig of 717 bp in length
* 16954 17053: gap of 100 bp
* 17054 17775: contig of 722 bp in length
* 17776 17875: gap of 100 bp
* 17876 18608: contig of 733 bp in length
* 18609 18708: gap of 100 bp
* 18709 19430: contig of 722 bp in length
* 19431 19530: gap of 100 bp
* 19531 20240: contig of 710 bp in length
* 20241 20340: gap of 100 bp
* 20341 21052: contig of 712 bp in length
* 21053 21152: gap of 100 bp
* 21153 21872: contig of 720 bp in length
* 21873 21972: gap of 100 bp
* 21973 22694: contig of 722 bp in length
* 22695 22794: gap of 100 bp
* 22795 23520: contig of 726 bp in length
* 23521 23620: gap of 100 bp
* 23621 24348: contig of 728 bp in length
* 24349 24448: gap of 100 bp
* 24449 25178: contig of 730 bp in length
* 25179 25278: gap of 100 bp
* 25279 25954: contig of 676 bp in length
* 25955 26054: gap of 100 bp
* 26055 26767: contig of 713 bp in length
* 26768 26867: gap of 100 bp
* 26868 27577: contig of 710 bp in length
* 27578 27677: gap of 100 bp
* 27678 28382: contig of 705 bp in length
* 28383 28482: gap of 100 bp
* 28483 29191: contig of 709 bp in length
* 29192 29291: gap of 100 bp
* 29292 30008: contig of 717 bp in length
* 30009 30108: gap of 100 bp
* 30109 30828: contig of 720 bp in length
* 30829 30928: gap of 100 bp
* 30929 31656: contig of 728 bp in length
* 31657 31756: gap of 100 bp
* 31757 32483: contig of 727 bp in length
* 32484 32583: gap of 100 bp
* 32584 33319: contig of 736 bp in length
* 33320 33419: gap of 100 bp
* 33420 34136: contig of 717 bp in length
* 34137 34236: gap of 100 bp
* 34237 34954: contig of 718 bp in length
* 34955 35054: gap of 100 bp
* 35055 35765: contig of 711 bp in length
* 35766 35865: gap of 100 bp
* 35866 36588: contig of 723 bp in length
* 36589 36688: gap of 100 bp
* 36689 37414: contig of 726 bp in length
* 37415 37514: gap of 100 bp
* 37515 38246: contig of 732 bp in length
* 38247 38346: gap of 100 bp
* 38347 39063: contig of 717 bp in length
* 39064 39163: gap of 100 bp
* 39164 39862: contig of 699 bp in length
* 39863 39962: gap of 100 bp
* 39963 40680: contig of 718 bp in length
* 40681 40780: gap of 100 bp
* 40781 41486: contig of 706 bp in length
* 41487 41586: gap of 100 bp
* 41587 42310: contig of 724 bp in length
* 42311 42410: gap of 100 bp
* 42411 43135: contig of 725 bp in length

```

```

* 43136 43235: gap of 100 bp
* 43236 43963: contig of 728 bp in length
* 43964 44063: gap of 100 bp
* 44064 44797: contig of 734 bp in length
* 44798 44897: gap of 100 bp
* 44898 45635: contig of 738 bp in length
* 45636 45735: gap of 100 bp
* 45736 46475: contig of 740 bp in length
* 46476 46575: gap of 100 bp
* 46576 47296: contig of 721 bp in length
* 47297 47396: gap of 100 bp
* 47397 48125: contig of 729 bp in length
* 48126 48225: gap of 100 bp
* 48226 48953: contig of 728 bp in length
* 48954 49053: gap of 100 bp
* 49054 49799: contig of 746 bp in length.

FEATURES
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      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /db_xref="taxon:10090"
      /clone="RP23-70124"
      /clone_1kb="RP23-70124"
      /clone_1kb="RP23-70124"

ORIGIN
  Query Match      77.8%; Score 14; DB 2; Length 49799;
  Best Local Similarity 85.7%; Pred. No. 1e+02;
  Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy      5 UCCUGAGAGNNNNNN 18
Db      45628 TCCTGAGAGNNNNNN 45641

RESULT 49
AC100333
LOCUS      55662 bp      DNA      linear      HTG 22-NOV-2001
DEFINITION Mus musculus clone RP23-126H4, LOW-PASS SEQUENCE SAMPLING.
ACCESSION  AC100333.1 GI:17047699
VERSION     AC100333.1 GI:17047699
KEYWORDS    HTG; HTGS PHASE0.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 55662)
            Birren, B., Linton, L., Nuebaum, C. and Lander, E.
            Mus musculus, clone RP23-126H4
            Unpublished
            2 (bases 1 to 55662)
            Birren, B., Linton, L., Nuebaum, C., Lander, E., Ali, A., Allen, N.,
            Anderson, S., Barina, N., Bastien, V., Boguslavsky, L., Bouckgalter, B.,
            Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazarov, B.,
            Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
            Cooke, P., D'Arellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
            Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
            Ginde, S., Gord, S., Goyette, W., Graham, L., Grand-Pierre, N.,
            Hagos, B., Hatford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
            Jones, C., Kamat, A., Karatas, A., Kells, C., Labrecque, K.,
            Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,
            Maclean, C., MacDonald, P., Major, J., Marguis, N., Matthews, C.,
            McCarthy, M., McEwan, P., McKernan, K., Mcpheeters, R., Meldrum, J.,
            Meneses, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
            Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
            Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
            Raymond, C., Retter, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
            Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R.,
            Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
            Strauss, N., Sudramanian, A., Talamas, J., Teste, S., Theodore, J.,
            Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,
            Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
            Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
            Direct Submission

```

## JOURNAL

## COMMENT

Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

## ----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www.seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L15120

Center clone name: 126\_H\_4

\* NOTE: This record contains 68 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 740: contig of 740 bp in length  
\* 741 840: gap of 100 bp in length  
\* 841 1580: contig of 740 bp in length  
\* 1581 1680: gap of 100 bp in length  
\* 1681 2386: contig of 706 bp in length  
\* 2387 2486: gap of 100 bp in length  
\* 2487 3189: contig of 703 bp in length  
\* 3190 3289: gap of 100 bp in length  
\* 3290 3996: contig of 707 bp in length  
\* 3997 4096: gap of 100 bp in length  
\* 4097 4829: contig of 733 bp in length  
\* 4830 4929: gap of 100 bp in length  
\* 4930 5658: contig of 729 bp in length  
\* 5659 5759: gap of 100 bp in length  
\* 5759 6497: contig of 739 bp in length  
\* 6498 6597: gap of 100 bp in length  
\* 6598 7326: contig of 729 bp in length  
\* 7327 7427: gap of 100 bp in length  
\* 7427 8125: contig of 699 bp in length  
\* 8126 8225: gap of 100 bp in length  
\* 8226 8939: contig of 714 bp in length  
\* 8940 9039: gap of 100 bp in length  
\* 9040 9747: contig of 708 bp in length  
\* 9748 9847: gap of 100 bp in length  
\* 9848 10664: contig of 717 bp in length  
\* 10665 11396: gap of 100 bp in length  
\* 11397 11496: contig of 732 bp in length  
\* 11497 12177: contig of 681 bp in length  
\* 12178 12277: gap of 100 bp in length  
\* 12278 13011: contig of 734 bp in length  
\* 13012 13112: gap of 100 bp in length  
\* 13112 13854: contig of 743 bp in length  
\* 13855 13954: gap of 100 bp in length  
\* 13955 14689: contig of 735 bp in length  
\* 14690 14789: gap of 100 bp in length  
\* 14790 15484: contig of 695 bp in length  
\* 15485 15585: gap of 100 bp in length  
\* 15586 16282: contig of 698 bp in length  
\* 16283 16383: gap of 100 bp in length  
\* 16384 17083: contig of 701 bp in length  
\* 17084 17183: gap of 100 bp in length  
\* 17184 17883: contig of 700 bp in length  
\* 17884 17983: gap of 100 bp in length  
\* 17984 18713: contig of 730 bp in length  
\* 18714 18814: gap of 100 bp in length  
\* 18814 19552: contig of 739 bp in length  
\* 19553 19652: gap of 100 bp in length

19653 20349: contig of 697 bp in length  
\* 20350 20449: gap of 100 bp in length  
\* 20450 21188: contig of 739 bp in length  
\* 21189 21288: gap of 100 bp in length  
\* 21289 22032: contig of 744 bp in length  
\* 22033 22133: gap of 100 bp in length  
\* 22134 22933: contig of 701 bp in length  
\* 22934 23645: gap of 100 bp in length  
\* 23646 23746: contig of 712 bp in length  
\* 23746 24454: gap of 100 bp in length  
\* 24455 24554: contig of 709 bp in length  
\* 24555 25280: gap of 100 bp in length  
\* 25281 25380: contig of 726 bp in length  
\* 25381 26121: gap of 100 bp in length  
\* 26122 26221: contig of 741 bp in length  
\* 26222 26968: gap of 100 bp in length  
\* 26969 27069: contig of 747 bp in length  
\* 27069 27811: gap of 100 bp in length  
\* 27812 27911: contig of 743 bp in length  
\* 27912 28611: gap of 100 bp in length  
\* 28612 28711: contig of 700 bp in length  
\* 28712 29461: gap of 100 bp in length  
\* 29462 29561: contig of 750 bp in length  
\* 29562 30303: gap of 100 bp in length  
\* 30304 30403: contig of 742 bp in length  
\* 30404 31117: gap of 100 bp in length  
\* 31118 31217: contig of 714 bp in length  
\* 31218 31936: gap of 100 bp in length  
\* 31937 32036: contig of 719 bp in length  
\* 32037 32758: gap of 100 bp in length  
\* 32759 32858: contig of 722 bp in length  
\* 32859 33583: gap of 100 bp in length  
\* 33584 33684: contig of 725 bp in length  
\* 33685 34383: gap of 100 bp in length  
\* 34384 34484: contig of 700 bp in length  
\* 34484 35225: gap of 100 bp in length  
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\* 35326 36026: gap of 100 bp in length  
\* 36027 36126: contig of 701 bp in length  
\* 36127 36859: gap of 100 bp in length  
\* 36860 36959: contig of 733 bp in length  
\* 36960 37674: gap of 100 bp in length  
\* 37675 37775: contig of 715 bp in length  
\* 37775 38489: gap of 100 bp in length  
\* 38490 38589: contig of 713 bp in length  
\* 38590 39299: gap of 100 bp in length  
\* 39300 39399: contig of 710 bp in length  
\* 39400 40103: gap of 100 bp in length  
\* 40104 40203: contig of 704 bp in length  
\* 40204 40928: gap of 100 bp in length  
\* 40929 41028: contig of 725 bp in length  
\* 41029 41761: gap of 100 bp in length  
\* 41762 41861: contig of 733 bp in length  
\* 41862 42589: gap of 100 bp in length  
\* 42590 42689: contig of 728 bp in length  
\* 42690 43426: gap of 100 bp in length  
\* 43427 43526: contig of 737 bp in length  
\* 43527 44206: gap of 100 bp in length  
\* 44207 44306: contig of 680 bp in length  
\* 44307 45039: gap of 100 bp in length  
\* 45040 45139: contig of 733 bp in length  
\* 45140 45834: gap of 100 bp in length  
\* 45835 45934: contig of 695 bp in length  
\* 45935 46618: gap of 100 bp in length  
\* 46619 46718: contig of 684 bp in length  
\* 46719 47442: gap of 100 bp in length  
\* 47443 47542: contig of 724 bp in length  
\* 47543 48376: gap of 100 bp in length  
\* 48377 48376: contig of 734 bp in length  
\* 48377 49111: gap of 100 bp in length  
\* 49112 49211: contig of 735 bp in length  
\* 49212 49953: gap of 100 bp in length  
\* 49953 49953: contig of 742 bp in length



```

* 49954 50053: gap of 100 bp
* 50054 50757: contig of 704 bp in length
* 50758 50857: gap of 100 bp
* 50858 51593: contig of 736 bp in length
* 51594 51693: gap of 100 bp
* 51694 52397: contig of 703 bp in length
* 52397 52496: gap of 100 bp
* 52497 53205: contig of 709 bp in length
* 53206 53305: gap of 100 bp
* 53306 54007: contig of 701 bp in length
* 54007 54106: gap of 100 bp
* 54107 54835: contig of 729 bp in length
* 54836 54935: gap of 100 bp
* 54936 55662: contig of 727 bp in length.
FEATURES
    source
        Location/Qualifiers
            1..55662
                /organism="Mus musculus"
Query Match      77.8%; Score 14; DB 2; Length 55662;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 5 UCCUGAGAGNNNNNN 18
Db 11389 TCCTGAGAGNNNNNN 11402
RESULT 50
AC100339
LOCUS      AC100339      59918 bp      DNA      linear      HTG 22-NOV-2001
DEFINITION Mus musculus clone RP23-127B24, LOW-PASS SEQUENCE SAMPLING.
ACCESSION  AC100339
VERSION     AC100339.1 GI:17047705
KEYWORDS   HTG; HTGS_PHASED.
SOURCE     Mus musculus
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 59918)
AUTHORS    Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N.,
            Anderson,S., Bartha,N., Baeten,V., Boguslavsky,L., Bourkhalter,B.,
            Brown,A., Camarata,J., Campoliano,A., Chang,J., Chazaro,B.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
            Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
            Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
            Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
            Hagob,B., Heatford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
            Jones,C., Kamat,A., Karatas,A., Kells,C., Lacroque,K.,
            Lamasares,R., Landers,T., Lehoczy,J., Levine,N., Matthews,C.,
            Maclean,C., MacDonald,P., Major,J., Marguis,N., McCarthy,M.,
            McEwan,P., McKernan,K., McPheters,R., Meidrim,J.,
            Menes,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
            Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
            Oliver,J., Peterson,K., Phunhahang,P., Pierre,N., Pollard,V.,
            Raymond,C., Retter,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
            Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupbach,R.,
            Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Strauss,N., Subramanian,A., Talamae,J., Teefaye,S., Theodore,J.,
            Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,
            Vei,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
            Zaitoun,J., Zembek,L., Zimmer,A. and Zody,M.
JOURNAL    Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT    All repeats were identified using RepeatMasker:
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            Center: Whitehead Institute/ MIT Center for Genome Research

```

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Center code: WTRB
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L15132
Center clone name: 127_B_24
* NOTE: This record contains 73 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1 701: contig of 701 bp in length
702 801: gap of 100 bp
802 1516: contig of 715 bp in length
1517 1616: gap of 100 bp
1617 2343: contig of 727 bp in length
2344 2443: gap of 100 bp
2443 3177: contig of 734 bp in length
3178 3277: gap of 100 bp
3277 4007: contig of 730 bp in length
4008 4107: gap of 100 bp
4107 4834: contig of 727 bp in length
4835 4934: gap of 100 bp
4935 5674: contig of 740 bp in length
5675 5774: gap of 100 bp
5775 6482: contig of 708 bp in length
6483 6582: gap of 100 bp
6583 7293: contig of 711 bp in length
7294 7393: gap of 100 bp
7394 8131: contig of 738 bp in length
8132 8231: gap of 100 bp
8232 8957: contig of 726 bp in length
8958 9057: gap of 100 bp
9058 9789: contig of 732 bp in length
9790 9889: gap of 100 bp
9890 10623: contig of 733 bp in length
10623 10723: gap of 100 bp
10723 11428: contig of 706 bp in length
11429 11528: gap of 100 bp
11529 12116: contig of 588 bp in length
12117 12216: gap of 100 bp
12217 12935: contig of 719 bp in length
12936 13035: gap of 100 bp
13036 13754: contig of 719 bp in length
13755 13854: gap of 100 bp
13855 14594: contig of 740 bp in length
14595 14694: gap of 100 bp
14695 15421: contig of 727 bp in length
15422 15521: gap of 100 bp
15522 16272: contig of 751 bp in length
16273 16372: gap of 100 bp
16373 17116: contig of 744 bp in length
17117 17216: gap of 100 bp
17217 17960: contig of 744 bp in length
17961 18060: gap of 100 bp
18061 18783: contig of 723 bp in length
18784 18883: gap of 100 bp
18884 19602: contig of 719 bp in length
19603 19702: gap of 100 bp
19703 20433: contig of 731 bp in length
20434 20533: gap of 100 bp
20534 21285: contig of 732 bp in length
21286 21365: gap of 100 bp
21366 22083: contig of 718 bp in length
22084 22183: gap of 100 bp
22184 22910: contig of 727 bp in length

```

```

* 22911 23010: gap of 100 bp
* 23011 23740: contig of 730 bp in length
* 23741 23840: gap of 100 bp
* 23841 24589: contig of 749 bp in length
* 24590 24689: gap of 100 bp
* 24690 25411: contig of 722 bp in length
* 25412 25511: gap of 100 bp
* 25512 26241: contig of 730 bp in length
* 26242 26341: gap of 100 bp
* 26342 26892: contig of 551 bp in length
* 26893 27716: contig of 724 bp in length
* 27717 28535: contig of 100 bp in length
* 28537 28636: gap of 100 bp
* 28637 29351: contig of 715 bp in length
* 29352 29451: gap of 100 bp
* 30183 30282: contig of 731 bp in length
* 30283 31031: gap of 100 bp
* 31032 31131: contig of 749 bp in length
* 31132 31864: contig of 733 bp in length
* 31865 32700: contig of 736 bp in length
* 31965 32701: gap of 100 bp
* 32701 32800: gap of 100 bp
* 32801 33537: contig of 737 bp in length
* 33538 33637: gap of 100 bp
* 33638 34375: contig of 738 bp in length
* 34376 34475: gap of 100 bp
* 34476 35215: contig of 740 bp in length
* 35216 35315: gap of 100 bp
* 35316 36035: contig of 720 bp in length
* 36036 36135: gap of 100 bp
* 36136 36859: contig of 724 bp in length
* 36860 36959: gap of 100 bp
* 36960 37681: contig of 722 bp in length
* 37682 37781: gap of 100 bp
* 37782 38521: contig of 740 bp in length
* 38522 38621: gap of 100 bp
* 38622 39345: contig of 725 bp in length
* 39346 39445: gap of 100 bp
* 39447 40183: contig of 737 bp in length
* 40184 40283: gap of 100 bp
* 40284 40990: contig of 707 bp in length
* 40991 41090: gap of 100 bp
* 41091 41830: contig of 740 bp in length
* 41831 41930: gap of 100 bp
* 41931 42669: contig of 739 bp in length
* 42670 42769: gap of 100 bp
* 42770 43503: contig of 734 bp in length
* 43504 43603: gap of 100 bp
* 43604 44317: contig of 714 bp in length
* 44318 44417: gap of 100 bp
* 44419 45132: contig of 715 bp in length
* 45133 45232: gap of 100 bp
* 45233 45954: contig of 722 bp in length
* 45955 46054: gap of 100 bp
* 46055 46768: contig of 714 bp in length
* 46769 46868: gap of 100 bp
* 46869 47613: contig of 745 bp in length
* 47614 47713: gap of 100 bp
* 47714 48455: contig of 742 bp in length
* 48456 48555: gap of 100 bp
* 48556 49289: contig of 734 bp in length
* 49290 49389: gap of 100 bp
* 49390 50129: contig of 740 bp in length
* 50130 50229: gap of 100 bp
* 50230 50969: contig of 740 bp in length
* 50970 51069: gap of 100 bp
* 51070 51800: contig of 731 bp in length
* 51801 51900: gap of 100 bp
* 51901 52622: contig of 722 bp in length
* 52623 52722: gap of 100 bp

```

```

Query Match      77.8%   Score 14; DB 2; Length 59918;
Best Local Similarity 85.7%   Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Cy 5 UCCUGAGGNNNNNN 18
Db 4827 TCCTGAGNNNNNN 4840

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RESULT 51
LOCUS
AC125441
DEFINITION
Mus musculus clone RP24-487N17, LOW-PASS SEQUENCE SAMPLING.
ACCESSION
AC125441
VERSION
AC125441.1 GI:21591995
KEYWORDS
HTG; HTGS PHASE0.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 62676)
AUTHORS
Birren, B., Nussbaum, C. and Lander, E.
TITLE
Mus musculus, clone RP24-487N17
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 62676)
AUTHORS
Birren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B.,
Cammarata, U., Chang, J., Charazro, B., Choepel, Y., Collamore, A.,
Cook, A., Cooke, P., DeArillano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagob, B.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Kartas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
McCarthy, M., Meldrum, J., Menues, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,
O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schauer, S., Schuback, R., Sejanovic, N., Talama, J.,
Smith, C., Spencer, B., Strange-Rhmann, N., Stojanovic, N., Talamas, J.,
Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Zemek, L., Zimmer, A. and Zody, M.
TITLE
Direct Submission
JOURNAL
Submitted (26-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

```

```

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L26703
Center clone name: 487_N_17

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* NOTE: This record contains 74 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely

```

\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

\* 1 712: contig of 712 bp in length  
\* 713 812: gap of 100 bp  
\* 813 1582: contig of 770 bp in length  
\* 1583 1682: gap of 100 bp  
\* 1683 2455: contig of 773 bp in length  
\* 2456 2555: gap of 100 bp  
\* 2556 3265: contig of 711 bp in length  
\* 3267 3365: gap of 100 bp  
\* 3367 4088: contig of 722 bp in length  
\* 4089 4188: gap of 100 bp  
\* 4189 4919: contig of 731 bp in length  
\* 4920 5019: gap of 100 bp  
\* 5020 5775: contig of 756 bp in length  
\* 5776 5875: gap of 100 bp  
\* 5876 6639: contig of 764 bp in length  
\* 6640 6739: gap of 100 bp  
\* 6740 7502: contig of 763 bp in length  
\* 7503 7602: gap of 100 bp  
\* 7603 8356: contig of 754 bp in length  
\* 8357 8456: gap of 100 bp  
\* 8457 9194: contig of 738 bp in length  
\* 9195 9294: gap of 100 bp  
\* 9295 10048: contig of 754 bp in length  
\* 10049 10148: gap of 100 bp  
\* 10149 10876: contig of 728 bp in length  
\* 10877 10976: gap of 100 bp  
\* 10977 11744: contig of 768 bp in length  
\* 11745 11844: gap of 100 bp  
\* 11845 12609: contig of 765 bp in length  
\* 12610 12709: gap of 100 bp  
\* 12710 13425: contig of 716 bp in length  
\* 13426 13525: gap of 100 bp  
\* 13526 14296: contig of 771 bp in length  
\* 14297 14396: gap of 100 bp  
\* 14397 15143: contig of 747 bp in length  
\* 15144 15243: gap of 100 bp  
\* 15244 15970: contig of 727 bp in length  
\* 15971 16070: gap of 100 bp  
\* 16071 16811: contig of 741 bp in length  
\* 16812 16911: gap of 100 bp  
\* 16912 17636: contig of 725 bp in length  
\* 17637 17736: gap of 100 bp  
\* 17737 18489: contig of 753 bp in length  
\* 18490 18589: gap of 100 bp  
\* 18590 19347: contig of 758 bp in length  
\* 19348 19447: gap of 100 bp  
\* 19448 20212: contig of 765 bp in length  
\* 20213 20312: gap of 100 bp  
\* 20313 21021: contig of 709 bp in length  
\* 21022 21121: gap of 100 bp  
\* 21122 21890: contig of 769 bp in length  
\* 21891 21990: gap of 100 bp  
\* 21991 22718: contig of 728 bp in length  
\* 22719 22818: gap of 100 bp  
\* 22819 23553: contig of 735 bp in length  
\* 23554 23653: gap of 100 bp  
\* 23654 24397: contig of 744 bp in length  
\* 24398 24497: gap of 100 bp  
\* 24498 25256: contig of 759 bp in length  
\* 25257 25356: gap of 100 bp  
\* 25357 26104: contig of 748 bp in length  
\* 26105 26204: gap of 100 bp  
\* 26205 26965: contig of 761 bp in length  
\* 26966 27065: gap of 100 bp  
\* 27066 27818: contig of 753 bp in length  
\* 27819 27918: gap of 100 bp

\* 27919 28681: contig of 763 bp in length  
\* 28682 28781: gap of 100 bp  
\* 28782 29492: contig of 711 bp in length  
\* 29493 29592: gap of 100 bp  
\* 29593 30353: contig of 761 bp in length  
\* 30354 30453: gap of 100 bp  
\* 30454 31230: contig of 777 bp in length  
\* 31231 31331: gap of 100 bp  
\* 31331 32081: contig of 751 bp in length  
\* 32082 32181: gap of 100 bp  
\* 32182 32897: contig of 716 bp in length  
\* 32898 32997: gap of 100 bp  
\* 32998 33718: contig of 721 bp in length  
\* 33719 33818: gap of 100 bp  
\* 33819 34565: contig of 747 bp in length  
\* 34566 34665: gap of 100 bp  
\* 34666 35410: contig of 745 bp in length  
\* 35411 35510: gap of 100 bp  
\* 35511 36277: contig of 767 bp in length  
\* 36278 36377: gap of 100 bp  
\* 36378 37130: contig of 753 bp in length  
\* 37131 37230: gap of 100 bp  
\* 37231 37997: contig of 767 bp in length  
\* 37998 38097: gap of 100 bp  
\* 38098 38863: contig of 766 bp in length  
\* 38864 38963: gap of 100 bp  
\* 38964 39719: contig of 756 bp in length  
\* 39720 39819: gap of 100 bp  
\* 39820 40572: contig of 753 bp in length  
\* 40573 40672: gap of 100 bp  
\* 40673 41416: contig of 744 bp in length  
\* 41417 41516: gap of 100 bp  
\* 41517 42238: contig of 722 bp in length  
\* 42239 42338: gap of 100 bp  
\* 42340 43072: contig of 734 bp in length  
\* 43073 43172: gap of 100 bp  
\* 43173 43923: contig of 751 bp in length  
\* 43924 44023: gap of 100 bp  
\* 44024 44785: contig of 762 bp in length  
\* 44786 44885: gap of 100 bp  
\* 44886 45637: contig of 752 bp in length  
\* 45638 45737: gap of 100 bp  
\* 45738 46491: contig of 753 bp in length  
\* 46491 46590: gap of 100 bp  
\* 46591 47355: contig of 765 bp in length  
\* 47356 47455: gap of 100 bp  
\* 47456 48219: contig of 764 bp in length  
\* 48220 48319: gap of 100 bp  
\* 48320 49027: contig of 708 bp in length  
\* 49028 49127: gap of 100 bp  
\* 49128 49885: contig of 758 bp in length  
\* 49886 49985: gap of 100 bp  
\* 49986 50743: contig of 758 bp in length  
\* 50744 50843: gap of 100 bp  
\* 50844 51597: contig of 754 bp in length  
\* 51598 51697: gap of 100 bp  
\* 51698 52398: contig of 701 bp in length  
\* 52399 52498: gap of 100 bp  
\* 52499 53237: contig of 739 bp in length  
\* 53238 53337: gap of 100 bp  
\* 53338 54097: contig of 760 bp in length  
\* 54098 54197: gap of 100 bp  
\* 54198 54952: contig of 755 bp in length  
\* 54953 55052: gap of 100 bp  
\* 55053 55818: contig of 766 bp in length  
\* 55819 55918: gap of 100 bp  
\* 55919 56683: contig of 765 bp in length  
\* 56684 56783: gap of 100 bp  
\* 56784 57512: contig of 729 bp in length  
\* 57513 57612: gap of 100 bp  
\* 57613 58380: contig of 768 bp in length  
\* 58381 58480: gap of 100 bp  
\* 58481 59236: contig of 756 bp in length

\* 59237 59336: gap of 100 bp  
\* 59337 60090: contig of 754 bp in length  
\* 60091 60190: gap of 100 bp

Query Match 77.8%; Score 14; DB 2; Length 62676;  
Best Local Similarity 85.7%; Pred. No. 1e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

5 UCCUGAGANNNNNN 18  
50735 TCCTGAGANNNNNN 50748

RESULT 52  
AC062003 64345 bp DNA linear HTG 21-APR-2000  
LOCUS AC062003  
DEFINITION Homo sapiens chromosome 11 clone RP11-132H5 map 11, LOW-PASS  
SEQUENCE SAMPLING.  
AC062003.1 GI:7630742  
VERSION AC062003.1  
KEYWORDS HTG; HTGS\_PHASED.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 64345)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
Anderson,S., Baldwin,J., Barra,N., Baerlein,V., Beda,F.,  
Boguslavsky,L., Bouckigalter,B., Brown,A., Burkett,G.,  
Campiano,A., Casale,A., Choquet,Y., Colangelo,M., Collins,S.,  
Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,D.S.,  
Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,  
Galagan,J., Gardina,S., Ginde,S., Goyette,M., Graham,L.,  
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatae,A.,  
Klein,J., Laroque,K., Lamazares,R., Lander,T., Lehocsky,J.,  
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Margulis,N.,  
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,  
Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,  
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,  
Pisan,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,  
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,  
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission  
Submitted (21-APR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

Project Information  
Center project name: L9886  
Center Clone name: 132\_H\_5

\* NOTE: This record contains 80 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.

However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 696: contig of 696 bp in length  
697 796: gap of 100 bp  
797 1500: contig of 704 bp in length  
1501 1600: gap of 100 bp  
1601 2298: contig of 698 bp in length  
2299 2398: gap of 100 bp  
2399 3099: contig of 701 bp in length  
3100 3199: gap of 100 bp  
3200 3907: contig of 708 bp in length  
3908 4007: gap of 100 bp  
4008 4683: contig of 676 bp in length  
4684 4783: gap of 100 bp  
4784 5495: contig of 712 bp in length  
5496 5595: gap of 100 bp  
5596 6303: contig of 708 bp in length  
6304 6403: gap of 100 bp  
6404 7109: contig of 706 bp in length  
7110 7209: gap of 100 bp  
7210 7917: contig of 708 bp in length  
7918 8017: gap of 100 bp  
8018 8720: contig of 703 bp in length  
8721 8820: gap of 100 bp  
8821 9522: contig of 702 bp in length  
9523 9622: gap of 100 bp  
9623 10322: contig of 700 bp in length  
10323 10422: gap of 100 bp  
10423 11149: contig of 727 bp in length  
11150 11249: gap of 100 bp  
11250 11962: contig of 713 bp in length  
11963 12062: gap of 100 bp  
12063 12767: contig of 705 bp in length  
12768 12867: gap of 100 bp  
12868 13575: contig of 708 bp in length  
13576 13675: gap of 100 bp  
13676 14364: contig of 689 bp in length  
14365 14464: gap of 100 bp  
14465 15167: contig of 703 bp in length  
15168 15267: gap of 100 bp  
15268 15968: contig of 701 bp in length  
15969 16068: gap of 100 bp  
16070 16771: contig of 703 bp in length  
16772 16872: gap of 100 bp  
16873 17567: contig of 696 bp in length  
17568 18372: gap of 100 bp  
18373 18472: gap of 100 bp  
18473 19172: contig of 700 bp in length  
19173 19272: gap of 100 bp  
19273 19993: contig of 721 bp in length  
19994 20093: gap of 100 bp  
20094 20813: contig of 720 bp in length  
20814 20913: gap of 100 bp  
20914 21626: contig of 713 bp in length  
21627 21726: gap of 100 bp  
21727 22425: contig of 699 bp in length  
22426 22525: gap of 100 bp  
22526 23319: contig of 694 bp in length  
23319 23319: gap of 100 bp  
23320 24037: contig of 718 bp in length  
24038 24137: gap of 100 bp  
24138 24853: contig of 716 bp in length  
24854 24953: gap of 100 bp  
24954 25669: contig of 716 bp in length  
25670 25769: gap of 100 bp  
25770 26479: contig of 710 bp in length  
26480 26579: gap of 100 bp  
26580 27282: contig of 703 bp in length  
27283 27382: gap of 100 bp  
27383 28102: contig of 720 bp in length

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* 28103 28202: gap of 100 bp
* 28203 28912: contig of 710 bp in length
* 28913 29012: gap of 100 bp
* 29013 29739: contig of 727 bp in length
* 29740 29839: gap of 100 bp
* 29840 30552: contig of 713 bp in length
* 30553 30652: gap of 100 bp
* 30653 31339: contig of 687 bp in length
* 31340 31439: gap of 100 bp
* 31440 32115: contig of 676 bp in length
* 32116 32917: contig of 702 bp in length
* 32918 33017: gap of 100 bp
* 33018 33728: contig of 711 bp in length
* 33729 33828: gap of 100 bp
* 33829 34540: contig of 712 bp in length
* 34541 34641: gap of 100 bp
* 34641 35349: contig of 709 bp in length
* 35350 35449: gap of 100 bp
* 35450 36170: contig of 721 bp in length
* 36171 36270: gap of 100 bp
* 36271 36980: contig of 710 bp in length
* 36981 37080: gap of 100 bp
* 37081 37809: contig of 729 bp in length
* 37810 37909: gap of 100 bp
* 37910 38612: contig of 703 bp in length
* 38613 38712: gap of 100 bp
* 38713 39412: contig of 700 bp in length
* 39413 39512: gap of 100 bp
* 39513 40207: contig of 695 bp in length
* 40208 40307: gap of 100 bp
* 40308 41001: contig of 694 bp in length
* 41002 41101: gap of 100 bp
* 41102 41812: contig of 711 bp in length
* 41813 41912: gap of 100 bp
* 41913 42613: contig of 701 bp in length
* 42614 42713: gap of 100 bp
* 42714 43421: contig of 708 bp in length
* 43422 43521: gap of 100 bp
* 43522 44236: contig of 715 bp in length
* 44237 44336: gap of 100 bp
* 44337 45045: contig of 709 bp in length
* 45046 45145: gap of 100 bp
* 45146 45831: contig of 686 bp in length
* 45832 45931: gap of 100 bp
* 45932 46638: contig of 707 bp in length
* 46639 46738: gap of 100 bp
* 46739 47452: contig of 714 bp in length
* 47453 47552: gap of 100 bp
* 47553 48261: contig of 709 bp in length
* 48262 48361: gap of 100 bp
* 48362 49059: contig of 698 bp in length
* 49060 49159: gap of 100 bp
* 49160 49862: contig of 703 bp in length
* 49863 49962: gap of 100 bp
* 49963 50667: contig of 705 bp in length
* 50668 50767: gap of 100 bp
* 50768 51462: contig of 695 bp in length
* 51463 51562: gap of 100 bp
* 51563 52280: contig of 718 bp in length
* 52281 52380: gap of 100 bp
* 52381 53094: contig of 714 bp in length
* 53095 53194: gap of 100 bp
* 53195 53865: contig of 671 bp in length
* 53866 54663: contig of 688 bp in length
* 54664 54763: gap of 100 bp
* 54764 55470: contig of 707 bp in length
* 55471 55570: gap of 100 bp

```

```

Query Match 77.8%; Score 14; DB 2; Length 64345;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 5 UCCUGAGNNNNN 18
Db 49052 TCCTGAGNNNNN 49065

RESULT 53
AC025214
LOCUS
DEFINITION
Homo sapiens chromosome 1 clone RP11-25B7 map 1, LOW-PASS SEQUENCE
SMAPPING.
AC025214.1 GI:7188892
VERSION
AC025214.1
KEYWORDS
HTG, HTGS_Phrase0
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 65174)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS
Birren, B., Linton, J., Nusbaum, C. and Lander, E.
REFERENCE
2 (bases 1 to 65174)
Homo sapiens chromosome 1, clone RP11-25B7
Unpublished
AUTHORS
Birren, B., Linton, J., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bada, F.,
Boguslavsky, L., Bouknight, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., DeArrelano, K., Dewar, K., Diaz, J. S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardina, S., Glade, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hages, B., Harford, A., Horton, L.,
Howard, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karas, A.,
Klein, J., Lacroque, K., Lamazares, R., Landers, T., Lehotzky, J.,
Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPeckers, R.,
Meldrum, J., Menus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N.,
Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rotman, D.,
Roy, A., Santos, R., Schauer, S., Severi, R., Spencer, B.,
Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tefaye, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (07-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLE
JOURNAL
COMMENT
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center Project name: L7950
Center Clone name: 25_B_7

NOTE: This record contains 82 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1 689: contig of 689 bp in length
* 690 789: gap of 100 bp
* 790 1486: contig of 697 bp in length

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1487 1586: gap of 100 bp  
1587 2280: contig of 694 bp in length  
2281 2380: gap of 100 bp  
2381 3071: contig of 691 bp in length  
3072 3171: gap of 100 bp  
3172 3866: contig of 695 bp in length  
3867 3966: gap of 100 bp  
3967 4664: contig of 698 bp in length  
4665 4764: gap of 100 bp  
4765 5467: contig of 703 bp in length  
5468 5567: gap of 100 bp  
5568 6263: contig of 696 bp in length  
6264 6363: gap of 100 bp  
6364 7084: contig of 721 bp in length  
7085 7184: gap of 100 bp  
7185 7841: contig of 657 bp in length  
7842 7941: gap of 100 bp  
7942 8638: contig of 697 bp in length  
8639 8738: gap of 100 bp  
8739 9431: contig of 693 bp in length  
9432 9531: gap of 100 bp  
9532 10235: contig of 704 bp in length  
10236 10335: gap of 100 bp  
10336 11052: contig of 717 bp in length  
11053 11152: gap of 100 bp  
11153 11855: contig of 703 bp in length  
11856 11955: gap of 100 bp  
11956 12666: contig of 711 bp in length  
12667 12766: gap of 100 bp  
12767 13465: contig of 699 bp in length  
13466 13565: gap of 100 bp  
13566 14265: contig of 700 bp in length  
14266 14365: gap of 100 bp  
14366 15069: contig of 704 bp in length  
15070 15169: gap of 100 bp  
15170 15857: contig of 688 bp in length  
15858 15957: gap of 100 bp  
15959 16643: contig of 686 bp in length  
16644 16743: gap of 100 bp  
16744 17437: contig of 694 bp in length  
17438 17537: gap of 100 bp  
17538 18221: contig of 684 bp in length  
18222 18321: gap of 100 bp  
18322 19004: contig of 683 bp in length  
19005 19104: gap of 100 bp  
19105 19819: contig of 715 bp in length  
19820 19919: gap of 100 bp  
19920 20604: contig of 685 bp in length  
20605 20704: gap of 100 bp  
20705 21403: contig of 699 bp in length  
21404 21503: gap of 100 bp  
21504 22200: contig of 697 bp in length  
22201 22300: gap of 100 bp  
22301 23007: contig of 707 bp in length  
23008 23107: gap of 100 bp  
23108 23805: contig of 698 bp in length  
23806 23905: gap of 100 bp  
23906 24597: contig of 692 bp in length  
24598 24697: gap of 100 bp  
24698 25394: contig of 697 bp in length  
25395 25494: gap of 100 bp  
25495 26178: contig of 684 bp in length  
26179 26278: gap of 100 bp  
26279 26970: contig of 692 bp in length  
26971 27070: gap of 100 bp  
27071 27783: contig of 713 bp in length  
27784 27883: gap of 100 bp  
27884 28583: contig of 700 bp in length  
28584 29408: contig of 725 bp in length  
29409 29508: gap of 100 bp  
29509 30221: contig of 713 bp in length  
30222 30321: gap of 100 bp

30322 31022: contig of 701 bp in length  
31023 31122: gap of 100 bp  
31123 31808: contig of 686 bp in length  
31809 31908: gap of 100 bp  
31909 32583: contig of 675 bp in length  
32584 32683: gap of 100 bp  
32684 33371: contig of 688 bp in length  
33372 33471: gap of 100 bp  
33472 34163: contig of 692 bp in length  
34164 34263: gap of 100 bp  
34264 34933: contig of 670 bp in length  
34934 35033: gap of 100 bp  
35034 35680: contig of 647 bp in length  
35681 35780: gap of 100 bp  
35781 36484: contig of 704 bp in length  
36485 36584: gap of 100 bp  
36585 37306: contig of 722 bp in length  
37307 37406: gap of 100 bp  
37407 38105: contig of 699 bp in length  
38106 38205: gap of 100 bp  
38206 38897: contig of 692 bp in length  
38898 38997: gap of 100 bp  
38998 39694: contig of 697 bp in length  
39695 39794: gap of 100 bp  
39795 40492: contig of 698 bp in length  
40493 40592: gap of 100 bp  
40593 41279: contig of 687 bp in length  
41280 41379: gap of 100 bp  
41380 42055: contig of 676 bp in length  
42056 42155: gap of 100 bp  
42156 42850: contig of 695 bp in length  
42851 42950: gap of 100 bp  
42952 43552: contig of 702 bp in length  
43553 43752: gap of 100 bp  
43753 44467: contig of 715 bp in length  
44468 44567: gap of 100 bp  
44568 45268: contig of 701 bp in length  
45269 45368: gap of 100 bp  
45369 46078: contig of 710 bp in length  
46079 46178: gap of 100 bp  
46179 46860: contig of 682 bp in length  
46861 46960: gap of 100 bp  
46961 47663: contig of 703 bp in length  
47664 47763: gap of 100 bp  
47764 48430: contig of 667 bp in length  
48431 48530: gap of 100 bp  
48531 49221: contig of 691 bp in length  
49222 49321: gap of 100 bp  
49322 50016: contig of 695 bp in length  
50017 50116: gap of 100 bp  
50117 50830: contig of 714 bp in length  
50831 50930: gap of 100 bp  
50931 51612: contig of 682 bp in length  
51613 51712: gap of 100 bp  
51713 52400: contig of 688 bp in length  
52401 52500: gap of 100 bp  
52501 53210: contig of 710 bp in length  
53211 53310: gap of 100 bp  
53310 53996: contig of 666 bp in length  
53997 54096: gap of 100 bp  
54097 54810: contig of 714 bp in length  
54811 54910: gap of 100 bp

Query Match 77.8%; Score 14; DB 2; Length 65174;  
Best Local Similarity 85.7%; Pred. No. 1e+02; 0; Gaps 0;  
Matches 12; Conservative 2; Mismatches 0; Indels 0;

Qy 5 UCCUGAGNNNNNN 18  
:|||||  
Db 47656 TCCTGAGNNNNNN 47669

RESULT 54

AC100485  
 LOCUS AC100485 66795 bp DNA linear HTG 30-Jul-2002  
 DEFINITION Mus musculus clone RP23-142A10, LOW-PASS SEQUENCE SAMPLING.  
 ACCESSION AC100485  
 VERSION AC100485.2 GI:22004531  
 KEYWORDS HTG; HTGS PHASE0.  
 ORGANISM Mus musculus (house mouse)  
 SOURCE Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 66795)  
 AUTHORS Birren, B., Nusbaum, C. and Lander, E.  
 TITLE Mus musculus, clone RP23-142A10  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 66795)  
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barina, N., Baatien, V., Boguslavskiy, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fato, S., Ferreira, P., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelle, C., Lacroque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Major, J., Marguis, N., Matthews, C., McCarthy, M., McKernan, P., McKernan, K., McNetters, R., Meldrum, J., Menue, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Roserli, M., Roy, A., Santoe, R., Schauer, S., Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J., Tophan, K., Travers, M., Travis, N., Trigilio, J., Vassiliou, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 DIRECT SUBMISSION  
 JOURNAL Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 REFERENCE 3 (bases 1 to 66795)  
 AUTHORS Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barina, N., Baatien, V., Bloom, T., Boguslavskiy, L., Boukhalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fato, S., Ferreira, P., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Menue, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Teefaye, S., Theodore, J., Tophan, K., Travers, M., Vassiliou, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 DIRECT SUBMISSION  
 JOURNAL Submitted (30-Jul-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 COMMENT On Jul 30, 2002 this sequence version replaced gi:117047851.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/MIT Center for Genome Research  
 Center code: WIDR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L15450

Center clone name: 142\_A\_10  
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 \* NOTE: This record contains 86 individual  
 \* sequencing reads that have not been assembled into  
 \* contigs. Runs of N are used to separate the reads  
 \* and the order in which they appear is completely  
 \* arbitrary. Low-pass sequence sampling is useful for  
 \* identifying clones that may be gene-rich and allows  
 \* overlap relationships among clones to be deduced.  
 \* However, it should not be assumed that this clone  
 \* will be sequenced to completion. In the event that  
 \* the record is updated, the accession number will  
 \* be preserved.  
 \*  
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 \* 664 663: contig of 663 bp in length  
 \* 764 763: gap of 100 bp  
 \* 1438 1437: contig of 674 bp in length  
 \* 1538 1537: gap of 100 bp  
 \* 2213 2212: contig of 675 bp in length  
 \* 2313 2312: gap of 100 bp  
 \* 2997 2997: contig of 685 bp in length  
 \* 3097 3097: gap of 100 bp  
 \* 3785 3784: contig of 687 bp in length  
 \* 3885 3884: gap of 100 bp  
 \* 4574 4574: contig of 690 bp in length  
 \* 4675 4674: gap of 100 bp  
 \* 5351 5350: contig of 676 bp in length  
 \* 5451 5450: gap of 100 bp  
 \* 6105 6104: contig of 654 bp in length  
 \* 6205 6204: gap of 100 bp  
 \* 6875 6874: contig of 670 bp in length  
 \* 6975 6974: gap of 100 bp  
 \* 7656 7655: contig of 681 bp in length  
 \* 7756 7755: gap of 100 bp  
 \* 8433 8432: contig of 677 bp in length  
 \* 8533 8532: gap of 100 bp  
 \* 9209 9208: contig of 676 bp in length  
 \* 9309 9308: gap of 100 bp  
 \* 9982 9982: contig of 674 bp in length  
 \* 10082 10082: gap of 100 bp  
 \* 10755 10754: contig of 672 bp in length  
 \* 10855 10854: gap of 100 bp  
 \* 11536 11535: contig of 681 bp in length  
 \* 11636 11635: gap of 100 bp  
 \* 12322 12322: contig of 687 bp in length  
 \* 12323 12422: gap of 100 bp  
 \* 12423 13114: contig of 692 bp in length  
 \* 13115 13214: gap of 100 bp  
 \* 13215 13894: contig of 680 bp in length  
 \* 13895 13994: gap of 100 bp  
 \* 13995 14655: contig of 661 bp in length  
 \* 14656 14755: gap of 100 bp  
 \* 14756 15418: contig of 663 bp in length  
 \* 15419 15518: gap of 100 bp  
 \* 15519 16196: contig of 678 bp in length  
 \* 16197 16296: gap of 100 bp  
 \* 16297 16968: contig of 673 bp in length  
 \* 16970 17069: gap of 100 bp  
 \* 17070 17758: contig of 689 bp in length  
 \* 17759 17858: gap of 100 bp  
 \* 17859 18543: contig of 685 bp in length  
 \* 18544 18643: gap of 100 bp  
 \* 18644 19318: contig of 675 bp in length  
 \* 19319 19418: gap of 100 bp  
 \* 19419 20095: contig of 677 bp in length  
 \* 20096 20195: gap of 100 bp  
 \* 20196 20888: contig of 693 bp in length  
 \* 20889 20988: gap of 100 bp  
 \* 20989 21680: contig of 692 bp in length  
 \* 21681 21780: gap of 100 bp  
 \* 21781 22461: contig of 681 bp in length  
 \* 22462 22561: gap of 100 bp  
 \* 22562 23228: contig of 667 bp in length  
 \* 23229 23328: gap of 100 bp

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* 23379 24012: contig of 684 bp in length
* 24013 24112: gap of 100 bp
* 24113 24790: contig of 678 bp in length
* 24791 24890: gap of 100 bp
* 24891 25664: contig of 674 bp in length
* 25665 26354: gap of 100 bp
* 26355 26533: contig of 689 bp in length
* 26534 27116: gap of 100 bp
* 27117 27217: gap of 100 bp
* 27217 27891: contig of 674 bp in length
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* 28687 28786: gap of 100 bp
* 28787 29472: contig of 685 bp in length
* 29472 29571: gap of 100 bp
* 29571 30236: contig of 665 bp in length
* 30237 30336: gap of 100 bp
* 30337 31024: contig of 688 bp in length
* 31025 31124: gap of 100 bp
* 31125 31801: contig of 677 bp in length
* 31802 31901: gap of 100 bp
* 31902 32570: contig of 669 bp in length
* 32571 32670: gap of 100 bp
* 32671 33351: contig of 681 bp in length
* 33352 33451: gap of 100 bp
* 33452 34117: contig of 666 bp in length
* 34118 34217: gap of 100 bp
* 34218 34894: contig of 677 bp in length
* 34895 34994: gap of 100 bp
* 34995 35668: contig of 674 bp in length
* 35669 35768: gap of 100 bp
* 35769 36443: contig of 674 bp in length
* 36443 37225: gap of 100 bp
* 37226 37325: contig of 683 bp in length
* 37326 37998: contig of 673 bp in length
* 37999 38098: gap of 100 bp
* 38099 38786: contig of 687 bp in length
* 38787 38886: gap of 100 bp
* 38887 39566: contig of 681 bp in length
* 39567 39666: gap of 100 bp
* 39667 40345: contig of 679 bp in length
* 40346 40445: gap of 100 bp
* 40446 41124: contig of 679 bp in length
* 41125 41224: gap of 100 bp
* 41225 41900: contig of 676 bp in length
* 41901 42000: gap of 100 bp
* 42001 42693: contig of 693 bp in length
* 42694 42793: gap of 100 bp
* 42794 43469: contig of 676 bp in length
* 43470 43569: gap of 100 bp
* 43570 44232: contig of 663 bp in length
* 44233 44332: gap of 100 bp
* 44333 45033: contig of 701 bp in length

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Query Match 77.8%; Score 14; DB 2; Length 66795;  
 Best Local Similarity 85.7%; Pred. No. 1e+02;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 UCCUGAGANNNNNN 18  
 Db 44225 TCCTGAGANNNNNN 44238

RESULT 55  
 AC027792  
 LOCUS AC027792 Homo sapiens chromosome 17 clone RP11-222B7 map 17, LOW-PASS  
 DEFINITION AC027792 SEQUENCE SAMPLING.  
 ACCESSION AC027792.1 GI:7382634  
 VERSION AC027792.1  
 KEYWORDS HTG; HTGS\_PHASE0.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 67822)  
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
 TITLE Homo sapiens chromosome 17, clone RP11-222B7  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 67822)  
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
 Anderson, S., Baldwin, J., Barua, N., Baetien, V., Bede, F.,  
 Boguslavsky, L., Boukhalter, J., Brown, A., Burkett, G.,  
 Campiagno, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S.,  
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 Meldrum, J., Menus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J.,  
 Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,  
 O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,  
 Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,  
 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,  
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talmap, J.,  
 Testaye, S., Theodore, J., Titzell, A., Travers, M., Trigg, J.,  
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,  
 Young, G., Zainoun, J., Zimmer, A. and Zody, M.  
 Direct Submission

TITLE  
 JOURNAL  
 COMMENT  
 Submitted (01-APR-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www.seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 Project Information  
 Center project name: L9026  
 Center clone name: 222\_B.7

NOTE: This record contains 76 individual  
 sequencing reads that have not been assembled into  
 contigs. Runs of N are used to separate the reads  
 and the order in which they appear is completely  
 arbitrary. Low-pass sequence sampling is useful for  
 identifying clones that may be gene-rich and allows  
 overlap relationships among clones to be deduced.  
 However, it should not be assumed that this clone  
 will be sequenced to completion. In the event that  
 the record is updated, the accession number will  
 be preserved.

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1 778: contig of 778 bp in length
779 779: gap of 100 bp
879 1676: contig of 798 bp in length
1677 1776: gap of 100 bp
1777 2564: contig of 788 bp in length
2565 2664: gap of 100 bp
2665 3450: contig of 786 bp in length
3451 3550: gap of 100 bp
3551 4345: contig of 795 bp in length
4346 4445: gap of 100 bp
4446 5232: contig of 787 bp in length
5233 6138: contig of 806 bp in length
6139 6238: gap of 100 bp
6239 7032: contig of 794 bp in length
7033 7132: gap of 100 bp
7133 7920: contig of 788 bp in length

```



```

* 7921 8020: gap of 100 bp
* 8021 8813: contig of 793 bp in length
* 8814 8914: gap of 100 bp
* 8914 9690: contig of 777 bp in length
* 9691 9791: gap of 100 bp
* 9791 10568: contig of 778 bp in length
* 10569 10669: gap of 100 bp
* 10669 11453: contig of 785 bp in length
* 11454 11553: gap of 100 bp
* 11554 12321: contig of 768 bp in length
* 12322 12421: gap of 100 bp
* 12421 13216: contig of 795 bp in length
* 13217 13316: gap of 100 bp
* 13317 14121: contig of 805 bp in length
* 14122 14221: gap of 100 bp
* 14222 14996: contig of 775 bp in length
* 14997 15096: gap of 100 bp
* 15097 15903: contig of 807 bp in length
* 15904 16004: gap of 100 bp
* 16004 16810: contig of 807 bp in length
* 16811 16910: gap of 100 bp
* 16911 17716: contig of 806 bp in length
* 17717 17817: gap of 100 bp
* 17817 18607: contig of 791 bp in length
* 18608 18707: gap of 100 bp
* 18708 19492: contig of 785 bp in length
* 19493 19593: gap of 100 bp
* 19593 20373: contig of 781 bp in length
* 20374 20473: gap of 100 bp
* 20474 21283: contig of 810 bp in length
* 21284 21383: gap of 100 bp
* 21384 22166: contig of 783 bp in length
* 22167 22266: gap of 100 bp
* 22267 23063: contig of 797 bp in length
* 23064 23163: gap of 100 bp
* 23164 23956: contig of 793 bp in length
* 23957 24056: gap of 100 bp
* 24057 24858: contig of 802 bp in length
* 24859 24959: gap of 100 bp
* 24959 25760: contig of 802 bp in length
* 25761 25861: gap of 100 bp
* 25862 26662: contig of 802 bp in length
* 26663 26763: gap of 100 bp
* 26763 27537: contig of 774 bp in length
* 27537 27637: gap of 100 bp
* 27637 28430: contig of 794 bp in length
* 28431 29333: gap of 100 bp
* 29333 29433: contig of 803 bp in length
* 29434 30240: gap of 100 bp
* 30240 30339: contig of 806 bp in length
* 30339 31121: gap of 100 bp
* 31122 32013: contig of 792 bp in length
* 32014 32113: gap of 100 bp
* 32114 32908: contig of 795 bp in length
* 32909 33008: gap of 100 bp
* 33009 33806: contig of 798 bp in length
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* 33907 34692: contig of 786 bp in length
* 34693 34793: gap of 100 bp
* 34793 35568: contig of 776 bp in length
* 35569 35668: gap of 100 bp
* 35669 36465: contig of 797 bp in length
* 36466 37354: gap of 100 bp
* 37355 37454: contig of 789 bp in length
* 37455 38242: gap of 100 bp
* 38243 38342: contig of 788 bp in length
* 38343 39138: gap of 100 bp
* 39139 39238: contig of 796 bp in length
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* 40129 40909: contig of 781 bp in length
* 40910 41010: gap of 100 bp
* 41010 41826: contig of 817 bp in length
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* 41927 42720: contig of 794 bp in length
* 42721 42820: gap of 100 bp
* 42821 43631: contig of 811 bp in length
* 43632 43731: gap of 100 bp
* 43732 44532: contig of 801 bp in length
* 44533 44633: gap of 100 bp
* 44633 45451: contig of 819 bp in length
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* 45552 46335: contig of 784 bp in length
* 46336 46435: gap of 100 bp
* 46436 47246: contig of 811 bp in length
* 47247 47347: gap of 100 bp
* 47347 48126: contig of 780 bp in length
* 48127 48226: gap of 100 bp
* 48227 49003: contig of 777 bp in length
* 49004 49103: gap of 100 bp
* 49104 49900: contig of 797 bp in length
* 49901 50001: gap of 100 bp
* 50001 50779: contig of 779 bp in length
* 50780 50879: gap of 100 bp
* 50880 51676: contig of 797 bp in length
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* 51777 52552: contig of 776 bp in length
* 52553 52652: gap of 100 bp
* 52653 53450: contig of 798 bp in length
* 53451 53550: gap of 100 bp
* 53551 54352: contig of 802 bp in length
* 54353 54452: gap of 100 bp
* 54453 55253: contig of 803 bp in length
* 55256 55355: gap of 100 bp
* 55356 56151: contig of 796 bp in length
* 56152 56251: gap of 100 bp
* 56252 57033: contig of 782 bp in length
* 57034 57134: gap of 100 bp
* 57134 57925: contig of 792 bp in length
* 57926 58025: gap of 100 bp
* 58026 58857: contig of 832 bp in length
* 58858 59748: gap of 100 bp
* 59749 59848: contig of 791 bp in length
* 59849 60650: gap of 100 bp
* 60651 60751: contig of 802 bp in length
* 60752 61554: gap of 804 bp in length
* 61555 61654: gap of 100 bp

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Query Match 77.8%; Score 14; DB 2; Length 67822;  
Best Local Similarity 85.7%; Pred. No. le+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 5 UCCUGAGNNNNNN 18  
Db 33799 TCCTGAGNNNNNN 33812

RESULT 56  
AC102023  
LOCUS  
DEFINITION Mus musculus clone RP24-68N17, LOW-PASS SEQUENCE SAMPLING.  
AC102023  
VERSION AC102023.1 GI:17061109  
KEYWORDS HTG; HTGS PHASE0.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 73882)  
AUTHORS Birren,B., Linton,L., Nuebaum,C. and Lander,E.  
TITLE Mus musculus, clone RP24-68N17  
JOURNAL Unpublished

REFERENCE  
AUTHORS

2 (bases 1 to 73882)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,  
Anderson, S., Batra, N., Biedt, V., Boguslavsky, L., Bouckgalter, B.,  
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,  
Choepe, T., Colangelo, M., Collins, S., Collymore, A., Cook, A.,  
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McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Melidrin, J.,  
Menesh, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,  
Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D.,  
Oliver, J., Peterson, K., Phunhang, P., Pierre, N., Pollard, V.,  
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,  
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,  
Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N.,  
Strauss, N., Subramanian, A., Talmas, J., Teafaye, S., Theodore, J.,  
Topham, K., Travers, M., Travis, N., Trigglio, J., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,  
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome  
Research, 330 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Sait, A. F. A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
Project Information  
Center project name: L17890  
Center clone name: 68\_N\_17

## COMMENT

NOTE: This record contains 88 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1  
747 746: contig of 746 bp in length  
847 846: gap of 100 bp  
1577 1576: contig of 730 bp in length  
1677 1676: gap of 100 bp  
2426 2425: contig of 749 bp in length  
2526 2525: gap of 100 bp  
3221 3221: contig of 696 bp in length  
3322 3321: gap of 100 bp  
4086 4085: contig of 764 bp in length  
4186 4185: gap of 100 bp  
4890 4889: contig of 704 bp in length  
4990 4989: gap of 100 bp  
5704 5704: contig of 715 bp in length  
5804 5804: gap of 100 bp  
5805 5804: contig of 774 bp in length  
6579 6578: gap of 100 bp  
7423 7423: contig of 745 bp in length  
7523 7523: gap of 100 bp  
8270 8270: contig of 747 bp in length  
8371 8370: gap of 100 bp  
9117 9117: contig of 747 bp in length  
9217 9217: gap of 100 bp  
9926 9926: contig of 709 bp in length  
10026 10026: gap of 100 bp

10027 10773: contig of 747 bp in length  
10774 10873: gap of 100 bp  
10874 11635: contig of 762 bp in length  
11636 11735: gap of 100 bp  
11736 12489: contig of 754 bp in length  
12490 12589: gap of 100 bp  
12590 13332: contig of 743 bp in length  
13333 13432: gap of 100 bp  
13433 14169: contig of 737 bp in length  
14170 14269: gap of 100 bp  
14270 15000: contig of 731 bp in length  
15001 15100: gap of 100 bp  
15101 15839: contig of 738 bp in length  
15839 15938: gap of 100 bp  
15939 16653: contig of 715 bp in length  
16654 16753: gap of 100 bp  
16754 17495: contig of 742 bp in length  
17496 17595: gap of 100 bp  
17596 18344: contig of 749 bp in length  
18345 18444: gap of 100 bp  
18445 19165: contig of 721 bp in length  
19166 19265: gap of 100 bp  
19266 20001: contig of 736 bp in length  
20002 20101: gap of 100 bp  
20102 20862: contig of 761 bp in length  
20863 20952: gap of 100 bp  
20963 21714: contig of 752 bp in length  
21715 22575: contig of 761 bp in length  
22576 22675: gap of 100 bp  
22676 23434: contig of 759 bp in length  
23435 23534: gap of 100 bp  
23535 24285: contig of 761 bp in length  
24296 24395: gap of 100 bp  
24396 25146: contig of 751 bp in length  
25147 25246: gap of 100 bp  
25247 25970: contig of 724 bp in length  
25971 26070: gap of 100 bp  
26071 26810: contig of 740 bp in length  
26811 26910: gap of 100 bp  
26910 27670: contig of 760 bp in length  
27671 27770: gap of 100 bp  
27771 28520: contig of 750 bp in length  
28521 28620: gap of 100 bp  
28621 29349: contig of 729 bp in length  
29349 29449: gap of 100 bp  
29450 30205: contig of 756 bp in length  
30206 30305: gap of 100 bp  
30306 31039: contig of 734 bp in length  
31039 31139: gap of 100 bp  
31140 31882: contig of 743 bp in length  
31883 31982: gap of 100 bp  
31983 32734: contig of 752 bp in length  
32735 32834: gap of 100 bp  
32835 33587: contig of 753 bp in length  
33588 33687: gap of 100 bp  
33688 34423: contig of 756 bp in length  
34424 34523: gap of 100 bp  
34524 35254: contig of 731 bp in length  
35255 35354: gap of 100 bp  
35355 36083: contig of 729 bp in length  
36084 36183: gap of 100 bp  
36184 36938: contig of 755 bp in length  
36939 37038: gap of 100 bp  
37039 37761: contig of 723 bp in length  
37762 37861: gap of 100 bp  
37862 38553: contig of 632 bp in length  
38554 38653: gap of 100 bp  
38654 39391: contig of 738 bp in length  
39391 39491: gap of 100 bp  
39492 40238: contig of 747 bp in length  
40238 40338: gap of 100 bp  
40339 41094: contig of 756 bp in length

```

* 41095 41194: gap of 100 bp
* 41195 41949: contig of 755 bp in length
* 41950 42049: gap of 100 bp
* 42050 42791: contig of 742 bp in length
* 42792 42891: gap of 100 bp
* 42892 43626: contig of 735 bp in length
* 43627 43726: gap of 100 bp
* 43727 44466: contig of 740 bp in length
* 44467 44566: gap of 100 bp
* 44567 45302: contig of 736 bp in length
* 45303 45402: gap of 100 bp
* 45403 46150: contig of 748 bp in length
* 46151 46250: gap of 100 bp
* 46251 47000: contig of 750 bp in length
* 47001 47100: gap of 100 bp
* 47101 47805: contig of 705 bp in length
* 47806 47905: gap of 100 bp
* 47906 48646: contig of 741 bp in length
* 48647 48746: gap of 100 bp
* 48747 49499: contig of 753 bp in length
* 49500 49599: gap of 100 bp
* 49600 50345: contig of 746 bp in length
* 50346 50445: gap of 100 bp
* 50446 51185: contig of 740 bp in length
* 51186 51285: gap of 100 bp
* 51286 52048: contig of 763 bp in length
* 52049 52148: gap of 100 bp
* 52149 52875: contig of 727 bp in length
* 52876 52975: gap of 100 bp
* 52976 53699: contig of 724 bp in length
* 53700 53799: gap of 100 bp
* 53800 54514: contig of 715 bp in length
* 54515 54614: gap of 100 bp
* 54616 55372: contig of 758 bp in length
* 55373 55472: gap of 100 bp
* 55473 56192: contig of 720 bp in length
* 56193 56292: gap of 100 bp
* 56293 57036: contig of 744 bp in length
* 57037 57136: gap of 100 bp
* 57137 57873: contig of 737 bp in length
* 57874 57973: gap of 100 bp

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Query Match      77.8%: Score 14; DB 2; Length 73882;
Best Local Similarity 85.7%: Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 5 UCCUGAGAGNNNNNN 18
Db 31032 TCCTGAGAGNNNNN 31045

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RESULT 57
LOCUS AC021390 81233 bp DNA linear HTG 13-JUL-2000
DEFINITION Homo sapiens clone RP11-27N15, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC021390
VERSION AC021390.2 GI:9136426
KEYWORDS HTG; HTGS_PHASEO.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 81233)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP11-27N15
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 81233)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguslavsky,I., Bouckgalter,B., Brown,A., Burkett,G., Castle,A.,
Choapel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
Darellano,K., Dewar,K., Domino,M., Doyle,M., Fenescor,J.,
Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J.,

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# JOURNAL COMMENT

```

Gardyna,S., Grant,G., Hages,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kam,L., Kartas,A., Klein,J.,
Landers,T., Lehoczy,D., Levine,R., Liu,C., Liu,G., Locke,K.,
Mcdonald,P., Margulis,N., McEwan,P., McGuck,A., McKernan,K.,
Mephesters,R., Meldrum,J., Menus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivari,T.M., Peterson,K.,
Pierre,N., Pisanic,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talmas,J., Teefaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (16-JUN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6705716.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4723
Center clone name: 27_N_15
-----
* NOTE: This record contains 90 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
784 883: contig of 783 bp in length
884 1668: contig of 785 bp in length
1669 1768: gap of 100 bp
1769 2571: contig of 803 bp in length
2572 2672: gap of 100 bp
2673 3492: contig of 821 bp in length
3493 3592: gap of 100 bp
3593 4378: contig of 786 bp in length
4379 4479: gap of 100 bp
4479 5320: contig of 842 bp in length
5321 5420: gap of 100 bp
5421 6248: contig of 828 bp in length
6249 6349: gap of 100 bp
6349 7149: contig of 801 bp in length
7150 7249: gap of 100 bp
7250 8080: contig of 831 bp in length
8081 8180: gap of 100 bp
8181 8991: contig of 811 bp in length
8992 9091: gap of 100 bp
9091 9897: contig of 806 bp in length
9897 9997: gap of 100 bp
9998 10787: contig of 790 bp in length
10788 10887: gap of 100 bp
10888 11681: contig of 794 bp in length
11682 11781: gap of 100 bp
11782 12604: contig of 823 bp in length
12605 12704: gap of 100 bp
12705 13499: contig of 795 bp in length
13500 13599: gap of 100 bp
13600 14431: contig of 832 bp in length
14432 14531: gap of 100 bp
14532 15338: contig of 807 bp in length
15339 15438: gap of 100 bp
15439 16259: contig of 821 bp in length

```

```

* 16260 16359: gap of 100 bp
* 16360 17159: contig of 800 bp in length
* 17160 17259: gap of 100 bp
* 17260 18071: contig of 812 bp in length
* 18072 18171: gap of 100 bp
* 18172 18933: contig of 762 bp in length
* 18934 19033: gap of 100 bp
* 19034 19832: contig of 799 bp in length
* 19833 19933: gap of 100 bp
* 19933 20759: contig of 827 bp in length
* 20760 20860 21633: contig of 774 bp in length
* 20860 21733: gap of 100 bp
* 21634 21734 22552: contig of 819 bp in length
* 22553 22653 23465: contig of 813 bp in length
* 23466 23565: gap of 100 bp
* 23566 24369: contig of 804 bp in length
* 24370 24470 25295: gap of 100 bp
* 25296 25395: gap of 100 bp
* 25396 26214: contig of 819 bp in length
* 26215 26315 27131: contig of 817 bp in length
* 27132 27232 28055: contig of 824 bp in length
* 28056 28155: gap of 100 bp
* 28156 28961: contig of 806 bp in length
* 28962 29062 29622: contig of 561 bp in length
* 29623 29723 30529: gap of 100 bp
* 30530 30629: gap of 100 bp
* 30630 31415: contig of 786 bp in length
* 31416 31515: gap of 100 bp
* 31516 32337: contig of 822 bp in length
* 32338 32437: gap of 100 bp
* 32438 33250: contig of 813 bp in length
* 33251 33351 34141: contig of 791 bp in length
* 33351 34142 34241: gap of 100 bp
* 34242 35058: contig of 817 bp in length
* 35059 35158: gap of 100 bp
* 35159 35955: contig of 798 bp in length
* 35957 36056: gap of 100 bp
* 36057 36886: contig of 830 bp in length
* 36887 36986: gap of 100 bp
* 36987 37796: contig of 810 bp in length
* 37797 37896: gap of 100 bp
* 37897 38696: contig of 800 bp in length
* 38697 38796: gap of 100 bp
* 38797 39595: contig of 799 bp in length
* 39596 39695: gap of 100 bp
* 39696 40484: contig of 789 bp in length
* 40485 40584: gap of 100 bp
* 40585 41392: contig of 808 bp in length
* 41393 41493: gap of 100 bp
* 41493 42281: contig of 789 bp in length
* 42282 42381: gap of 100 bp
* 42382 43197: contig of 816 bp in length
* 43198 43297: gap of 100 bp
* 43298 44107: contig of 810 bp in length
* 44108 44207: gap of 100 bp
* 44208 44991: contig of 784 bp in length
* 44992 45091: gap of 100 bp
* 45092 45921: contig of 830 bp in length
* 45922 46021: gap of 100 bp
* 46022 46847: contig of 826 bp in length
* 46848 46947: gap of 100 bp
* 46948 47770: contig of 823 bp in length
* 47771 47870: gap of 100 bp
* 47871 48692: contig of 822 bp in length
* 48693 48792: gap of 100 bp

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* 48793 49602: contig of 810 bp in length
* 49603 49702: gap of 100 bp
* 49703 50512: contig of 810 bp in length
* 50513 50612: gap of 100 bp
* 50613 51396: contig of 784 bp in length
* 51397 51496: gap of 100 bp
* 51497 52303: contig of 807 bp in length
* 52304 52403: gap of 100 bp
* 52404 53235: gap of 831 bp in length
* 53235 53335 54128: contig of 793 bp in length
* 54128 54227: gap of 100 bp
* 54228 55034: contig of 807 bp in length
* 55035 55134: gap of 100 bp
* 55135 55927: contig of 793 bp in length
* 55928 56027: gap of 100 bp
* 56028 56841: contig of 814 bp in length
* 56842 56941: gap of 100 bp
* 56942 57765: contig of 824 bp in length
* 57766 57865: gap of 100 bp
* 57866 58666: contig of 801 bp in length
* 58667 58766: gap of 100 bp
* 58767 59570: contig of 804 bp in length
* 59571 59670: gap of 100 bp
* 59671 60468: contig of 798 bp in length
* 60469 60568: gap of 100 bp
* 60569 61348: contig of 780 bp in length
* 61349 61448: gap of 100 bp
* 61449 62272: contig of 824 bp in length
* 62273 62373 63167: contig of 795 bp in length
* 63168 63267: gap of 100 bp
* 63268 64080: contig of 813 bp in length
* 64081 64180: gap of 100 bp

Query Match
Best Local Similarity 77.8%; Score 14; DB 2; Length 81233;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGNNNNNN 18
Db 11674 TCCTGAGNNNNNN 11687

RESULT 58
AC022890 83547 bp DNA linear HTG 24-AUG-2002
LOCUS Homo sapiens chromosome 6 clone RP11-516A8 map 6, LOW-PASS SEQUENCE
DEFINITION SAMPLING.
ACCESSION AC022890.2 GI:9160241
VERSION HTG; HTGS_PHASE0.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 83547)
REFERENCE 1 Birren,B., Linton,L., Nusbaum,C. and Lander,E.
AUTHORS Homo sapiens chromosome 6, clone RP11-516A8
JOURNAL Unpublished
TITLE 2 (bases 1 to 83547)
REFERENCE 1 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
AUTHORS Anderson,S., Balwin,J., Barina,N., Beckert,J., Beda,F.,
Boguslavsky,L., Bouknight,J., Brown,A., Burkett,G., Castle,A.,
Chapel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
Dearellano,K., Dewar,K., Domino,M., Doyle,M., Fencsator,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hages,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kam,L., Karatas,A., Klein,J.,
Lander,T., Lehotzky,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Maddison,P., Margulis,N., McEwan,P., McGuirk,A., McKernan,K.,
McPheeters,R., Meldrum,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K.,

```

Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
(bases 1 to 83547)

Bliren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavsky, L., Bouhgalter, B., Brown, A., Burkett, G., Campoliano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J. S., Dodge, S., Domingo, M., Doyle, M., Ferreira, P., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand, P., Grant, N., Grant, G., Hagos, B., Heasford, A., Horton, L., Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karacas, A., Klein, J., Laroque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Margie, N., McCarthy, M., McKean, P., McQuirk, A., McKernan, K., McPheters, R., Melidym, J., Meneus, L., Minova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced gi:6922031.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: I62230  
Center clone name: 516\_A\_8

\*\*\*\*\*  
\* NOTE: This record contains 88 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
\*\*\*\*\*

1 847: contig of 847 bp in length  
848 947: gap of 100 bp  
948 1811: contig of 864 bp in length  
1812 1911: gap of 100 bp  
1912 2767: contig of 856 bp in length  
2768 2867: gap of 100 bp  
2868 3724: contig of 857 bp in length  
3725 3824: gap of 100 bp  
3825 4676: contig of 852 bp in length  
4677 4776: gap of 100 bp  
4777 5611: contig of 835 bp in length  
5612 5711: gap of 100 bp  
5712 6524: contig of 813 bp in length  
6525 7481: contig of 857 bp in length  
7482 7581: gap of 100 bp

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7582 8426: contig of 845 bp in length  
8427 8525: gap of 100 bp  
8527 9380: contig of 854 bp in length  
9381 9480: gap of 100 bp  
9481 10323: contig of 843 bp in length  
10324 10423: gap of 100 bp  
10424 11259: contig of 836 bp in length  
11260 11359: gap of 100 bp  
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12215 12313: gap of 100 bp  
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13164 13263: gap of 100 bp  
13264 14140: contig of 877 bp in length  
14141 14240: gap of 100 bp  
14241 15103: contig of 863 bp in length  
15104 15203: gap of 100 bp  
15204 16065: contig of 862 bp in length  
16066 16165: gap of 100 bp  
16166 17031: contig of 866 bp in length  
17032 17131: gap of 100 bp  
17132 17987: contig of 856 bp in length  
17988 18087: gap of 100 bp  
18088 18931: contig of 844 bp in length  
18932 19031: gap of 100 bp  
19032 19851: contig of 820 bp in length  
19852 19951: gap of 100 bp  
19952 20798: contig of 847 bp in length  
20799 20898: gap of 100 bp  
20899 21729: contig of 831 bp in length  
21730 21829: gap of 100 bp  
21830 22679: contig of 850 bp in length  
22679 22779: gap of 100 bp  
22780 23637: contig of 858 bp in length  
23638 23737: gap of 100 bp  
23738 24597: contig of 860 bp in length  
24598 24697: gap of 100 bp  
24698 25531: contig of 834 bp in length  
25532 25631: gap of 100 bp  
25632 26435: contig of 804 bp in length  
26436 26535: gap of 100 bp  
26536 27344: contig of 809 bp in length  
27345 27444: gap of 100 bp  
27445 28309: contig of 865 bp in length  
28310 28409: gap of 100 bp  
28410 29259: contig of 850 bp in length  
29260 29359: gap of 100 bp  
29360 30200: contig of 841 bp in length  
30201 30300: gap of 100 bp  
30301 31162: contig of 862 bp in length  
31163 31262: gap of 100 bp  
31263 32112: contig of 850 bp in length  
32113 32212: gap of 100 bp  
32213 33069: contig of 857 bp in length  
33070 33169: gap of 100 bp  
33170 34006: contig of 837 bp in length  
34007 34106: gap of 100 bp  
34107 34972: contig of 866 bp in length  
34973 35072: gap of 100 bp  
35073 35924: contig of 852 bp in length  
35925 36024: gap of 100 bp  
36025 36864: contig of 840 bp in length  
36865 36964: gap of 100 bp  
36965 37823: contig of 859 bp in length  
37824 37923: gap of 100 bp  
37924 38773: contig of 850 bp in length  
38774 38873: gap of 100 bp  
38874 39728: contig of 855 bp in length  
39729 39828: gap of 100 bp  
39829 40690: contig of 862 bp in length  
40691 40790: gap of 100 bp  
40791 41636: contig of 846 bp in length  
41637 41736: gap of 100 bp  
41737 42566: contig of 830 bp in length

```

* 42567 42666: gap of 100 bp
* 42667 43520: contig of 854 bp in length
* 43521 43620: gap of 100 bp
* 43621 44487: contig of 867 bp in length
* 44488 44587: gap of 100 bp
* 44588 44549: contig of 862 bp in length
* 44550 45549: gap of 100 bp
* 45550 46389: contig of 840 bp in length
* 46390 46489: gap of 100 bp
* 46490 47342: contig of 853 bp in length
* 47343 47442: gap of 100 bp
* 47443 48298: contig of 856 bp in length
* 48299 48398: gap of 100 bp
* 48399 49262: contig of 864 bp in length
* 49263 49363: gap of 100 bp
* 49363 50208: contig of 846 bp in length
* 50209 50308: gap of 100 bp
* 50309 51167: contig of 859 bp in length
* 51168 51267: gap of 100 bp
* 51268 52131: contig of 864 bp in length
* 52132 52231: gap of 100 bp
* 52231 53103: contig of 872 bp in length
* 53104 53203: gap of 100 bp
* 53204 54032: contig of 829 bp in length
* 54033 54132: gap of 100 bp
* 54133 54993: contig of 861 bp in length
* 54994 55093: gap of 100 bp

```

```

Query Match 77.8% Score 14; DB 2; Length 83547;
Best Local Similarity 85.7% Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 5 UCCUGGAGNNNNN 18
Db 50201 TCCTGGAGNNNNN 50214

```

```

RESULT 59
AC034264
LOCUS
DEFINITION Mus musculus clone RP23-390D17, LOW-PASS SEQUENCE SAMPLING.
AC034264
VERSION AC034264.1 GI:7417775
KEYWORDS HTG; HTGS PHASE0.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 85440)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-390D17
Unpublished
2 (bases 1 to 85440)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Baastien,V., Beda,F.,
Boguslavsky,L., Bouckhalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., DeArrelano,K., Dewar,K., Diaz,J.S.,
Dodgson,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Gallagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoccky,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheters,R.,
Melidim,J., Menus,L., Mihova,T., Mironov,C., Mlenka,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talmas,J.,
Testaye,S., Theodore,J., Tirelli,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,

```

# TITLE JOURNAL COMMENT

Young, G., Zainoun, J., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (05-APR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.P.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L5036  
Center clone name: 390\_D\_17  
-----  
\* NOTE: This record contains 89 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

```

1 850: contig of 850 bp in length
* 851 950: gap of 100 bp
* 951 1835: contig of 885 bp in length
* 1836 1935: gap of 100 bp
* 1936 2781: contig of 846 bp in length
* 2782 2881: gap of 100 bp
* 2882 3753: contig of 872 bp in length
* 3754 3853: gap of 100 bp
* 3854 4683: contig of 830 bp in length
* 4684 4783: gap of 100 bp
* 4784 5651: contig of 868 bp in length
* 5652 5751: gap of 100 bp
* 5752 6617: contig of 866 bp in length
* 6618 7563: contig of 846 bp in length
* 7564 7663: gap of 100 bp
* 7664 8537: contig of 874 bp in length
* 8538 8638: gap of 100 bp
* 8638 9495: contig of 858 bp in length
* 9496 9595: gap of 100 bp
* 9596 10445: contig of 850 bp in length
* 10446 10545: gap of 100 bp
* 10546 11424: contig of 879 bp in length
* 11425 11524: gap of 100 bp
* 11525 12407: contig of 883 bp in length
* 12408 12507: gap of 100 bp
* 12508 13367: contig of 860 bp in length
* 13368 13467: gap of 100 bp
* 13468 14333: contig of 866 bp in length
* 14334 14433: gap of 100 bp
* 14434 15296: contig of 863 bp in length
* 15297 15396: gap of 100 bp
* 15397 16271: contig of 875 bp in length
* 16272 16371: gap of 100 bp
* 16372 17240: contig of 865 bp in length
* 17241 17340: gap of 100 bp
* 17341 18227: contig of 887 bp in length
* 18228 18327: gap of 100 bp
* 18328 19192: contig of 865 bp in length
* 19193 19292: gap of 100 bp
* 19293 20169: contig of 877 bp in length
* 20170 20269: gap of 100 bp
* 20270 21116: contig of 847 bp in length
* 21117 22057: contig of 841 bp in length
* 22058 22157: gap of 100 bp

```

```

* 22158 22987: contig of 830 bp in length
* 22988 23087: gap of 100 bp
* 23088 23925: contig of 838 bp in length
* 23926 24025: gap of 100 bp
* 24026 24912: contig of 887 bp in length
* 24913 25012: gap of 100 bp
* 25013 25879: contig of 867 bp in length
* 25880 25979: gap of 100 bp
* 25980 26839: contig of 860 bp in length
* 26840 26939: gap of 100 bp
* 26940 27768: contig of 828 bp in length
* 27769 27868: gap of 100 bp
* 27869 28749: contig of 881 bp in length
* 28750 28849: gap of 100 bp
* 28850 29690: contig of 841 bp in length
* 29691 29790: gap of 100 bp
* 29791 30656: contig of 866 bp in length
* 30657 30756: gap of 100 bp
* 30757 31645: contig of 889 bp in length
* 31646 31745: gap of 100 bp
* 31746 32637: contig of 882 bp in length
* 32638 32737: gap of 100 bp
* 32738 33611: contig of 874 bp in length
* 33612 34563: contig of 852 bp in length
* 34564 35518: gap of 100 bp
* 35519 35618: gap of 100 bp
* 35619 36511: contig of 893 bp in length
* 36512 37487: contig of 876 bp in length
* 37488 37588: gap of 100 bp
* 37589 38427: contig of 839 bp in length
* 38428 38527: gap of 100 bp
* 38528 39372: contig of 846 bp in length
* 39373 39473: gap of 100 bp
* 39474 40331: contig of 859 bp in length
* 40332 40431: gap of 100 bp
* 40432 41244: contig of 812 bp in length
* 41245 42165: contig of 822 bp in length
* 42166 42266: gap of 100 bp
* 42267 43103: contig of 838 bp in length
* 43104 43203: gap of 100 bp
* 43204 44032: contig of 829 bp in length
* 44033 44132: gap of 100 bp
* 44133 44989: contig of 857 bp in length
* 44990 45089: gap of 100 bp
* 45090 45967: contig of 878 bp in length
* 45968 46068: gap of 100 bp
* 46069 46924: contig of 857 bp in length
* 46925 47024: gap of 100 bp
* 47025 47868: contig of 844 bp in length
* 47869 47968: gap of 100 bp
* 47969 48846: contig of 878 bp in length
* 48847 48946: gap of 100 bp
* 48947 49814: contig of 868 bp in length
* 49815 49914: gap of 100 bp
* 49915 50765: contig of 851 bp in length
* 50766 50865: gap of 100 bp
* 50866 51729: contig of 864 bp in length
* 51730 51829: gap of 100 bp
* 51830 52708: contig of 879 bp in length
* 52709 52808: gap of 100 bp
* 52809 53684: contig of 876 bp in length
* 53685 53784: gap of 100 bp
* 53785 54646: contig of 862 bp in length
* 54647 54746: gap of 100 bp
* 54747 55641: contig of 895 bp in length
* 55642 55741: gap of 100 bp
* 55742 56601: contig of 860 bp in length
* 56602 57577: gap of 100 bp
* 57578 57677: contig of 876 bp in length

```

```

* 57578 57677: gap of 100 bp
* 57678 58550: contig of 873 bp in length
* 58551 58650: gap of 100 bp
* 58651 59526: contig of 876 bp in length
* 59527 59626: gap of 100 bp
* 59627 60500: contig of 874 bp in length
* 60501 60600: gap of 100 bp
* 60601 61448: contig of 848 bp in length
* 61449 61548: gap of 100 bp
* 61549 62398: contig of 850 bp in length
* 62399 62498: gap of 100 bp
* 62499 63363: contig of 865 bp in length
* 63364 63464: gap of 100 bp
* 63465 64326: contig of 863 bp in length
* 64327 64426: gap of 100 bp
* 64427 65285: contig of 859 bp in length
* 65286 65385: gap of 100 bp
* 65386 66245: contig of 860 bp in length
* 66246 66345: gap of 100 bp
* 66346 67188: contig of 843 bp in length

Query Match      77.8%; Score 14; DB 2; Length 85440;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy      5 UCCUGGAGNNNNN 18
Db      20162 TCCTGAGNNNNN 20175

RESULT 60
AC138602
LOCUS      Mus musculus clone RP23-9113, LOW-PASS SEQUENCE SAMPLING.
DEFINITION
ACCESSION  AC138602
VERSION    AC138602.1 GI:27573472
KEYWORDS   HTG; HTGS PHASED.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 88940)
REFERENCE  Birren,B., Nusbaum,C. and Lander,E.
            Mus musculus, clone RP23-9113
            Unpublished
            2 (bases 1 to 88940)
AUTHORS   Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
            Barina,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B.,
            Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
            Cook,A., Cooke,P., Deakrellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Fairo,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
            Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N.,
            Hago,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
            Kamat,A., Karacas,A., Kells,C., Lander,T., Levine,R.,
            Lindblad-Toh,K., Liu,G., Maclean,C., MacDonald,P., Major,T.,
            Matthews,C., McCarthy,M., Meldrum,D., Menus,L., Mitova,T.,
            Mienna,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
            Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
            Peterson,K., Phukhang,P., Pierre,N., Raymond,C., Retta,R.,
            Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schnuppman,N.,
            Seojanovic,N., Talamas,J., Teste,S., Theodore,J., Topham,K.,
            Travers,M., Vaseiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,
            Wyman,D., Young,G., Zaitoun,J., Zembek,L., Zimmer,A. and Zody,M.
            Direct Submission
            Submitted (10-JAN-2003) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            All repeats were identified using RepeatMasker:
            Smit,A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            ----- Genome Center
            Center: Whitehead Institute/ MIT Center for Genome Research
            Center code: WIBR

```

Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center Project name: L22378  
Center clone name: 91\_I\_3  
-----

\* NOTE: This record contains 83 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 976: contig of 976 bp in length  
\* 977 1076: gap of 100 bp  
\* 1077 2028: contig of 952 bp in length  
\* 2029 2128: gap of 100 bp  
\* 2129 3050: contig of 922 bp in length  
\* 3051 3150: gap of 100 bp  
\* 3151 4111: contig of 961 bp in length  
\* 4112 4211: gap of 100 bp  
\* 4212 5202: contig of 991 bp in length  
\* 5203 5302: gap of 100 bp  
\* 5303 6279: contig of 977 bp in length  
\* 6280 6379: gap of 100 bp  
\* 6380 7406: contig of 1027 bp in length  
\* 7407 8478: contig of 972 bp in length  
\* 8479 8578: gap of 100 bp  
\* 8579 9600: contig of 1022 bp in length  
\* 9601 9700: gap of 100 bp  
\* 9701 10655: contig of 955 bp in length  
\* 10656 11729: contig of 974 bp in length  
\* 11730 11828: gap of 100 bp  
\* 11830 12796: contig of 967 bp in length  
\* 12797 12896: gap of 100 bp  
\* 12897 13853: contig of 957 bp in length  
\* 13854 13953: gap of 100 bp  
\* 13954 14907: contig of 954 bp in length  
\* 14908 15007: gap of 100 bp  
\* 15008 15941: contig of 934 bp in length  
\* 15942 16041: gap of 100 bp  
\* 16042 17009: contig of 968 bp in length  
\* 17010 17109: gap of 100 bp  
\* 17110 18086: contig of 977 bp in length  
\* 18087 18186: gap of 100 bp  
\* 18187 19158: contig of 972 bp in length  
\* 19159 19258: gap of 100 bp  
\* 19259 20253: contig of 995 bp in length  
\* 20254 20353: gap of 100 bp  
\* 20354 21335: contig of 982 bp in length  
\* 21336 21435: gap of 100 bp  
\* 21436 22392: contig of 957 bp in length  
\* 22393 22492: gap of 100 bp  
\* 22493 23452: contig of 960 bp in length  
\* 23453 24532: contig of 980 bp in length  
\* 24533 24632: gap of 100 bp  
\* 24633 25633: contig of 1001 bp in length  
\* 25634 25733: gap of 100 bp  
\* 25734 26729: contig of 996 bp in length  
\* 26730 26829: gap of 100 bp  
\* 26830 27804: contig of 975 bp in length  
\* 27805 27904: gap of 100 bp  
\* 27905 28888: contig of 984 bp in length  
\* 28889 28975: gap of 100 bp  
\* 28976 30075: contig of 987 bp in length  
\* 30075: gap of 100 bp

30076 31045: contig of 970 bp in length  
\* 31046 31145: gap of 100 bp  
\* 31146 32118: contig of 973 bp in length  
\* 32119 32218: gap of 100 bp  
\* 32219 33151: contig of 933 bp in length  
\* 33152 33251: gap of 100 bp  
\* 33252 34237: contig of 986 bp in length  
\* 34238 34337: gap of 100 bp  
\* 34338 35324: contig of 987 bp in length  
\* 35325 35424: gap of 100 bp  
\* 35425 36413: contig of 989 bp in length  
\* 36414 36513: gap of 100 bp  
\* 36514 37512: contig of 999 bp in length  
\* 37513 37612: gap of 100 bp  
\* 37613 38602: contig of 990 bp in length  
\* 38603 38702: gap of 100 bp  
\* 38703 39704: contig of 1002 bp in length  
\* 39705 39804: gap of 100 bp  
\* 39805 40782: contig of 978 bp in length  
\* 40783 40882: gap of 100 bp  
\* 40883 41876: contig of 994 bp in length  
\* 41877 41976: gap of 100 bp  
\* 41977 42950: contig of 974 bp in length  
\* 42951 43050: gap of 100 bp  
\* 43051 44022: contig of 972 bp in length  
\* 44023 44122: gap of 100 bp  
\* 44123 45074: contig of 952 bp in length  
\* 45075 45174: gap of 100 bp  
\* 45175 46161: contig of 987 bp in length  
\* 46162 46261: gap of 100 bp  
\* 46262 47237: contig of 976 bp in length  
\* 47238 47337: gap of 100 bp  
\* 47338 48343: contig of 1006 bp in length  
\* 48344 48443: gap of 100 bp  
\* 48444 49414: contig of 971 bp in length  
\* 49415 49514: gap of 100 bp  
\* 49515 50516: contig of 1002 bp in length  
\* 50517 50616: gap of 100 bp  
\* 50617 51589: contig of 973 bp in length  
\* 51590 51689: gap of 100 bp  
\* 51690 52676: contig of 987 bp in length  
\* 52677 52776: gap of 100 bp  
\* 52777 53758: contig of 982 bp in length  
\* 53759 53858: gap of 100 bp  
\* 53859 54818: contig of 960 bp in length  
\* 54819 54918: gap of 100 bp  
\* 54919 55873: contig of 955 bp in length  
\* 55874 55973: gap of 100 bp  
\* 55974 56931: contig of 956 bp in length  
\* 56932 57031: gap of 100 bp  
\* 57032 57973: contig of 942 bp in length  
\* 57974 58073: gap of 100 bp  
\* 58074 59046: contig of 973 bp in length  
\* 59047 59146: gap of 100 bp  
\* 59147 60133: contig of 987 bp in length  
\* 60134 60233: gap of 100 bp  
\* 60234 61221: contig of 988 bp in length  
\* 61222 61321: gap of 100 bp  
\* 61322 62303: contig of 982 bp in length  
\* 62304 62404: gap of 100 bp  
\* 62404 63380: contig of 972 bp in length  
\* 63381 63480: gap of 100 bp  
\* 63481 64459: contig of 979 bp in length  
\* 64460 64559: gap of 100 bp  
\* 64560 65544: contig of 985 bp in length  
\* 65545 65644: gap of 100 bp  
\* 65645 66614: contig of 970 bp in length  
\* 66615 66714: gap of 100 bp  
\* 66715 67664: contig of 950 bp in length  
\* 67665 67764: gap of 100 bp  
\* 67765 68736: contig of 972 bp in length  
\* 68737 68836: gap of 100 bp  
\* 68837 69837: contig of 1001 bp in length



\* 69938 69937: gap of 100 bp  
\* 70938 70948: contig of 911 bp in length  
\* 70849 70948: gap of 100 bp  
\* 70949 71924: contig of 976 bp in length  
\* 71925 72024: gap of 100 bp  
\* 72025 72989: contig of 965 bp in length  
\* 72990 73089: gap of 100 bp  
\* 73090 74074: contig of 985 bp in length  
\* 74075 74174: gap of 100 bp  
\* 74175 75149: contig of 975 bp in length  
\* 75150 75249: gap of 100 bp  
\* 75250 76211: contig of 962 bp in length  
\* 76212 76311: gap of 100 bp

Query Match 77.8% Score 14; DB 2; Length 88940;  
Best Local Similarity 85.7% Pred. No. 1e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 UCCUGAGAGNNNNNN 18  
Db 86791 TCCTGAGAGNNNNNN 86804

# RESULT 61

AC095920\_03

WPCOMMENT

Sequence split into 10 fragments LOCUS AC095920 Accession AC095920

Fragment Name	Begin	End
AC095920_00	1	110000
AC095920_01	100001	210000
AC095920_02	200001	310000
AC095920_03	300001	410000
AC095920_04	400001	510000
AC095920_05	500001	610000
AC095920_06	600001	710000
AC095920_07	700001	810000
AC095920_08	800001	910000
AC095920_09	900001	1005083

Continuation (4 of 10) of AC095920 From Base 300001 (AC095920 Rattus norvegicus clone CH

Query Match 77.8% Score 14; DB 2; Length 110000;  
Best Local Similarity 85.7% Pred. No. 1e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 UCCUGAGAGNNNNNN 18  
Db 85215 TCCTGAGAGNNNNNN 85228

# RESULT 62

AC096315\_3

WPCOMMENT

Sequence split into 9 fragments LOCUS AC096315 Accession AC096315

Fragment Name	Begin	End
AC096315_0	1	110000
AC096315_1	100001	210000
AC096315_2	200001	310000
AC096315_3	300001	410000
AC096315_4	400001	510000
AC096315_5	500001	610000
AC096315_6	600001	710000
AC096315_7	700001	810000
AC096315_8	800001	848038

Continuation (4 of 9) of AC096315 From Base 300001 (AC096315 Rattus norvegicus clone CH2

Query Match 77.8% Score 14; DB 2; Length 110000;  
Best Local Similarity 85.7% Pred. No. 1e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 UCCUGAGAGNNNNNN 18  
Db 83645 TCCTGAGAGNNNNNN 83658

# RESULT 63

AC112872\_0

WPCOMMENT

Sequence split into 5 fragments LOCUS AC112872 Accession AC112872

Fragment Name	Begin	End
AC112872_0	1	110000
AC112872_1	100001	210000
AC112872_2	200001	310000
AC112872_3	300001	410000
AC112872_4	400001	421172

LOCUS AC112872 421172 bp DNA linear HTG 11-OCT-2002

DEFINITION Rattus norvegicus clone CH230-221D7, \*\*\* SEQUENCING IN PROGRESS

\*\*\* 18 unordered pieces.

AC112872 GI:23817694  
VERSION AC112872.6  
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_ENRICHED.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus

# REFERENCE

AUTHORS

1 (bases 1 to 421172)

Muzny,D.,Marie.,Metzker,M.,Lee.,Abramson,S.,Adams,C.,Alder,J.,

Allen,C.,Allen,H.,Alibrook,S.,Amin,A.,Anguiano,D.,

Anyalebechi,V.,Aoyagi,A.,Ayodeji,M.,Baca,E.,Baden,H.,

Baldwin,D.,Bandaranaike,D.,Barber,M.,Barnstead,M.,Benahmed,F.,

Biswal,R.,Blair,J.,Blankenburg,K.,Blyth,P.,Brown,M.,

Bryant,N.,Buhay,C.,Burch,P.,Burrell,K.,Calderon,E.,

Cardenas,V.,Carter,K.,Cavazos,I.,Ceasar,H.,Center,A.,

Chacko,J.,Chavez,D.,Chen,G.,Chen,R.,Chen,Y.,Chen,Z.,Chu,J.,

Cleveland,C.,Cockrell,R.,Cox,C.,Coyle,M.,Cree,A.,D'Souza,L.,

Devila,M.L.,Davis,C.,Davy-Carroll,L.,De Anda,C.,Dedrich,D.,

Delgado,O.,Denson,S.,Deramo,C.,Ding,Y.,Dinh,H.,Divya,K.,

Draper,H.,Dugan-Rocha,S.,Dunn,A.,Durbin,K.,Dvali,B.,Eaves,K.,

Egan,A.,Escotto,M.,Eugene,C.,Evans,C.A.,Fallis,T.,Fan,G.,

Farrandez,S.,Finley,M.,Flagg,N.,Forbes,L.,Foster,M.,Foster,P.,

Fraser,C.M.,Gabris,A.,Ganter,R.,Garcia,A.,Garner,T.,Garza,M.,

Gedraetogis,E.,Geer,K.,Gill,R.,Grady,M.,Guerra,M.,Guevara,W.,

Gubaratine,P.,Haaland,W.,Hamill,C.,Hamilton,C.,Hamilton,K.,

Harvey,Y.,Havlak,P.,Hawes,A.,Henderson,N.,Hernandez,J.,

Hernandez,R.,Hines,S.,Hladun,S.L.,Hodgeson,A.,Hogues,M.,

Hollins,B.,Howells,S.,Hulky,S.,Hume,J.,Idlebird,D.,Jackson,A.,

Jackson,L.,Jacob,L.,Jiang,H.,Johnson,B.,Johnson,R.,Jolivet,A.,

Karpachy,S.,Kelly,S.,Kelly,S.,Khan,Z.,King,L.,Kovar,C.,

Kowis,C.,Kraft,C.L.,Lebow,H.,Levan,J.,Lewis,L.,Li,Z.,Liu,J.,

Liu,J.,Liu,M.,Liu,Y.,London,P.,Longacre,S.,Lopez,J.,

Lorenshewa,L.,Loulseged,H.,Lozado,R.J.,Lu,X.,Ma,J.,

Maheshwari,M.,Mahindartne,M.,Mahmoud,M.,Malloy,K.,Mangum,A.,

Mangum,B.,Mapua,P.,Martin,K.,Martin,R.,Martinez,B.,

Mawhinney,S.,McLeod,M.P.,McNeill,T.Z.,Meenen,E.,

Mlosoavlevic,A.,Miner,G.,Minga,E.,Montemayor,J.,Moore,S.,

Morgan,M.,Morris,K.,Morris,S.,Munidas,M.,Murphy,S.,

Nankervis,C.,Neal,D.,Newton,N.,Nguyen,N.,Norris,S.,

Nwokeneme,O.,Okwunonu,G.,Olanunnsagun,A.,Pal,S.,Parks,K.,

Pastermak,S.,Paul,H.,Perez,A.,Perez,L.,Pfannkuch,C.,

Pieterman,S.,Polindexter,A.,Popovic,D.,Primus,E.,Pu,L.,L.,

Piazzi,M.,Quiroz,J.,Rachlin,E.,Reeves,K.,Regier,M.A.,Reigh,R.,

Reilly,B.,Reilly,M.,Ren,Y.,Reuter,M.,Richard,S.,Riggs,F.,

Rivers,C.,Rodkey,T.,Rojas,A.,Rose,M.,Rose,R.,Ruiz,S.J.,

Sanders,W.,Savery,G.,Scherer,S.,Scott,G.,Shatsman,S.,Shen,H.,

Shetty,J.,Shvartsbeyn,A.,Sisson,I.,Sitter,C.D.,Smaiz,D.,

Sneed,A.,Sodergren,E.,Song,X.-Z.,Sotelle,R.,Sosa,J.,

Steinle,M.,Strong,R.,Sutton,A.,Svatek,A.,Taber,P.,Taylor,C.,

Taylor,T.,Thomas,N.,Thomas,S.,Tingey,A.,Trejos,Z.,Usmani,K.,

Valas,R.,Vera,V.,Villaana,D.,Waldron,L.,Walker,B.,Wang,J.,

Wang,Q.,Wang,S.,Warren,J.,Warren,R.,Wei,X.,White,F.,

Williams,G.,Willson,R.,Wiczek,R.,Wooden,H.,Worley,K.,

Wright,D.,Wright,R.,Wu,J.,Yakub,S.,Yen,J.,Yoon,L.,Yoon,V.,

Yu,F.,Zhang,J.,Zhou,J.,Zhou,X.,Zhou,S.,Dunn,D.,von

Niederhausen,A.,Weiss,R.,Smith,D.R.,Holt,R.A.,Smith,H.O.,

Weinstock,G.,and Gibbs,R.A.

TITLE

Direct Submission

JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Unpublished  
2 (bases 1 to 421172)  
Worley, K.C.  
Direct Submission  
Submitted (25-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 421172)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (11-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Oct 11, 2002 this sequence version replaced gi:21743603.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GRWG  
Center clone name: CH230-231D7  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329  
Consensus quality: 302679 bases at least Q40  
Consensus quality: 309380 bases at least Q30  
Consensus quality: 313052 bases at least Q20  
Estimated insert size: 328717; sum-of-contigs estimation  
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html))  
\* NOTE: This sequence may represent more than one clone.  
\* NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence, as soon as it is available and the accession number will be preserved.

1 5264: contig of 5264 bp in length  
\* 5265 5364: gap of unknown length  
\* 5365 23206: contig of 17842 bp in length  
\* 23307 23306: gap of unknown length  
\* 23307 51321: contig of 28015 bp in length  
\* 51322 51421: gap of unknown length  
\* 51422 68374: contig of 16953 bp in length  
\* 68375 68474: gap of unknown length  
\* 68475 73067: contig of 4593 bp in length  
\* 73068 73167: gap of unknown length  
\* 73168 259372: contig of 186205 bp in length  
\* 259373 259472: gap of unknown length  
\* 259473 267150: contig of 7678 bp in length  
\* 267151 267250: gap of unknown length  
\* 267251 308706: contig of 41456 bp in length  
\* 308707 308806: gap of unknown length  
\* 308807 341693: contig of 32887 bp in length  
\* 341694 341793: gap of unknown length  
\* 341794 379744: contig of 37951 bp in length  
\* 379745 379844: gap of unknown length

FEATURES  
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1. 421172  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-231D7"  
963. 1760  
/note="clone\_boundary  
site: EcoRI  
end\_sequence: RWBOK16T0"  
1678. 5264  
/note="wgs\_contig"  
23307. 26161  
/note="wgs\_contig"  
26212. 29344  
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71261. 73067  
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73168. 74530  
/note="wgs\_contig"  
259473. 261100  
/note="wgs\_contig"  
261928. 267150  
/note="wgs\_contig"  
308807. 310434  
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337486. 341693  
/note="wgs\_contig"  
341794. 345624  
/note="wgs\_contig"  
349912. 351036  
/note="wgs\_contig"

ORIGIN  
Query Match 77.8%; Score 14; DB 2; Length 110000;  
Best Local Similarity 85.7%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;  
Matches 12; Conservative 2; Mismatches 0;  
Qy 5 UCCUGAGNNNNN 18  
Db 26154 TCCTGAGNNNNN 26167

RESULT 64  
AC025433/c 133614 bp DNA linear HTG 18-JUL-2000  
LOCUS Homo sapiens chromosome 5 clone CTB-17D7, WORKING DRAFT SEQUENCE,  
DEFINITION Homo sapiens chromosome 5 clone CTB-17D7, WORKING DRAFT SEQUENCE,  
AC025433  
AC025433.4 GI:9256471  
VERSION HTG; HTGS PHASE2; HTGS\_DRAFT.  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 133614)  
DOE Joint Genome Institute.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Sequencing of Human Chromosome 5  
Unpublished  
2 (bases 1 to 133614)  
DOE Joint Genome Institute.  
Direct Submission  
Submitted (09-MAR-2000) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
On Jul 18, 2000 this sequence version replaced gi:7711806.

-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: <http://www.jgi.doe.gov>  
-----

Project Information  
Center Project Name: 70811, H232  
Center clone name: CIT978SKB\_17D7  
-----

Summary Statistics  
Consensus quality: 117171 bases at least Q40  
Consensus quality: 127725 bases at least Q20  
Consensus quality: 130109 bases at least Q30  
Estimated insert size: 137000; pulse field gel estimation  
Estimated insert size: 132714; sum-of-contigs estimation  
Quality coverage: 4.57 in Q20 bases; pulse field gel estimation  
Quality coverage: 4.72 in Q20 bases; sum-of-contigs estimation.

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 20 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.

\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

1  
1671: contig of 1671 bp in length  
1671: contig of 1671 bp in length

1672 1771: gap of unknown length  
1772 2774: contig of 1003 bp in length  
2775 2874: gap of unknown length  
2875 6617: contig of 3743 bp in length  
6618 6717: gap of unknown length  
6718 8135: contig of 1418 bp in length  
8136 8235: gap of unknown length  
8236 12447: contig of 4212 bp in length  
12448 12547: gap of unknown length  
12548 14359: contig of 1812 bp in length  
14360 14459: gap of unknown length  
14460 29085: contig of 14626 bp in length  
29086 29185: gap of unknown length  
29186 35376: contig of 6191 bp in length  
35377 35476: gap of unknown length  
35477 46481: contig of 11005 bp in length  
46482 46581: gap of unknown length  
46582 50727: contig of 4146 bp in length  
50728 50827: gap of unknown length  
50829 54905: contig of 4078 bp in length  
54906 55005: gap of unknown length  
55006 58540: contig of 3535 bp in length  
58541 58640: gap of unknown length  
58641 59894: contig of 1254 bp in length  
59895 59994: gap of unknown length  
59996 63699: contig of 3705 bp in length  
63700 63799: gap of unknown length  
63800 66138: contig of 2339 bp in length  
66139 66238: gap of unknown length  
66239 67963: contig of 1725 bp in length  
67964 68063: gap of unknown length  
68064 87222: contig of 19159 bp in length  
87223 87322: gap of unknown length  
87323 90431: contig of 3109 bp in length  
90432 90531: gap of unknown length  
90532 121085: contig of 30554 bp in length  
121086 121185: gap of unknown length  
121186 133614: contig of 12429 bp in length.

FEATURES  
SOURCE

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/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="5"  
/clone="CTB-17D7"  
/clone\_lib="Caltech human BAC library B"

ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 133614;  
Best Local Similarity 85.7%; Pred. No. 1e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGGNNNNN 18  
:|||||  
Db 35484 TCCTGGAGNNNNN 35471

RESULT 65  
AC023576  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AC023576 150695 bp DNA linear HTG 30-MAY-2000  
Homo sapiens chromosome 1 clone RP11-574J7 map 1, LOW-PASS SEQUENCE  
SMAPPING.  
AC023576  
AC023576.2 GI:8112081  
HTG; HTGS\_PHASE0.  
Homo sapiens (human)  
Homo sapiens  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

1 (bases 1 to 150695)  
Homo sapiens chromosome 1, clone RP11-574J7  
Unpublished  
2 (bases 1 to 150695)  
Birren, B., Linton, L., Nussbaum, C., Lander, E., Abraham, H., Allen, N.,  
Anderson, S., Baldwin, J., Barna, N., Bede, F., Boguslavsky, L.,  
Boukhalil, B., Brown, A., Burkett, G., Campoliano, A., Cattle, A.,  
Choepel, Y., Collinge, M., Collins, S., Collipalmo, A., Cooke, P.,  
Darellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M.,  
Feneator, J., Ferreira, P., FitzHugh, M., Forrest, C., Gage, D.,  
Galaan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,  
Grand-Pierre, N., Grant, G., Hages, B., Heaford, A., Horton, L.,  
Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karacas, A.,  
Klein, J., Landers, T., Largocque, K., Lehocsky, J., Levine, R.,  
Lieu, C., Liu, G., Locke, K., MacDonald, P., Margulis, N., McCarthy, M.,  
McEwan, P., McGurk, A., McKernan, K., McPheters, R., Meldrum, J.,  
Meneas, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Naylor, J.,  
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T. M.,  
Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C.,  
Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,  
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
Stribermanian, A., Talamas, J., Testaye, S., Theodore, J., Tirrell, A.,  
Travers, M., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.,  
Xu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, D., Zimmer, A. and  
Zody, M.

Direct Submission  
Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On May 30, 2000 this sequence version replaced gi:6978288.  
All repeats were identified using RepeatMasker:  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
-----Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIRB  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
-----Project Information  
Center Project name: L6803  
Center clone name: 574\_J\_7

TITLE  
JOURNAL  
COMMENT

\* NOTE: This record contains 166 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

\* 1 714: contig of 714 bp in length  
\* 715 814: gap of 100 bp  
\* 815 1518: contig of 704 bp in length  
\* 1519 1618: gap of 100 bp  
\* 1619 2321: contig of 703 bp in length  
\* 2322 2421: gap of 100 bp  
\* 2422 3108: contig of 687 bp in length  
\* 3109 3208: gap of 100 bp  
\* 3209 3915: contig of 708 bp in length  
\* 3917 4016: gap of 100 bp  
\* 4017 4721: contig of 705 bp in length  
\* 4722 4821: gap of 100 bp  
\* 4822 5530: contig of 709 bp in length  
\* 5531 5630: gap of 100 bp  
\* 5631 6340: contig of 710 bp in length  
\* 6341 6440: gap of 100 bp  
\* 6441 7124: contig of 684 bp in length  
\* 7125 7224: gap of 100 bp  
\* 7225 7922: contig of 698 bp in length  
\* 7923 8022: gap of 100 bp  
\* 8023 8737: contig of 715 bp in length  
\* 8738 8837: gap of 100 bp  
\* 8838 9520: contig of 683 bp in length  
\* 9521 9620: gap of 100 bp  
\* 9621 10304: contig of 684 bp in length  
\* 10305 10404: gap of 100 bp  
\* 10405 11118: contig of 714 bp in length  
\* 11119 11218: gap of 100 bp  
\* 11219 11926: contig of 708 bp in length  
\* 11927 12026: gap of 100 bp  
\* 12027 12719: contig of 693 bp in length  
\* 12720 12819: gap of 100 bp  
\* 12820 13544: contig of 725 bp in length  
\* 13545 13644: gap of 100 bp  
\* 13645 14339: contig of 695 bp in length  
\* 14340 14439: gap of 100 bp  
\* 14440 15153: contig of 714 bp in length  
\* 15154 15253: gap of 100 bp  
\* 15254 15959: contig of 706 bp in length  
\* 15960 16059: gap of 100 bp  
\* 16060 16734: contig of 675 bp in length  
\* 16735 16834: gap of 100 bp  
\* 16835 17501: contig of 667 bp in length  
\* 17502 17601: gap of 100 bp  
\* 17603 18238: contig of 637 bp in length  
\* 18239 18338: gap of 100 bp  
\* 18339 19048: contig of 710 bp in length  
\* 19049 19148: gap of 100 bp  
\* 19149 19804: contig of 656 bp in length  
\* 19805 19904: gap of 100 bp  
\* 19905 20630: contig of 726 bp in length  
\* 20631 20730: gap of 100 bp  
\* 20731 21437: contig of 707 bp in length  
\* 21438 21537: gap of 100 bp  
\* 21538 22248: contig of 711 bp in length  
\* 22249 22348: gap of 100 bp  
\* 22349 23072: contig of 724 bp in length  
\* 23073 23172: gap of 100 bp  
\* 23173 23878: contig of 706 bp in length  
\* 23879 23978: gap of 100 bp  
\* 23979 24670: contig of 692 bp in length  
\* 24671 24770: gap of 100 bp

\* 24771 25448: contig of 678 bp in length  
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\* 25549 26230: contig of 682 bp in length  
\* 26231 26330: gap of 100 bp  
\* 26331 27021: contig of 691 bp in length  
\* 27022 27121: gap of 100 bp  
\* 27122 27833: contig of 712 bp in length  
\* 27834 27933: gap of 100 bp  
\* 27934 28620: contig of 687 bp in length  
\* 28621 28720: gap of 100 bp  
\* 28721 29420: contig of 700 bp in length  
\* 29421 29520: gap of 100 bp  
\* 29521 30235: contig of 715 bp in length  
\* 30236 30335: gap of 100 bp  
\* 30336 31031: contig of 696 bp in length  
\* 31032 31131: gap of 100 bp  
\* 31132 31848: contig of 717 bp in length  
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\* 32658 32767: gap of 100 bp  
\* 32768 33483: contig of 716 bp in length  
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\* 33584 34244: contig of 661 bp in length  
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\* 34345 35031: contig of 687 bp in length  
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\* 35132 35783: contig of 652 bp in length  
\* 35784 36597: contig of 714 bp in length  
\* 36598 36697: gap of 100 bp  
\* 36698 37417: contig of 720 bp in length  
\* 37418 37517: gap of 100 bp  
\* 37518 38228: contig of 711 bp in length  
\* 38229 38328: gap of 100 bp  
\* 38329 39042: contig of 714 bp in length  
\* 39043 39142: gap of 100 bp  
\* 39143 39827: contig of 686 bp in length  
\* 39828 39927: gap of 100 bp  
\* 39928 40615: contig of 688 bp in length  
\* 40616 40715: gap of 100 bp  
\* 40716 41396: contig of 681 bp in length  
\* 41397 41496: gap of 100 bp  
\* 41497 42299: contig of 703 bp in length  
\* 42300 42399: gap of 100 bp  
\* 42400 43002: contig of 703 bp in length  
\* 43003 43102: gap of 100 bp  
\* 43103 43806: contig of 704 bp in length  
\* 43807 43906: gap of 100 bp  
\* 43907 44612: contig of 706 bp in length  
\* 44613 44712: gap of 100 bp  
\* 44713 45428: contig of 716 bp in length  
\* 45429 45528: gap of 100 bp  
\* 45529 46243: contig of 715 bp in length  
\* 46244 46343: gap of 100 bp  
\* 46344 47017: contig of 674 bp in length  
\* 47018 47117: gap of 100 bp  
\* 47118 47824: contig of 707 bp in length  
\* 47825 47924: gap of 100 bp  
\* 47925 48610: contig of 686 bp in length  
\* 48611 48710: gap of 100 bp  
\* 48711 49421: contig of 711 bp in length  
\* 49422 49521: gap of 100 bp  
\* 49521 50341: contig of 720 bp in length  
\* 50342 51017: contig of 676 bp in length  
\* 51018 51117: gap of 100 bp  
\* 51118 51827: contig of 710 bp in length  
\* 51828 51927: gap of 100 bp  
\* 51928 52556: contig of 729 bp in length  
\* 52557 52756: gap of 100 bp  
\* 52757 53471: contig of 715 bp in length  
\* 53472 53571: gap of 100 bp  
\* 53572 54254: contig of 683 bp in length

\* 54355 54354: gap of 100 bp  
 \* 54355 55047: contig of 693 bp in length

Query Match 77.8%; Score 14; DB 2; Length 150695;  
 Best Local Similarity 85.7%; Pred. No. 1e+02;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

5 UCCUGAGANNNNNN 18  
 :||:|||||||  
 114977 TCCTGAGANNNNNN 114990

RESULT 66  
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 LOCUS  
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 AC142149 151097 bp DNA linear HTG 20-APR-2003  
 AC142149.4 GI:30026070  
 HTG: HTGS.PHASE1.  
 Rattus norvegicus (Norway rat)  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 151097)  
 Muzny,D,Marie, Metzker,M,Lee, Abrazon,S, Adams,C, Alder,J, Allen,C, Allen,H, Albrooks,S, Amin,A, Angiano,D, Anyalibechi,V, Aoyagi,A, Ayodeji,M, Baca,E, Baden,H, Baldwin,D, Bandaranaike,D, Barber,M, Barnstead,M, Benahmed,F, Biewald,K, Blair,J, Blankenburg,K, Blyth,P, Brown,M, Bryant,N, Buhay,C, Burch,P, Burrell,K, Calderon,E, Cadenas,V, Carter,K, Cavazos,I, Caesar,H, Center,A, Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J, Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L, Davila,M,L, Davis,C, Davy-Carroll,L, De Anda,C, Dederich,D, Delgado,O, Denison,S, Deramo,C, Ding,Y, Dinh,H, Divya,K, Draper,H, Dugan-Rocha,S, Dunn,A, Durbin,K, Duval,B, Evans,K, Egan,A, Escotto,M, Eugene,C, Evans,C,A, Falls,T, Fan,G, Fernandez,S, Finley,M, Flagg,N, Forbes,L, Foster,M, Foster,P, Fraser,C,M, Gabisi,A, Ganta,R, Garcia,A, Garner,T, Garza,M, Gebregorgis,E, Geer,K, Gill,R, Grady,M, Guerra,M, Guevara,W, Gunaratne,P, Haaland,M, Hamill,C, Hamilton,C, Hamilton,K, Harvey,Y, Havlak,P, Hawes,A, Henderson,N, Hernandez,J, Hernandez,R, Hines,S, Hladun,S,L, Hodgson,A, Hogues,M, Hollins,B, Howells,S, Hulik,S, Hume,J, Idlebird,D, Jackson,A, Jackson,L, Jacob,L, Jiang,H, Johnson,B, Johnson,R, Jolivet,A, Karpathy,S, Kelly,S, Kelly,S, Khan,Z, King,L, Kovar,C, Kowis,C, Kraft,C,L, Lebow,H, Levan,J, Lewis,L, Li,Z, Liu,J, Liu,J, Liu,W, Liu,Y, London,P, Longacre,S, Lopez,J, Lorenuhewa,L, Louisedge,H, Lozada,R,J, Lu,X, Ma,J, Maheshwari,M, Mahindaratne,M, Mahmoud,M, Malloy,K, Mangum,A, Mangum,B, Mapua,P, Martin,K, Martin,R, Martinez,B, Mawhinley,S, McLeod,M, McNeill,T, Meenen,E, Milosavljevic,A, Miner,G, Minja,E, Montemayor,J, Moore,S, Morgan,M, Morris,K, Morris,S, Munidasa,M, Murphy,M, Nair,L, Nankevris,C, Neal,D, Newton,S, Nguyen,N, Norris,S, Nwaokemele,O, Okwona,G, Olariunpaaogon,A, Pal,S, Parks,K, Paeternak,S, Paul,H, Popovic,D, Primus,E, Pu,L-L, Puazo,M, Quiroz,J, Rachlin,E, Reeves,K, Regier,M, Riggall,F, Rives,C, Rodkey,T, Rojas,A, Reuter,M, Richards,S, Riggs,F, Rives,C, Rodkey,T, Rojas,A, Rose,M, Rose,R, Ruiz,S,J, Sanders,W, Saverly,G, Scherer,S, Scott,G, Shatman,S, Shen,H, Shetty,J, Shvartsbeyn,A, Sisson,I, Sitter,C,D, Smajd,D, Sneed,A, Sodergren,E, Song,X-Z, Sorelle,R, Sosa,J, Steimle,M, Strong,R, Sutton,A, Staveler,A, Tabor,P, Taylor,C, Taylor,T, Thomas,N, Thomas,S, Tinger,A, Trejos,Z, Umani,K, Valas,R, Vera,V, Villasana,D, Waldron,L, Walker,B, Wang,J, Wang,Q, Wang,S, Warren,J, Warren,R, Wei,X, White,F, Williams,G, Willson,R, Wleczyk,R, Woodden,H, Worley,K, Wright,D, Wright,R, Wu,J, Yakub,S, Yan,J, Yoon,L, Yoon,V, Yu,F, Zhang,J, Zhou,J, Zhou,X, Zhao,S, Dunn,D, von Niederhausern,A, Weiss,R, Smith,D,R,

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 151097)  
 Worley,K.C.  
 Direct Submission  
 Submitted (23-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 151097)  
 Worley,K.C.  
 Direct Submission  
 Submitted (20-APR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 On Apr 20, 2003 this sequence version replaced gi:29366866.  
 ----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: KEOP  
 Center clone name: CH230-245G14  
 ----- Summary Statistics  
 Sequencing vector: Plasmid;  
 Chemistry: Dye-terminator Big Dye 100% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 128586 bases at least Q40  
 Consensus quality: 136602 bases at least Q30  
 Consensus quality: 142934 bases at least Q20  
 Estimated insert size: 13336; sum-of-coverage  
 Quality coverage: 2x in Q20 bases; sum-of-coverage estimation

NOTE: Estimated insert size may differ from sequence length  
 (see <http://www.hgsc.bcm.tmc.edu/docs/genbankdraft.data.html>).  
 NOTE: This is a "working draft" sequence. It currently consists of 53 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1101: contig of 1101 bp in length  
 1102 1201: gap of unknown length  
 1202 2666: contig of 1465 bp in length  
 2667 2766: gap of unknown length  
 2767 3805: contig of 1039 bp in length  
 3806 3905: gap of unknown length  
 3906 5001: contig of 1096 bp in length  
 5002 5101: gap of unknown length  
 5102 6205: contig of 1104 bp in length  
 6206 6305: gap of unknown length  
 6306 7492: contig of 1187 bp in length  
 7493 7592: gap of unknown length  
 7593 8734: contig of 1142 bp in length  
 8735 8834: gap of unknown length  
 8835 10072: contig of 1237 bp in length  
 10072 10171: gap of unknown length  
 10172 11381: contig of 1210 bp in length  
 11382 11481: gap of unknown length  
 11482 12810: contig of 1329 bp in length  
 12811 12910: gap of unknown length  
 12911 14287: contig of 1377 bp in length  
 14288 14387: gap of unknown length  
 14388 15797: contig of 1410 bp in length  
 15798 15897: gap of unknown length  
 15898 17405: contig of 1508 bp in length  
 17406 17505: gap of unknown length  
 17506 18656: contig of 1151 bp in length  
 18657 18756: gap of unknown length  
 18757 19886: contig of 1130 bp in length

```

* 19887 19986: gap of unknown length
* 19987 21267: contig of 1281 bp in length
* 21268 21367: gap of unknown length
* 21368 23384: contig of 2017 bp in length
* 23385 23484: gap of unknown length
* 23485 24781: contig of 1297 bp in length
* 24782 24881: gap of unknown length
* 24882 26325: contig of 1444 bp in length
* 26326 26425: gap of unknown length
* 26426 27891: contig of 1466 bp in length
* 27892 29249: contig of 1258 bp in length
* 29250 29349: gap of unknown length
* 29350 30511: contig of 1162 bp in length
* 30512 30612: gap of unknown length
* 30613 31639: contig of 1028 bp in length
* 31640 33262: contig of 1523 bp in length
* 33263 33362: gap of unknown length
* 33363 34819: contig of 1457 bp in length
* 34820 34919: gap of unknown length
* 34920 36444: contig of 1525 bp in length
* 36445 36544: gap of unknown length
* 36545 38154: contig of 1610 bp in length
* 38155 38254: gap of unknown length
* 38255 40652: contig of 2398 bp in length
* 40653 40752: gap of unknown length
* 40753 42596: contig of 1846 bp in length
* 42599 42698: gap of unknown length
* 42699 45341: contig of 2643 bp in length
* 45342 45441: gap of unknown length
* 45442 47416: contig of 1975 bp in length
* 47417 47516: gap of unknown length
* 47517 50148: contig of 2632 bp in length
* 50149 50248: gap of unknown length
* 50249 53066: contig of 2818 bp in length
* 53067 53166: gap of unknown length
* 53167 55930: contig of 2764 bp in length
* 55931 56031: gap of unknown length
* 56032 58774: contig of 2743 bp in length
* 58775 58874: gap of unknown length
* 58875 62176: contig of 3303 bp in length
* 62177 62276: gap of unknown length
* 62277 65607: contig of 3331 bp in length
* 65608 65707: gap of unknown length
* 65708 69755: contig of 4048 bp in length
* 69756 69855: gap of unknown length
* 69856 72866: contig of 3011 bp in length
* 72867 72966: gap of unknown length
* 72967 76494: contig of 3528 bp in length
* 76495 76594: gap of unknown length
* 76595 79874: contig of 3280 bp in length
* 79875 79974: gap of unknown length
* 79975 82982: contig of 3008 bp in length
* 82983 83082: gap of unknown length
* 83083 88834: contig of 5752 bp in length
* 88835 88934: gap of unknown length
* 88935 92177: contig of 3243 bp in length
* 92178 92277: gap of unknown length
* 92278 97659: contig of 5382 bp in length
* 97660 97759: gap of unknown length
* 97760 102398: contig of 4639 bp in length
* 102399 108654: gap of unknown length
* 108655 108754: contig of 6156 bp in length
* 108755 116575: gap of unknown length
* 116576 116675: contig of 7821 bp in length
* 116676 124086: contig of 7411 bp in length

```

Query Match 77.8%; Score 14; DB 2; Length 151097;  
 Best Local Similarity 85.7%; Pred. No. 1e+02; Indels 0; Gaps 0;  
 Matches 12; Conservative 2; Mismatches 0;

```

Qy 5 UCCUGAGANNNNNN 18
Db 144288 TCCTGGAGNNNNNN 144275

RESULT 67
AC074261
LOCUS
DEFINITION
ACCESSION
AC074261
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITILE
JOURNAL
REFERENCE
AUTHORS
TITILE
JOURNAL

COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0055F19
----- Summary Statistics -----
Sequencing vector: M3; 100%
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 145424 bases at least Q40
Consensus quality: 147251 bases at least Q30
Insert size: 14600; agarose-fp
Insert size: 149444; sum-of-contigs
Quality coverage: 5.22 in Q20 bases; agarose-fp
Quality coverage: 5.13 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1452: contig of 1452 bp in length
1553
1553: gap of unknown length
3955
4054: gap of unknown length
4055
5943: contig of 1889 bp in length
5944
6043: gap of unknown length
6044
10527: contig of 4484 bp in length
10528
10627: gap of unknown length
10628
15918: contig of 5291 bp in length
15919
20749: gap of unknown length
16019
20749: contig of 4731 bp in length
20750
20849: gap of unknown length
20850
27240: contig of 6391 bp in length
27241
27340: gap of unknown length
27341
36787: contig of 9447 bp in length
36788
36887: gap of unknown length

```

\* 36888 47572: contig of 10685 bp in length  
\* 47573 47672: contig of unknown length  
\* 47673 66286: contig of 18614 bp in length  
\* 66287 66386: gap of unknown length  
\* 66387 84036: contig of 17650 bp in length  
\* 84037 84137: gap of unknown length  
\* 84137 106069: contig of 21933 bp in length  
\* 106070 106169: gap of unknown length  
\* 106170 126375: contig of 20206 bp in length  
\* 126376 126475: gap of unknown length  
\* 126476 150744: contig of 24269 bp in length  
\* 150745 150844: gap of unknown length  
\* 150845 151448: contig of 604 bp in length.

## FEATURES

## source

location/Qualifiers  
1. 151448  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="12"  
/clone="RP11-55F19"

misc\_feature 1. 1452  
/note="assembly\_name:Contig11"  
misc\_feature 1553. 3954  
/note="assembly\_name:Contig12"  
misc\_feature 4055. 5943  
/note="assembly\_name:Contig13"  
misc\_feature 6044. 10527  
/note="assembly\_name:Contig14"  
misc\_feature 10628. 15918  
/note="assembly\_name:Contig15"  
misc\_feature 16019. 20749  
/note="assembly\_name:Contig16"  
misc\_feature 20850. 27240  
/note="assembly\_name:Contig17"  
misc\_feature 27341. 36787  
/note="assembly\_name:Contig18"  
misc\_feature 36888. 47572  
/note="assembly\_name:Contig19"  
misc\_feature 47673. 66286  
/note="assembly\_name:Contig20"  
misc\_feature 66387. 84036  
/note="assembly\_name:Contig21"  
misc\_feature 84137. 106069  
/note="assembly\_name:Contig22"  
misc\_feature 106170. 126375  
/note="assembly\_name:Contig23"  
misc\_feature 126476. 150744  
/note="assembly\_name:Contig24"  
misc\_feature 150845. 151448  
/note="assembly\_name:Contig7"

## ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 151448;  
Best Local Similarity 85.7%; Pred. No. 1e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGAGNNNNNN 18  
Db 3947 TCCTGAGAGNNNNN 3960

RESULT 68  
LOCUS BX927200 152420 bp DNA linear HTG 24-JAN-2004  
DEFINITION Danio rerio clone CH211-116A20, WORKING DRAFT SEQUENCE, 8 unordered  
pieces.  
ACCESSION BX927200  
VERSION BX927200.2 GI:41322788  
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_FULLTOP.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

## COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 152420)  
Burton, J.  
Direct Submission  
Submitted (23-JUN-2004) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
On Jan 25, 2004 this sequence version replaced gi:41223462.  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: zfish-help@sanger.ac.uk  
----- Project Information  
Center project name: ZC116A20  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 10% of reads  
Consensus quality: 150420 bases at least Q40  
Consensus quality: 151102 bases at least Q30  
Consensus quality: 151513 bases at least Q20  
Insert size: 151720; sum-of-contigs  
Insert size: 167766; 4.0% error; agarose-1p  
Quality coverage: 9.55x in Q20 bases; sum-of-contigs Quality  
coverage: 8.84x in Q20 bases; agarose-1p  
-----

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 8 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 33759: contig of 33759 bp in length  
\* 33760 33859: gap of 100 bp  
\* 33860 43530: contig of 9671 bp in length  
\* 43531 43630: gap of 100 bp  
\* 43631 48335: contig of 4705 bp in length  
\* 48336 48435: gap of 100 bp  
\* 48436 65568: contig of 17133 bp in length  
\* 65569 65668: gap of 100 bp  
\* 65669 69685: contig of 4017 bp in length  
\* 69686 69785: gap of 100 bp  
\* 69786 76321: contig of 6536 bp in length  
\* 76322 76421: gap of 100 bp  
\* 76422 120851: contig of 44430 bp in length  
\* 120852 120951: gap of 100 bp  
\* 120952 152420: contig of 31469 bp in length.

## FEATURES

## source

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/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="CH211-116A20"  
/clone\_lib="CHORI-211"  
1. 33759  
/note="assembly\_fragment:01133  
fragment\_chain:1"

## misc\_feature

clone\_end:T7  
vector\_side:left  
33860. 43530  
/note="assembly\_fragment:00194  
fragment\_chain:1"

## misc\_feature

43631. 48335  
/note="assembly\_fragment:00100  
fragment\_chain:1"

## misc\_feature

48436. 65568  
/note="assembly\_fragment:00346  
fragment\_chain:1"

## misc\_feature

65669. 69685  
/note="assembly\_fragment:00346  
fragment\_chain:1"

## misc\_feature

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/misc_feature /note="assembly_fragment:00012
fragment_chain:1"
misc_feature /note="assembly_fragment:00044
fragment_chain:1"
misc_feature /note="assembly_fragment:01745
fragment_chain:1"
misc_feature /note="assembly_fragment:00585
fragment_chain:1"
clone_end:SP6
vector_side:right"

ORIGIN

Query Match 77.8% Score 14; DB 2; Length 152420;
Best Local Similarity 85.7%; Pred. NO. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGNNNNN 18
Db 43523 TCCTGAGNNNNN 43536

RESULT 69
AC117546/c 154474 bp DNA linear HTG 24-FEB-2003
LOCUS Mus musculus clone RP23-220E20, WORKING DRAFT SEQUENCE, 23
DEFINITION unsorted pieces.
AC117546
AC117546 GI:28475947
VERSION HTG; HTGS PHASE1; HTGS DRAFT.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 154474)
TITLE Birren,B., Nusbaum,C. and Lander,E.
JOURNAL Mus musculus, clone RP23-220E20
REFERENCE Unpublished
AUTHORS 2 (bases 1 to 154474)
Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhalter,B., Brown,A., Camarata,J., Campoliano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Deakellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagge,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Labrecque,K., Lamazares,R.,
Landers,T., Lehoczyk,J., Levine,R., Lindblad-Toh,K., Liu,G.,
Maclean,C., MacDonald,P., Major,J., Margulis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrum,J., Menais,L.,
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schnupack,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Sudrmanian,A., Talamas,J., Testaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 154474)
TITLE Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
JOURNAL Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
REFERENCE Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,
AUTHORS Collymore,A., Cook,A., Cooke,P., Corum,B., Deakellano,K.,
Diaz,J.S., Dodge,S., Doolley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,

```

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TITLE
JOURNAL
COMMENT
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Liu,A., Mabbitt,R., Maclean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrum,J., Menais,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schnupack,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-FEB-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 24, 2003 this sequence version replaced gi:21306852.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RV/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 220_E_20
Center clone name: L17227
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 148512 bases at least Q40
Consensus quality: 150760 bases at least Q30
Consensus quality: 151523 bases at least Q20
Insert size: 163000; agarose-fp
Insert size: 152274; sum-of-contigs
Quality coverage: 5.7 in Q20 bases; sum-of-contigs
Quality coverage: 6.1 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 11: contig of 11 bp in length
* 12 111: gap of 100 bp
* 112 945: contig of 834 bp in length
* 946 1045: gap of 100 bp
* 1046 1775: contig of 730 bp in length
* 1776 1875: gap of 100 bp
* 1876 3255: contig of 1380 bp in length
* 3256 3355: gap of 100 bp
* 3356 4362: contig of 1007 bp in length
* 4363 4462: gap of 100 bp
* 4463 5745: contig of 1283 bp in length
* 5746 5845: gap of 100 bp
* 5846 7326: contig of 1481 bp in length
* 7327 7426: gap of 100 bp
* 7427 8111: contig of 685 bp in length
* 8112 8211: gap of 100 bp
* 8212 10181: contig of 1970 bp in length
* 10182 10281: gap of 100 bp
* 10282 12496: contig of 2215 bp in length
* 12497 12596: gap of 100 bp
* 12597 14720: contig of 2124 bp in length
* 14721 14820: gap of 100 bp
* 14821 17328: contig of 2508 bp in length
* 17329 17428: gap of 100 bp

```



```

* 17429 21654: contig of 4226 bp in length
* 21755 28010: contig of 6256 bp in length
* 21755 28010: gap of 100 bp
* 28011 28110: gap of 100 bp
* 28111 32487: contig of 4377 bp in length
* 32488 32587: gap of 100 bp
* 32588 39138: contig of 6551 bp in length
* 39139 39238: gap of 100 bp
* 39239 46847: contig of 7609 bp in length
* 46848 46947: gap of 100 bp
* 46948 56206: contig of 9259 bp in length
* 56207 56307: gap of 100 bp
* 56307 66269: contig of 9963 bp in length
* 66270 66370: gap of 100 bp
* 66370 95113: contig of 28744 bp in length
* 95114 95213: gap of 100 bp
* 95214 118555: contig of 23342 bp in length
* 118556 141728: gap of 100 bp
* 118556 141728: contig of 23073 bp in length
* 141729 141829: gap of 100 bp
* 141829 154474: contig of 12646 bp in length.

FEATURES
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/mol_type="Genomic DNA"
/db_xref="taxon:10090"
/clone_id="RP23-220820"
/clone_lib="RPCI-23 Female Mouse BAC"
1. 11
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vector_side:left"
112. 345
/note="assembly_fragment"
1046. 1775
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1876. 3255
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3356. 4362
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4463. 5745
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5846. 7326
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7427. 8111
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8212. 10181
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17429. 21654
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39239. 46847
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46948. 56206
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56307. 66269
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66370. 95113
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95214. 118555
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118556. 141728
/note="assembly_fragment"

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```

misc_feature 141829..154474
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clone_end:17
vector_side:right"

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## ORIGIN

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Query Match 77.8%; Score 14; DB 2; Length 154474;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Oy 5 UCCUGAGANNNNNN 18
|||||
Db 1053 TCCTGGAGNNNNNN 1040

```

## RESULT 70

```

AC025626/c 154696 bp DNA linear HTG 28-MAY-2000
LOCUS Homo sapiens clone RP11-216B13, WORKING DRAFT SEQUENCE, 35
DEFINITION

```

```

AC025626 154696 bp DNA linear HTG 28-MAY-2000
unorderd pieces.

```

```

AC025626 GI:8099800
HTG; HTGS PHASE1; HTGS_DRAFT.

```

```

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 154696)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Unpublished
2 (bases 1 to 154696)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavsky,L., Bouckgalter,B., Brown,A., Buckett,G.,
Campoliano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeArrelino,K., Dewar,K., Diaz,J.S.,
Dodgson,S., Domingo,M., Doyle,W., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karakas,A.,
Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Margrie,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheters,R.,
Meldrum,T., Meneses,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rotman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Teafaye,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,D.,
Vassiliev,H., Vziel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (12-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 28, 2000 this sequence version replaced gi:7657088.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

```

## REFERENCE

```

AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

```

```

TITLE
JOURNAL
COMMENT

```

```

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 15807
Center clone name: 216_B_13
----- Summary Statistics
Sequencing vector: MJ3; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

```

Consensus quality: 135951 bases at least Q40  
Consensus quality: 145629 bases at least Q30  
Consensus quality: 148984 bases at least Q20  
Insert size: 149000; agarose-fp  
Insert size: 151296; sum-of-contigs  
Quality coverage: 3.7 in Q20 bases; agarose-fp  
Quality coverage: 3.7 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 35 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence, as soon as it is available and the accession number will be preserved.

1 1088: contig of 1088 bp in length  
1089 1188: gap of 100 bp  
1189 2246: contig of 1058 bp in length  
2247 2346: gap of 100 bp  
2347 3505: contig of 1159 bp in length  
3506 3605: gap of 100 bp  
3606 4777: contig of 1172 bp in length  
4778 4878: gap of 100 bp  
4878 6634: contig of 1757 bp in length  
6635 6735: gap of 100 bp  
6735 8097: contig of 1363 bp in length  
8098 8197: gap of 100 bp  
8198 10306: contig of 2109 bp in length  
10307 10406: gap of 100 bp  
10407 12406: contig of 2000 bp in length  
12407 12506: gap of 100 bp  
12507 14219: contig of 1713 bp in length  
14220 14319: gap of 100 bp  
14320 16072: contig of 1753 bp in length  
16073 16173: gap of 100 bp  
16173 17723: contig of 1551 bp in length  
17724 17823: gap of 100 bp  
17824 19608: contig of 1785 bp in length  
19609 19708: gap of 100 bp  
19709 22007: contig of 2239 bp in length  
22008 22107: gap of 100 bp  
22108 23950: contig of 1843 bp in length  
23951 24050: gap of 100 bp  
24051 26881: contig of 2831 bp in length  
26882 26981: gap of 100 bp  
26982 29772: contig of 2791 bp in length  
29773 29872: gap of 100 bp  
29873 32507: contig of 2635 bp in length  
32508 32607: gap of 100 bp  
32608 36314: contig of 3707 bp in length  
36315 36414: gap of 100 bp  
36415 38938: contig of 2424 bp in length  
38939 42279: contig of 3341 bp in length  
42280 42379: gap of 100 bp  
42380 44940: contig of 2561 bp in length  
44941 45041: gap of 100 bp  
45041 48484: contig of 3443 bp in length  
48485 48584: gap of 100 bp  
48585 52752: contig of 4169 bp in length  
52753 52852: gap of 100 bp  
52853 57772: contig of 4919 bp in length  
57773 57872: gap of 100 bp  
57873 61962: contig of 4091 bp in length  
61963 62062: gap of 100 bp  
62063 65728: contig of 3666 bp in length  
65729 65828: gap of 100 bp  
65829 69752: contig of 3924 bp in length  
69753 69853: gap of 100 bp  
69854 76487: contig of 6635 bp in length  
76488 76587: gap of 100 bp  
76588 84995: contig of 8408 bp in length

## FEATURES

\* 84996 85095: gap of 100 bp  
\* 85096 91863: contig of 6768 bp in length  
\* 91864 91963: gap of 100 bp  
\* 91964 104501: contig of 12538 bp in length  
\* 104502 104601: gap of 100 bp  
\* 104602 116857: contig of 12256 bp in length  
\* 116858 116957: gap of 100 bp  
\* 116958 127000: contig of 10043 bp in length  
\* 127001 127100: gap of 100 bp  
\* 127101 140329: contig of 13229 bp in length  
\* 140330 140429: gap of 100 bp  
\* 140430 154696: contig of 14267 bp in length.

## source

1. 154696 Location/Qualifiers  
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/clone\_lib="RP11-11 Human Male BAC"  
1. 1088  
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1189. 2246  
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 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNNN 18  
 :||:|||||  
 Db 76595 TCCTGGAGNNNNNN 76582

RESULT 71  
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 DEFINITION Macaca mulatta clone CH250-272M19, \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 AC144021  
 AC144021.1 GI:29649612  
 HTG; HTGS\_PHASE2; HTGS\_PGI.  
 Macaca mulatta (rhesus monkey)  
 Macaca mulatta  
 Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Eukaryota; Euteleostomi; Primates; Catarrhini; Cercopithecoidea;  
 Cercopithecinae; Macaca.  
 1 (bases 1 to 158981)  
 Cauros, M. and Mlosovlevic, A.  
 Pooled genomic indexing (PGI): mathematical analysis and experiment  
 design  
 (in) Guiso R. and Gusfield, D. (Eds.):  
 ALGORITHMS IN BIOINFORMATICS, SECOND INTERNATIONAL WORKSHOP, WABI  
 2002, ROME, ITALY, SEPTEMBER 17-21, 2002, PROCEEDINGS: 10-28;  
 Springer (2002)  
 2 (bases 1 to 158981)  
 Mlosovlevic, A., Sodergren, E., Cauros, M., Li, B., Jackson, A.R.,  
 Adams, C., Adio-oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L.,  
 Amaratunga, H.C., Are, J.R., Ayale, M., Banks, T., Barbata, J.,  
 Benton, J., Bimege, K., Blankenship, K., Bonnin, D., Bouck, O.,  
 Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bulhay, C.,  
 Burck, P., Burkett, C., Burrell, K.L., Byrd, N.C., Caron, T.F.,  
 Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,  
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 Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,  
 Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,  
 Denu, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,  
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 Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O.,  
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 Howard, S., Huber, J., Hulik, J., Hume, J., Ioshikes, I., Jackson, L.E.,  
 Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,  
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 Ma, J., Maheshwari, M., Mapa, P., Maronde, I., Martin, R.,  
 Martindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P.,  
 Medard, M., Mei, G., Mercher, S., Metzger, M., Miller, A., Miner, G.,  
 Miner, S., Mitchell, T., Monabhat, K., Montgomery, K.T., Morgan, M.,  
 Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N.,  
 Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nockenkov, S.,  
 Ough, M., Okunou, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,  
 Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pritchard, L.,  
 Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojdoxan, I., Rolfe, M.,  
 Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shih, C.,  
 Shiohata, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A.,  
 Stanley, H., Stone, H., Sutton, A., Svatek, A., Taber, P., Tamerisa, A.,  
 Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B.,  
 Thomas, N., Thomas, S., Usmani, K., Vazquez, L., Vera, V., Villalón, D.,  
 Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R.,  
 Washington, C., Watlington, S., Williams, G., Williamson, A.,  
 Wiczak, R., Woodson, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J.,  
 Zorilla, S., Zuerlein, R., Weinstein, G. and Gibbs, R.  
 Direct Submission

JOURNAL Unpublished  
 3 (bases 1 to 158981)  
 REFERENCES  
 Worley, K.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-APR-2003) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 COMMENT  
 ----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
 ----- Project Information  
 Center project name: LCVO  
 Center clone name: CH250-272M19  
 ----- Summary Statistics  
 Chemistry: Dye-terminator Big Dye; Int% of reads  
 Chemistry: Dye-terminator Big Dye; Int% of reads  
 Consensus quality: 8998 bases at least Q40  
 Consensus quality: 10656 bases at least Q30  
 Consensus quality: 12610 bases at least Q20  
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 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html))  
 \* NOTE: The config are based on the application  
 \* of the PGI method using the Human genome (NCBI build 31)  
 \* as the comparative genome.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 1 contigs. Gaps between the contigs  
 \* are represented as runs of N. The order of the pieces  
 \* is believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have  
 \* provided by the submitter.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
 1 158981: config of 158981 bp in length.  
 Location/Qualifiers  
 1. 158981  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9544"  
 /clone="CH250-272M19"  
 1. 158981  
 /note="assembly name: CH250-272M19.1B  
 CONFIDENCE: 0.83"

ORIGIN  
 misc\_feature  
 Query Match 77.8%; Score 14; DB 2; Length 158981;  
 Best Local Similarity 85.7%; Pred. No. 1e+02;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNNN 18  
 :||:|||||  
 Db 125578 TCCTGGAGNNNNNN 125591

RESULT 72  
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 DRAFT SEQUENCE, 208 unordered pieces.  
 AL627241  
 AL627241.2 GI:17154521  
 HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 Rattus norvegicus (Norway rat)  
 Rattus norvegicus  
 Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1  
 Subtrak, R., Borzym, K., Mueller, I., Klages, S., Kojima, A.,  
 Walter, L., Guenther, E., Hurt, P., Lehrach, H., Himmelbauer, H. and

Reinhardt, R.  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 159732)  
AUTHORS MOLGENR.  
TITLE Direct Submission  
JOURNAL Submitted (22-OCT-2001) MPIMG, Abt. Lehrach, Max Planck Institut  
Fuer Molekulare Genetik, Ihnestrasse 73, Berlin, 14195 Germany  
COMMENT On Nov 29, 2001 this sequence version replaced gi:16416083.  
contig 01 1..485  
contig 02 586..2139  
contig 03 2240..2622  
contig 04 2723..3242  
contig 05 3343..3741  
contig 06 3842..4514  
contig 07 4615..5100  
contig 08 5201..6281  
contig 09 6382..6795  
contig 10 6896..7823  
contig 11 7924..8859  
contig 12 8960..9970  
contig 13 10071..10603  
contig 14 10704..11117  
contig 15 11218..11541  
contig 16 11642..11836  
contig 17 11937..12664  
contig 18 12765..13209  
contig 19 13310..13840  
contig 20 13941..14593  
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contig 23 15537..15720  
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contig 25 17050..17480  
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contig 27 18588..19109  
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contig 39 24461..24929  
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contig 43 26038..26430  
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contig 48 28083..28319  
contig 49 28420..28534  
contig 50 28635..28991  
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contig 73 45521..46039  
contig 74 46140..46414  
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contig 77 47293..47450  
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contig 79 47961..48430  
contig 80 48531..48653  
contig 81 48754..49063  
contig 82 49164..49670  
contig 83 49771..50025  
contig 84 50126..50257  
contig 85 50358..50715  
contig 86 50816..51272  
contig 87 51373..52012  
contig 88 52113..52782  
contig 89 52883..53189  
contig 90 53290..53793  
contig 91 53894..55049  
contig 92 55150..55809  
contig 93 55910..56216  
contig 94 56317..56478  
contig 95 56579..56830  
contig 96 56931..58630  
contig 97 58731..61919  
contig 98 62020..63009  
contig 99 63110..64262  
contig 100 64363..66293  
contig 101 66394..69648  
contig 102 69749..70372  
contig 103 70373..71267  
contig 104 71368..71964  
contig 105 72065..73347  
contig 106 73448..76788  
contig 107 76889..77454  
contig 108 77555..77994  
contig 109 78095..78534  
contig 110 78635..79129  
contig 111 79230..80115  
contig 112 80216..80696  
contig 113 80797..81094  
contig 114 81195..81562  
contig 115 81663..82073  
contig 116 82174..82860  
contig 117 82961..83358  
contig 118 83459..84108  
contig 119 84209..85381  
contig 120 85482..86381  
contig 121 86482..89030  
contig 122 89131..89820  
contig 123 89921..90373  
contig 124 90474..91295  
contig 125 91396..91885  
contig 126 91986..92467  
contig 127 92568..93077  
contig 128 93178..94148  
contig 129 94249..94776  
contig 130 94877..95508  
contig 131 95609..96081  
contig 132 96182..96480  
contig 133 96581..96738  
contig 134 96839..97101  
contig 135 97202..97344  
contig 136 97445..98094  
contig 137 98195..98621  
contig 138 98722..99640

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contig 139      99741..100464
contig 140      100555..100972
contig 141      101073..102073
contig 142      102174..103405
contig 143      103506..104010
contig 144      104111..104848
contig 145      104949..105842
contig 146      105943..106363
contig 147      106464..107150
contig 148      107251..107535
contig 149      107636..108568
contig 150      108669..109539
contig 151      109640..110953
contig 152      111054..111648
contig 153      111749..112240
contig 154      112341..113299
contig 155      113400..114244
contig 156      114345..115184
contig 157      115285..116003
contig 158      116104..117167
contig 159      117268..117889
contig 160      117990..118432
contig 161      118533..119049
contig 162      119150..119723
contig 163      119824..120825
contig 164      120926..121983
contig 165      122084..122875
contig 166      122976..124559
contig 167      124660..125228
contig 168      125329..125919
contig 169      126020..126849
contig 170      126950..128084
contig 171      128185..129302
contig 172      129403..129777
contig 173      129878..130903
contig 174      131004..132380
contig 175      132481..133687
contig 176      133788..134549
contig 177      134650..135830
contig 178      135931..136817

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Query Match 77.8%; Score 14; DB 2; Length 159732;  
 Best Local Similarity 85.7%; Pred. No. 1e+02;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNNN 18  
 :||:|||||||  
 Db 2132 TCCTGAGAGNNNNNN 2145

RESULT 73  
 AC027535/c 161829 bp DNA linear HTG 25-JUN-2000  
 LOCUS Homo sapiens chromosome 3 clone RP11-80B17 map 3, WORKING DRAFT  
 DEFINITION  
 AC027535 20 unordered pieces.  
 AC027535 GI:8705144  
 VERSION  
 HTG; HTGS PHASE1; HTGS\_DRAFT.  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 161829)  
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
 Homo sapiens chromosome 3, clone RP11-80B17  
 Unpublished  
 2 (bases 1 to 161829)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
 Anderson,S., Baldwin,J., Barina,N., Baetsen,V., Beda,F.,  
 Boguslavsky,L., Boukhalter,B., Brown,A., Burkett,G.,  
 Campiano,A., Castle,A., Choe,Y., Colangelo,M., Collins,S.,  
 Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,  
 Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,

TITLE  
JOURNAL

## COMMENT

Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,  
 Grand-Pierre,N., Grant,G., Hagoe,B., Heaford,A., Horton,L.,  
 Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karakas,A.,  
 Klein,J., Lacroque,K., Lamazares,R., Landers,T., Lehotzky,U.,  
 Levine,R., Liu,G., Locke,K., Macdonald,P., Margulis,N.,  
 McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPeckers,R.,  
 Meldrum,T., Menes,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,  
 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
 O'Neil,D., Oliver,T.M., Oliver,U., Peterson,K., Pierre,N.,  
 Pisan,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,  
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,U.,  
 Teefage,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,  
 Vasiliiev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Jun 25, 2000 this sequence version replaced gi:7342280.  
 All repeats were identified using RepeatMasker:  
 Smc, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WtBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L8663  
 Center clone name: 80.B.17  
 ----- Summary Statistics  
 Sequencing vector: M13; M77815; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 150530 bases at least Q40  
 Consensus quality: 15616 bases at least Q30  
 Consensus quality: 158784 bases at least Q20  
 Insert size: 157000; agarose-fp  
 Insert size: 159929; sum-of-coverage  
 Quality coverage: 4.1 in Q20 bases; sum-of-coverage  
 Quality coverage: 4.1 in Q20 bases; sum-of-coverage  
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 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 20 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 1 1220: contig of 1220 bp in length  
 \* 1221 1320: gap of 100 bp  
 \* 1321 2400: contig of 1080 bp in length  
 \* 2401 2500: gap of 100 bp  
 \* 2501 4030: contig of 1530 bp in length  
 \* 4031 4130: gap of 100 bp  
 \* 4131 6165: contig of 2035 bp in length  
 \* 6166 6265: gap of 100 bp  
 \* 6266 8351: contig of 2086 bp in length  
 \* 8352 8451: gap of 100 bp  
 \* 8452 11132: contig of 2681 bp in length  
 \* 11133 11232: gap of 100 bp  
 \* 11233 14754: contig of 3522 bp in length  
 \* 14755 14854: gap of 100 bp  
 \* 14855 18511: contig of 3657 bp in length  
 \* 18512 18611: gap of 100 bp  
 \* 18612 21628: contig of 3017 bp in length  
 \* 21629 21728: gap of 100 bp  
 \* 21729 26262: contig of 4534 bp in length  
 \* 26263 31430: gap of 100 bp  
 \* 31431 31530: contig of 5068 bp in length  
 \* 31531 37366: contig of 5836 bp in length

	*	37367	37466:	gap of 100 bp			
	*	37467	44372:	contig of 6506 bp	in length		
	*	44373	44472:	gap of 100 bp			
	*	44473	44472:	gap of 100 bp	in length		
	*	54510	54503:	contig of 10037 bp	in length		
	*	54510	54609:	gap of 100 bp			
	*	54510	54522:	contig of 9913 bp	in length		
	*	64623	64622:	gap of 100 bp			
	*	74692	74692:	contig of 10070 bp	in length		
	*	74693	74792:	gap of 100 bp			
	*	74793	85848:	contig of 11056 bp	in length		
	*	85849	85948:	gap of 100 bp			
	*	85949	108162:	contig of 22214 bp	in length		
	*	108163	108262:	gap of 100 bp			
	*	108263	129110:	contig of 20848 bp	in length		
	*	129111	129210:	gap of 100 bp			
	*	129211	161829:	contig of 32619 bp	in length.		
FEATURES							
source							
location/Qualifiers							
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		/organism="Homo sapiens"					
		/mol_type="genomic DNA"					
		/db_xref="taxon:9606"					
		/chromosome="3"					
		/map="13"					
		/clone="RP11-80B17"					
		/clone_1id="RP11-11 Human Male BAC"					
		1.	1220				
misc_feature		/note="assembly_fragment"					
		131.	12400				
misc_feature		/note="assembly_fragment"					
		2501.	4030				
misc_feature		/note="assembly_fragment"					
		4131.	6165				
misc_feature		/note="assembly_fragment"					
		6266.	8351				
misc_feature		/note="assembly_fragment"					
		8452.	11132				
misc_feature		/note="assembly_fragment"					
		11233.	14754				
misc_feature		/note="assembly_fragment"					
		14855.	18511				
misc_feature		/note="assembly_fragment"					
		18612.	21628				
misc_feature		/note="assembly_fragment"					
		21729.	26262				
misc_feature		/note="assembly_fragment"					
		26363.	31430				
misc_feature		/note="assembly_fragment"					
		31531.	37366				
misc_feature		/note="assembly_fragment"					
		37467.	44372				
misc_feature		/note="assembly_fragment"					
		clone_end:SP6					
		vector_side:right					
		44473.	54509				
misc_feature		/note="assembly_fragment"					
		54610.	64522				
misc_feature		/note="assembly_fragment"					
		clone_end:T7					
		vector_side:right					
		64623.	74692				
misc_feature		/note="assembly_fragment"					
		74793.	85848				
misc_feature		/note="assembly_fragment"					
		85949.	108162				
misc_feature		/note="assembly_fragment"					
		108263.	129110				
misc_feature		/note="assembly_fragment"					
		129211.	161829				
misc_feature		/note="assembly_fragment"					
ORIGIN							
Query Match	77.8%;	Score 14;	DB				

Matches	12,	Conservative	2;	Mismatches	0;	Indels	0;	Gaps	0;
Ox	5	UCCUGAGGNNNNN	18	:	:	:	:	:	:
Db	108270	TCTGTGAGANNNNNN	108257						

RESULT 74  
BX908804/c

LOCUS	BX908804	163732 bp	DNA	linear	HTG 17-FEB-2004
DEFINITION	Danio rerio clone CH211-163M16, WORKING DRAFT SEQUENCE, 11				
ACCESSION	BX908804				
KEYWORDS	unordered pieces.				
SOURCE	BX908804.5 GI:42592630				
ORGANISM	HTG: HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP. Danio rerio [zebrafish]				
REFERENCE	Danio rerio Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio. 1 (bases 1 to 163732) Sims,S. Direct Submission Submitted (13-FEB-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 17, 2004 this sequence version replaced gi:42538895.				
AUTHORS	----- Genome Center				
JOURNAL	Center: Wellcome Trust Sanger Institute Center code: SC Web site: http://www.sanger.ac.uk Contact: zfish-help@sanger.ac.uk Project Information Center project name: ZC163M16 ----- Summary Statistics				
COMMENT	Assembly program: XGAP4; version 4.5 Chemistry: dye-terminator; 100% of reads Consensus quality: 160023 bases at least Q40 Consensus quality: 160522 bases at least Q30 Consensus quality: 160800 bases at least Q20 Insert size: 162732; sum-of-contigs Insert size: 173608; 1.2% error; agarose-fp Quality coverage: 11.84x in Q20 bases; sum-of-contigs Quality coverage: 11.22x in Q20 bases; agarose-fp ----- NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. 1 6995: contig of 6995 bp in length 6996 7095: gap of 100 bp 7096 16711: contig of 9616 bp in length 16712 16811: gap of 100 bp 16812 35552: contig of 18741 bp in length 35553 35652: gap of 100 bp 35653 38371: contig of 2719 bp in length 38372 38471: gap of 100 bp 38472 64553: contig of 26082 bp in length 64554 64653: gap of 100 bp 64654 109139: contig of 44466 bp in length 109140 109238: gap of 100 bp 109239 113076: contig of 3837 bp in length 113077 113176: gap of 100 bp 113177 137707: contig of 24531 bp in length 137708 137807: gap of 100 bp 137808 152500: contig of 14663 bp in length 152501 152600: gap of 100 bp 152601 160231: contig of 7631 bp in length 160232 160331: gap of 100 bp				

```

COMMENT
On Sep 1, 2000 this sequence version replaced gi:7523968.

MO 63108, USA
University School of Medicine, 4444 Forest Park Parkway, St. Louis,

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Project Information -----
Center project name: H_NH0424B07
Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 169510 bases at least Q40
Consensus quality: 170826 bases at least Q30
Consensus quality: 171573 bases at least Q20
Insert size: 15500; agarose-fp
Insert size: 172723; sum-of-contigs
Quality coverage: 5.33 in Q20 bases; agarose-fp
Quality coverage: 4.79 in Q20 bases; sum-of-contigs
-----contigs-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1      14541: contig of 14541 bp in length
*
*      14542      14641: gap of unknown length
*
*      14642      24352: contig of 9711 bp in length
*
*      24353      24452: gap of unknown length
*
*      24453      55873: contig of 31421 bp in length
*
*      55874      55973: gap of unknown length
*
*      55974      96383: contig of 40410 bp in length
*
*      96384      96483: gap of unknown length
*
*      96484      141828: contig of 45345 bp in length
*
*      141829      141928: gap of unknown length
*
*      141929      150686: contig of 8768 bp in length
*
*      150697      150796: gap of unknown length
*
*      150797      162246: contig of 11450 bp in length
*
*      162247      162347: gap of unknown length
*
*      162347      173423: contig of 11077 bp in length.
FEATURES
source
1..173423
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="12"
/clone="RP11-42AB7"
1..14541
/note="assembly_name:Contig10"
clone_end:SP6
vector_side:left"
14642..24352
/note="assembly_name:Contig8"
clone_end:T7
vector_side:right"
24453..55873
/note="assembly_name:Contig11"
55974..96383
/note="assembly_name:Contig12"
96484..141828
/note="assembly_name:Contig13"
141929..150696
/note="assembly_name:Contig6"
150797..162246
/note="assembly_name:Contig7"
162347..173423
misc_feature

```

```

ORIGIN /note="assembly_name:Contig9"
Query Match 77.8%; Score 14; DB 2; Length 173423;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNN 18
Db 162239 TCCTGAGAGNNNNN 162252

RESULT 76
CR339046 173705 bp DNA linear HTG 11-MAR-2004
LOCUS Danio rerio clone CH211-112C15, *** SEQUENCING IN PROGRESS ***, 9
DEFINITION unordered pieces.
ACCESSION CR339046
VERSION CR339046.4 GI:45381861
KEYWORDS HTG; HTGS PHASE1.
SOURCE Danio rerio (zebrafish)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 173705)
McLay, K.
Direct Submission
Submitted (08-MAR-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zf1sh-help@sanger.ac.uk Clone requests: clonequest@sanger.ac.uk
On Mar 11, 2004 this sequence version replaced gi:45238479.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zf1sh-help@sanger.ac.uk
----- Project Information
Center project name: ZC112C15
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 171047 bases at least Q40
Consensus quality: 171468 bases at least Q30
Consensus quality: 171906 bases at least Q20
Insert size: 172905; sum-of-contigs
Insert size: 176004; 4.4% error; agarose-fp
Quality coverage: 10.13x in Q20 bases; sum-of-contigs Quality
Coverage: 9.95x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 17494: contig of 17494 bp in length
* 17495 17594: gap of 100 bp
* 17595 30952: contig of 13358 bp in length
* 30953 31052: gap of 100 bp
* 31053 56754: contig of 25702 bp in length
* 56755 56854: gap of 100 bp
* 56855 61530: contig of 4676 bp in length
* 61531 61630: gap of 100 bp
* 61631 83735: contig of 22005 bp in length
* 83736 83791: gap of 100 bp
* 83791 87791: contig of 4056 bp in length
* 87792 87891: gap of 100 bp
* 87892 91726: contig of 3835 bp in length
* 91727 91826: gap of 100 bp
* 91827 139371: contig of 47545 bp in length

```

```

FEATURES
* 139372 139471: gap of 100 bp
* 139472 173705: contig of 34234 bp in length.
Location/Qualifiers
source
1. 173705
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-112C15"
/clone_1b="CHORI-211"
1. 17494
/note="assembly fragment:00399
fragment chain:1
clone_end:17
vector_side:left"
17595. 30952
/note="assembly fragment:00171
fragment chain:1"
31053. 56754
/note="assembly fragment:00394
fragment chain:1"
56855. 61530
/note="assembly fragment:00107
fragment chain:1"
61631. 83635
/note="assembly fragment:00638
fragment chain:1"
83736. 87791
/note="assembly fragment:00001
fragment chain:1"
87892. 91726
/note="assembly fragment:00050
fragment chain:1"
91827. 139371
/note="assembly fragment:01987
fragment chain:1"
139472. 173705
/note="assembly fragment:01449
fragment chain:1
clone_end:586
vector_side:right"

ORIGIN
Query Match 77.8%; Score 14; DB 2; Length 173705;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNN 18
Db 61523 TCCTGAGAGNNNNN 61536

RESULT 77
AP002368 175056 bp DNA linear HTG 31-MAY-2000
LOCUS Homo sapiens chromosome 11 clone RP11-152017 map 11q, WORKING DRAFT
DEFINITION SEQUENCE, 38 unordered pieces.
ACCESSION AP002368
VERSION AP002368.1 GI:8131632
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 175056)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 175,056 genomic DNA of 11q
Published only in Database (2000)
REFERENCE Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
JOURNAL Submitted (29-MAY-2000) Masahira Hattori, The Institute of Physical

```



and Chemical Research (RIKEN), Genomic Sciences Center (GSC),  
 Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,  
 Japan (E-mail: [natcori@gsc.riken.go.jp](mailto:natcori@gsc.riken.go.jp),  
<http://hngp.gsc.riken.go.jp/>, Tel: 01-42-778-9923,  
 Fax: 01-42-778-9924)

----- Genome Center -----

COMMENT

FEATURES

source

1. 175056  
Location/Qualifiers

171435 172584: contig of 1150 bp in length

172885 172684: gap of 100 bp

173766 173766: contig of 1082 bp in length

173767 173866: gap of 100 bp

173867 175056: contig of 1190 bp in length.

1. 175056  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="11"  
/map="11g"  
/clone="RP11-152017"  
1. 27556  
misc\_feature  
/note="assembly\_fragment"  
27657. 47715  
misc\_feature  
/note="assembly\_fragment"  
47816. 58290  
misc\_feature  
/note="assembly\_fragment"  
58391. 65882  
misc\_feature  
/note="assembly\_fragment"  
65983. 75140  
misc\_feature  
/note="assembly\_fragment"  
75241. 83735  
misc\_feature  
/note="assembly\_fragment"  
83836. 91075  
misc\_feature  
/note="assembly\_fragment"  
91176. 97301  
misc\_feature  
/note="assembly\_fragment"  
97402. 102966  
misc\_feature  
/note="assembly\_fragment"  
103067. 108296  
misc\_feature  
/note="assembly\_fragment"  
108397. 114679

Query Match 77.8%; Score 14; DB 2; Length 175056;  
Best Local Similarity 85.7%; Pred. No. 1e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGNNNNNN 18  
Db 58283 TCCTGAGNNNNNN 58296

RESULT 78  
AC144311 176565 bp DNA linear HTG 09-APR-2003  
LOCUS  
DEFINITION  
AC144311  
AC144311.1 GI:29650159  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
HTG: HTGS PHASE2; HTGS\_PGI.  
Macaaca mulatta (rhesus monkey)  
Macaaca mulatta  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopithecinae; Macaca.  
1 (bases 1 to 176565)  
Csuros,M. and Milosavljevic,A.  
Pooled genomic indexing (PGI): mathematical analysis and experiment  
design  
(in) Guigo,R. and Gusfield,D. (Eds.);  
ALGORITHMS IN BIOINFORMATICS, SECOND INTERNATIONAL WORKSHOP, WABI  
2002, ROME, ITALY, SEPTEMBER 17-21, 2002, PROCEEDINGS: 10-28;  
Springer (2002)

REFERENCE  
AUTHORS  
2 (bases 1 to 176565)  
Milosavljevic,A., Sodergren,E., Csuros,M., Li,B., Jackson,A.R.,  
Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C., Albrooks,S.L.,  
Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbara,J.,  
Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J.,  
Bowls,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Bunay,C.,  
Burch,P., Burckell,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,  
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,  
Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C., Cleveland,C.D.,

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT

Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,  
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,  
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Drexler,H.,  
Dugan-Rocha,S., Durbin,K.J., Egan,A., Earnhart,C., Edwards,C.C.,  
Elhaj,C., Emerling,S., Escoto,M., Falls,T., Ferraguto,D.,  
Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J.,  
Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,U.H., Guevara,W.,  
Gunnarathne,P., Hale,S., Hamilton,K., Han,J., Harris,C., Harris,K.,  
Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O.,  
Hodgson,A., Hogue,M., Holloway,C., Hollins,B., Homsi,F.,  
Howard,S., Huber,J., Hulyk,S., Hune,J., Ioshikbes,I., Jackson,L.E.,  
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,  
Karlsson,E., Kelly,S., Khan,U., King,L., Kovach,J., Kovar,C.,  
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lee,E., Lewis,L.C.,  
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,  
Lounsged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,  
Ma,J., Maheshwari,M., Mapua,P., Marondel,I., Martin,R.,  
Martindale,A., Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P.,  
Meador,M., Mei,G., Merscher,S., Metzger,M., Miller,A., Miner,G.,  
Miner,Z., Mitchell,T., Mohabbat,K., Montgomery,K.T., Morgan,M.,  
Morris,S., Moser,M., Neal,D., Nelson,D., Newton,J., Newton,N.,  
Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokemko,S.,  
Ogulu,M., Okunolu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B.,  
Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pul,L.,  
Quiles,M., Ren,Y., Rivers,M., Rojce,A., Rojupokan,I., Rolfe,M.,  
Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shum,C.,  
Shooshitari,N., Sisson,I., Sodergren,E., Sonalke,T., Sparks,A.,  
Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A.,  
Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B.,  
Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D.,  
Vinson,R., Wang,O., Wang,S., Ward-Moore,S., Warren,R.,  
Washington,C., Watlington,S., Williams,G., Williams,A., Zhou,J.,  
Wleczky,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J.,  
Zorilla,S., Kuchelapatti,R., Weinstein,G. and Gibbs,R.

Direct Submission  
Unpublished  
3 (bases 1 to 176565)  
Worley,K.C.  
Direct Submission  
Submitted (09-APR-2003) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

----- Genome Center -----  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information -----  
Center project name: LCIP  
Center clone name: CH250-271024  
----- Summary Statistics -----  
Chemistry: Dye-primer Bodipy: inf% of reads  
Chemistry: Dye-terminator Big Dye: inf% of reads  
Consensus quality: 7017 bases at least Q40  
Consensus quality: 8529 bases at least Q30  
Consensus quality: 10199 bases at least Q20

----- NOTE: -----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_difft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_difft_data.html))  
\* NOTE: The contigs are based on the application  
\* of the PGI method using the Human genome (NCBI build 31)  
\* as the comparative genome.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 1 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
1 176565: contig of 176565 bp in length.  
Location/Qualifiers

FEATURES

```

source
1. .176565
/organism="Macaca mulatta"
/mol_type="genomic DNA"
/db_xref="taxon:9544"
/clone="CH250-271024"
misc_feature
1. .176565
/feature="assembly name:CH250-271024.1B
CONFIDENCE: 0.83"

ORIGIN
Query Match 77.8%; Score 14; DB 2; Length 176565;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 5 UCCUGAGAGNNNNN 18
:|||||
29695 TCCTGAGAGNNNNN 29708

RESULT 79
AC151062 177380 bp DNA linear HTG 04-SEP-2004
LOCUS Bos taurus clone CH240-503N8, WORKING DRAFT SEQUENCE, 23 unordered
pieces.
AC151062
AC151062.1 GI:51468321
HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 177380)
Munzy,D., Metzker,M., Adams,C., Agbai II,O., Allen,C.,
Alabrooks,S., Archer,P., Arredondo,H., Bandaranaike,D., Bangura,L.,
Beltran,B., Beltran,R., Beraducci,A., Biswal,K., Blyth,P.,
Bonham,H., Buhay,C., Burch,P., Cadoree,I., Canada,A., Cardenas,V.,
Carter,K., Cavazos,I., Chacko,J., Chahrouh,M., Chavez,D., Chen,A.,
Chen,G., Chen,R., Cheng,M.-T., Chu,D., Clerc,K., Cockrell,R.,
Coyle,M., Cree,A., Curry,S., Dai,W., Davila,M.L., Davis,C.,
Davy-Carroll,L., De Anda,C., Delgado,O., Denson,S., Deramo,C.,
Ding,Y., Dinh,H., Donlin,J., McCauley,S., Dugan-Rocha,S., Dunn,A.,
Durbin,K., Dziuda,D., Egan,A., Escoto,M., Espinoza,E., Eugene,C.,
Fa,M., Fernandez,S., Fernando,P., Flagg,N., Forbes,L., Foster,P.,
Fowler,G., Fu,Q., Fun,E., Garcia,A., Garcia,R., Garner,T.,
Gaskin,C., Gench,S., Ghose,S., Gill,R., Gonzalez,D.,
Gonzalez-Garay,M., Guevara,W., Holder,M., Haaland,W., Haeblerlen,K.,
Hall,B., Hamid,H., Hamilton,K., Harbes,B., Harris,R., Havlak,P.,
Hawes,A., Hawkins,E., Hayes,S., Hemphill,L., Hernandez,J.,
Hines,S., Hitchens,M., Hodgson,A., Hogue,M., Hollins,B.,
Howell,L.T., Huylk,S., Hume,U., Imo,K., Jackson,A., Jackson,L.,
Jacob,L., Jiang,H., Johnson,B., Johnson,R., Kalatus,K., Kelly,S.,
Keys,T., Khan,Z., King,L., Kovar,C., Kowis,A., Kowis,C., Lara,F.,
Leal,S., Lee,K., Lee,S., Legall,F.I., Lemon,S., Lewis,L., Li,B.,
Li,Y., Li,Z., Linnell,M., Liu,W., Liu,Y.-S., Liu,Y., Llyanage,D.,
London,P., Lopez,J., Lorensunewa,L., Lorado,R., Luk,T., Madu,R.,
Maneswari,M., Mahoney,C., Malloy,K., Mansouri,D., Martinez,E.,
McClalland,H., McPherson,J., Mercadao,C., Milosavljevic,A.,
Minja,E., Morgan,M., Morris,S., Mundaas,M., Murray,D.,
Nazareth,L., Ngo,D., Nguyen,N., Norwig-Bastaguch,E., Nott,A.,
Naackeleh,O., Obregon,M., Och-Okorle,C., Odeh,E., Okunnu,G.,
Okunnu,K., Parker,D., Pasternak,S., Patel,B., Patel,V., Paul,H.,
Perez,A., Perez,L., Petrosino,J., Pham,T., Primus,E., Pu,L.-L.,
Puzio,M., Qin,X., Quinn,A., Quiroz,J., Rabata,D., Rachlin,E.,
Reigh,R., Ren,Y., Reuter,M., Richards,S., Rives,C., Rodriguez,F.,
Rojas,A., Ruiz,S.J., Sana,M., Sanders,W., Santibanez,J., Santos,R.,
Savery,G., Scherer,S., Shen,H., Shen,Y., Sison,I., Sneed,A.,
Sodergren,E., Song,X.-Z., Sorelle,R., Swatek,A., Taylor,E.,
Taylor,T., Thomas,N., Thorn,R., Thornton,R., Trejos,Z., Umaní,K.,
Vargo,C., Verdusco,D., Villaseña,D., Virk,D., Volkov,A.,
Waldron,L., Walker,B., Wang,Q., Wang,S., Warren,J., Wei,X.,
Wheeler,D., Williams,G., Williams,R., Worley,K., Wright,R., Wu,J.,
Yakub,S., Yan,K., Yaun,Y., Yu,F., Zhang,J., Zhang,L., Zhang,Z.,

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
Morley,K.C.
TITLE
Direct Submission
JOURNAL
Submitted (20-APR-2004) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 177380)
REFERENCE
AUTHORS
Morley,K.C.
TITLE
Direct Submission
JOURNAL
Submitted (04-SEP-2004) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help.tmc.edu
----- Project Information
Center project name: FBTU
Center clone name: CH240-503N8
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 18238 bases at least Q40
Consensus quality: 185027 bases at least Q30
Consensus quality: 188535 bases at least Q20
Estimated insert size: 190732; sum-of-coverage estimation
Estimated insert size: 189442; agarose-fp estimation
Quality coverage: 3x in Q20 bases; agarose-fp estimation
Quality coverage: 3x in Q20 bases; sum-of-coverage estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
2833: contig of 2833 bp in length
2834 2933: gap of unknown length
2934 6260: contig of 3327 bp in length
6261 6360: gap of unknown length
6361 12441: contig of 6081 bp in length
12442 12541: gap of unknown length
12542 15522: contig of 2981 bp in length
15523 15622: gap of unknown length
15623 22934: contig of 7312 bp in length
22935 23035: gap of unknown length
23035 37402: gap of 14368 bp in length
37403 37502: gap of unknown length
37503 41711: contig of 4209 bp in length
41712 41811: gap of unknown length
41812 49591: contig of 7780 bp in length
49592 49691: gap of unknown length
49692 70288: contig of 20558 bp in length
70289 70389: gap of unknown length
70390 77856: contig of 7467 bp in length
77857 77956: gap of unknown length
77957 80000: contig of 2044 bp in length
80001 80100: gap of unknown length
80101 83813: contig of 3713 bp in length
83814 83913: gap of unknown length
83914 89178: contig of 5265 bp in length
89179 89279: gap of unknown length
89280 98605: contig of 9327 bp in length
98606 98705: gap of unknown length

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* 98706 101016: contig of 2311 bp in length
* 101017 101116: gap of unknown length
* 101117 106474: contig of 5358 bp in length
* 106475 106474: gap of unknown length
* 106575 116243: contig of 9669 bp in length
* 116244 116343: gap of unknown length
* 116344 122675: contig of 6332 bp in length
* 122676 122775: gap of unknown length
* 122776 137611: contig of 14836 bp in length
* 137612 143280: contig of 5569 bp in length
* 143281 143380: gap of unknown length
* 143381 155847: contig of 12467 bp in length
* 155848 155947: gap of unknown length
* 155948 164900: contig of 8953 bp in length
* 164901 165001: gap of unknown length
* 165001 177380: contig of 12380 bp in length.

FEATURES
  source
    1. 177380
       /organism="Bos taurus"
       /mol_type="genomic DNA"
       /db_xref="taxon:9913"
       /clone="CH240-503N8"

ORIGIN
  Query Match      77.8%; Score 14; DB 2; Length 177380;
  Best Local Similarity 85.7%; Pred. No. 1e+02;
  Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      5 UCCUGAGAGNNNNNN 18
Db      15515 TCCTGAGAGNNNNNN 15528

RESULT 80
LOCUS   AC125597/c
DEFINITION
  Rattus norvegicus clone CH230-341P19, *** SEQUENCING IN PROGRESS
  *** 3 unordered pieces.
ACCESSION
  AC125597
  AC125597.3 GI:25074793
KEYWORDS
  HTG; HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.
SOURCE
  Rattus norvegicus (Norway rat)
  Rattus norvegicus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
  Rattus.
  1 (bases 1 to 178472)
  Muzny,D,Marie, Metzker,M,Lee, Abramson,S, Adams,C, Alder,J,
  Allen,C, Allen,H, Aisbrooke,S, Amin,A, Anguiano,D,
  Anyalebechi,V, Ayoyagi,A, Ayodeji,M, Baca,E, Baden,H,
  Baldwin,D, Bandaranaike,D, Barber,M, Barnstead,M, Benahmed,F,
  Bielawski,K, Blair,J, Blankenburg,K, Blyth,P, Brown,M,
  Bryant,N, Buhay,C, Burch,P, Burrell,K, Calderon,E,
  Cardenas,V, Carter,K, Cavazos,I, Caesar,H, Center,A,
  Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J,
  Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L,
  Davila,M,L, Davis,C, Davy-Carroll,L, De Anda,C, Deckerich,D,
  Delgado,O, Denson,S, Deramo,C, Ding,Y, Dinh,H, Divya,K,
  Draper,H, Dugan-Rocha,S, Dunn,A, Durbin,K, Duval,B, Evans,K,
  Egan,A, Escotto,M, Eugene,C, Evans,C,A, Falls,T, Fan,G,
  Fernandez,S, Finley,M, Flagg,N, Forbes,L, Foster,M, Foster,P,
  Fraser,C,M, Gabisi,A, Ganta,R, Garcia,A, Garner,T, Garza,M,
  Gebregergis,E, Geer,K, Gill,R, Grady,M, Guerra,M, Guevara,W,
  Gunaratne,P, Haaland,W, Hamill,C, Hamilton,C, Hamilton,J,
  Hernandez,R, Hines,S, Hladun,S,L, Hodgson,A, Hogue,M,
  Hollins,B, Howells,S, Hu,Y,S, Hume,J, Idlebird,D, Jackson,A,
  Jackson,L, Jacob,L, Jiang,H, Johnson,B, Johnson,R, Jolivet,A,
  Karpathy,S, Kelly,S, Kelly,S, Khan,Z, King,L, Kovar,C,
  Kowals,C, Kratic,C,L, Ledow,H, Levan,J, Lewis,L, Li,Z, Liu,J,
  Liu,J, Liu,W, Liu,Y, London,P, Longacre,S, Lopez,J,
  Lorenshewa,L, Loulseged,H, Lozano,R,J, Lu,X, Ma,J,

```

```

TITLE
  JOURNAL
REFERENCE
  AUTHORS
  TITLE
  JOURNAL
  Submitted (29-JUN-2002) Human Genome Sequencing Center, Department
  of Molecular and Human Genetics, Baylor College of Medicine, One
  Baylor Plaza, Houston, TX 77030, USA
  3 (bases 1 to 178472)
  Rat Genome Sequencing Consortium.
  Direct Submission
  Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
  of Molecular and Human Genetics, Baylor College of Medicine, One
  Baylor Plaza, Houston, TX 77030, USA
  On Nov 19, 2002 this sequence version replaced gi:23196214.
  The sequence in this assembly is a combination of BAC based reads
  and whole genome shotgun sequencing reads assembled using Atlas
  (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
  in the feature table below represents a scaffold in the Atlas
  assembly (a 'contig-scaffold'). Within each contig-scaffold,
  individual sequence contigs are ordered and oriented, and separated
  by sized gaps filled with Ns to the estimated size. The sequence
  may extend beyond the ends of the clone and there may be sequence
  contigs within a contig-scaffold that consist entirely of whole
  genome shotgun sequence reads. Both end sequences and whole genome
  shotgun sequence only contigs will be indicated in the feature
  table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: KADN
Center clone name: CH230-341P19
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 172947 bases at least Q40
Consensus quality: 174279 bases at least Q30
Consensus quality: 175219 bases at least Q20
Estimated insert size: 177582; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as

```

\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 91458: contig of 91458 bp in length  
\* 91459 91558: gap of unknown length  
\* 91559 176692: contig of 85134 bp in length  
\* 176693 176792: gap of unknown length  
\* 176793 178472: contig of 1680 bp in length.

Location/Qualifiers  
1. 178472  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-341P19"  
1. 1860  
/note="wgs\_end\_extension  
clone\_end:T7"  
1911. 3094  
/note="wgs\_end\_extension  
clone\_end:T7"  
3845. 4697  
/note="clone\_boundary  
clone\_end:T7  
site:  
end\_sequence:BZ205473"

ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 178472;  
Best Local Similarity 85.7%; Pred. No. 1e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGGNNNNN 18  
:|||||  
Db 91566 TCCTGAGGNNNNN 91553

RESULT 81  
BX927248/c 180506 bp DNA linear HTG 01-MAR-2004  
DEFINITION  
BX927248  
Accession  
BX927248.2 GI:41392805  
HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.  
KEYWORDS  
Danio rerio (zebrafish)  
SOURCE  
Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 180506)  
Sims, S.  
Direct Submission  
Submitted (26-FEB-2004) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
zf1sh-help@sanger.ac.uk Clone requests: clonesreqs@sanger.ac.uk  
On Jan 29, 2004 this sequence version replaced gi:4139613.  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: zf1sh-help@sanger.ac.uk  
----- Project Information  
Center project name: zc140C22  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 10% of reads  
Consensus quality: 178181 bases at least Q40  
Consensus quality: 178549 bases at least Q30  
Consensus quality: 178864 bases at least Q20  
Insert size: 179706; sum-of-contigs  
Insert size: 181854; 4.4% error; agarose-fp  
Quality coverage: 7.68x in Q20 bases; sum-of-contigs Quality

coverage: 8.04x in Q20 bases; agarose-fp  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 9 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 21382: contig of 21382 bp in length  
\* 21383 21482: gap of 100 bp  
\* 21483 39908: contig of 18426 bp in length  
\* 39909 40008: gap of 100 bp  
\* 40009 71058: contig of 31050 bp in length  
\* 71059 71159: gap of 100 bp  
\* 71159 81805: contig of 10647 bp in length  
\* 81806 81905: gap of 100 bp  
\* 81906 89850: contig of 7945 bp in length  
\* 89851 89951: gap of 100 bp  
\* 89951 95146: contig of 5196 bp in length  
\* 95147 95246: gap of 100 bp  
\* 95247 167183: contig of 71937 bp in length  
\* 167184 167283: gap of 100 bp  
\* 167284 170213: contig of 2930 bp in length  
\* 170214 170314: gap of 100 bp  
\* 170314 180506: contig of 10193 bp in length.

Location/Qualifiers  
1. 180506  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="CH211-140C22"  
/clone\_1b="CHOR1-211"  
1. 21382  
/note="assembly fragment: 00562  
fragment chain: 1  
clone\_end:SP6  
vector\_side:left"  
21483. 39908  
/note="assembly fragment: 00790  
fragment chain: 1"  
40009. 71058  
/note="assembly fragment: 01068  
fragment chain: 1"  
71159. 81805  
/note="assembly fragment: 00401  
fragment chain: 1"  
81906. 89850  
/note="assembly fragment: 00278  
fragment chain: 1"  
89951. 95146  
/note="assembly fragment: 00106  
fragment chain: 1"  
95247. 167183  
/note="assembly fragment: 01493  
fragment chain: 1"  
167284. 170213  
/note="assembly fragment: 00077  
fragment chain: 1"  
170314. 180506  
/note="assembly fragment: 00160  
fragment chain: 1"

ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 180506;  
Best Local Similarity 85.7%; Pred. No. 1e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGGNNNNN 18  
:|||||  
Db 170321 TCCTGAGGNNNNN 170308

RESULT 82  
AC015622  
LOCUS  
DEFINITION  
Homo sapiens clone RP11-45J14, WORKING DRAFT SEQUENCE, 33 unordered  
pieces.  
AC015622  
AC015622.4 GI:8096821  
HTG, HTGS\_PHASE1, HTGS\_DRAFT.  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 184869)  
Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
Homo sapiens, clone RP11-45J14  
Unpublished  
2 (bases 1 to 184869)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,  
Baldin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhalter,B.,  
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,  
Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,  
Ferrera,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,  
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,  
Lehoczky,J., Lien,C., Locke,K., Macdonald,P., Marguis,N.,  
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,  
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,  
Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
Teste,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,  
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On May 26, 2000 this sequence version replaced gi:5604528.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L1170  
Center clone name: 45-J\_14  
----- Summary Statistics  
Sequencing vector: M13; M77815; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 147749 bases at least Q40  
Consensus quality: 168400 bases at least Q30  
Consensus quality: 176223 bases at least Q20  
Insert size: 152000; agarose-fp  
Insert size: 181669; sum-of-contigs  
Quality coverage: 4.6 in Q20 bases; agarose-fp  
Quality coverage: 3.8 in Q20 bases; sum-of-contigs  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 33 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\*  
\* 1 1226: contig of 1226 bp in length  
\* 1227 1326: gap of 100 bp  
\* 1327 1360: contig of 1034 bp in length  
\* 2361 2460: gap of 100 bp  
\* 2461 3510: contig of 1050 bp in length  
\* 3511 3610: gap of 100 bp

3611 4882: contig of 1272 bp in length  
\* 4883 4982: gap of 100 bp  
\* 4983 6425: contig of 1443 bp in length  
\* 6426 6525: gap of 100 bp  
\* 6526 7693: contig of 1168 bp in length  
\* 7694 7793: gap of 100 bp  
\* 7794 8950: contig of 1157 bp in length  
\* 8951 9050: gap of 100 bp  
\* 9051 10082: contig of 1032 bp in length  
\* 10083 10182: gap of 100 bp  
\* 10183 11513: contig of 1331 bp in length  
\* 11514 11614: gap of 100 bp  
\* 11614 12762: contig of 1149 bp in length  
\* 12763 12862: gap of 100 bp  
\* 12863 14245: contig of 1383 bp in length  
\* 14246 14345: gap of 100 bp  
\* 14346 15528: contig of 1183 bp in length  
\* 15529 15628: gap of 100 bp  
\* 15629 16803: contig of 1175 bp in length  
\* 16804 16903: gap of 100 bp  
\* 16904 18547: contig of 1644 bp in length  
\* 18548 18647: gap of 100 bp  
\* 18648 19920: contig of 1273 bp in length  
\* 19921 20020: gap of 100 bp  
\* 20021 22262: contig of 2242 bp in length  
\* 22263 22362: gap of 100 bp  
\* 22363 24001: contig of 1639 bp in length  
\* 24002 24101: gap of 100 bp  
\* 24102 26555: contig of 2554 bp in length  
\* 26556 26755: gap of 100 bp  
\* 26756 28646: contig of 1891 bp in length  
\* 28647 28746: gap of 100 bp  
\* 28747 31056: contig of 2310 bp in length  
\* 31057 31156: gap of 100 bp  
\* 31157 33922: contig of 2766 bp in length  
\* 33923 34022: gap of 100 bp  
\* 34023 36450: contig of 2428 bp in length  
\* 36451 36550: gap of 100 bp  
\* 36551 40183: contig of 3633 bp in length  
\* 40184 40283: gap of 100 bp  
\* 40283 45282: contig of 4999 bp in length  
\* 45283 45382: gap of 100 bp  
\* 45383 50884: contig of 5502 bp in length  
\* 50885 50984: gap of 100 bp  
\* 50985 61265: contig of 10281 bp in length  
\* 61266 61365: gap of 100 bp  
\* 61366 71108: contig of 9743 bp in length  
\* 71109 71208: gap of 100 bp  
\* 71209 85877: contig of 14669 bp in length  
\* 85878 85977: gap of 100 bp  
\* 85978 97906: contig of 11929 bp in length  
\* 97907 98006: gap of 100 bp  
\* 98007 112916: contig of 14910 bp in length  
\* 112917 113016: gap of 100 bp  
\* 113017 129210: contig of 16194 bp in length  
\* 129211 129310: gap of 100 bp  
\* 129311 152603: contig of 23293 bp in length  
\* 152604 152703: gap of 100 bp  
\* 152704 184869: contig of 32166 bp in length.  
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Location/Qualifiers  
1..184869  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone\_lib="RP11-45J14"  
/clone\_lib="RP11-45J14" Human Male BAC"  
1..1226  
/note="assembly\_fragment"  
1327..2360  
/note="assembly\_fragment"  
2461..3510  
/note="assembly\_fragment"  
3611..4882

FEATURES  
source  
misc\_feature  
misc\_feature  
misc\_feature  
misc\_feature  
misc\_feature

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misc_feature      /note="assembly_fragment"
                    4983..6425
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    6526..7693
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    7794..8950
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    9051..10082
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    10183..11513
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    11614..12762
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    12863..14245
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    14346..15528
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    15629..16803
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    16904..18547
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    18648..19920
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    20021..22262
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    22363..24001
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    24102..26655
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    26756..28646
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    28747..31056
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    31157..33922
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    34023..36450
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    36551..40183
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    40284..45282
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    45383..50884
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    50985..61265
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    61366..71108
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    71209..85877
                    /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                    clone_end:T7
                    vector_side:left"
misc_feature      85978..97906
                    /note="assembly_fragment"
misc_feature      98007..112916
                    /note="assembly_fragment"
misc_feature      113017..129210
                    /note="assembly_fragment"

Query Match      77.8%; Score 14; DB 2; Length 184869;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      5 UCCUGAGNNNNNN 18
       :|||:|||||
       22255 TCCTGAGNNNNNN 22268

RESULT 83
LOCUS      BX927379      187478 bp      DNA      linear      HTG 05-FEB-2004
DEFINITION Danio rerio clone DKEY-11H12, *** SEQUENCING IN PROGRESS ***, 5
ACCESSION      BX927379

```

```

VERSION      BX927379.3      GI:42414941
KEYWORDS
SOURCE      HTG; HTGS PHASE1
ORGANISM      Danio rerio (zebrafish)
              Danio rerio
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
              Cypriniformes; Cyprinidae; Danio.
REFERENCE
AUTHORS      McIay,K.
TITLE      Direct Submission
JOURNAL      Submitted (04-FEB-2004) Wellcome Trust Sanger Institute, Hinxton,
              Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
              fish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
              On Feb 5, 2004 this sequence version replaced gi:42406562.

COMMENT
              ----- Genome Center
              Center: Wellcome Trust Sanger Institute
              Center code: SC
              Web site: http://www.sanger.ac.uk
              Contact: zfish-help@sanger.ac.uk
              ----- Project Information
              Center project name: ZK11H12
              ----- Summary Statistics
              Assembly program: XGAP4; version 4.5
              Chemistry: Dye-terminator; 100% of reads
              Consensus quality: 186191 bases at least Q40
              Consensus quality: 186506 bases at least Q30
              Consensus quality: 186799 bases at least Q20
              Insert size: 187078; sum-of-ctrls
              Insert size: 179723; 3.4% error; agarose-fp
              Quality coverage: 8.73x in Q20 bases; sum-of-ctrls Quality
              coverage: 9.09x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 75787: contig of 75787 bp in length
* 75788 75887: gap of 100 bp
* 75888 82568: contig of 6681 bp in length
* 82568 82668: gap of 100 bp
* 82668 87993: contig of 5325 bp in length
* 87993 88093: gap of 100 bp
* 88093 130375: contig of 42282 bp in length
* 130375 130475: gap of 100 bp
* 130475 187478: contig of 57003 bp in length.

FEATURES
Source
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/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-11H12"
/clone_1lb="DanioKey"
1..75787
/note="assembly_fragment:01538
fragment chain:1"
75888..82568
/note="assembly_fragment:00004
fragment chain:1"
82669..87993
/note="assembly_fragment:00091.0"
88094..130375
/note="assembly_fragment:00180"
130476..187478
/note="assembly_fragment:00791"

ORIGIN
Query Match      77.8%; Score 14; DB 2; Length 187478;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

QY 5 UCCUGAGNNNNN 18  
 Db 75780 TCCTGAGANNNNN 75793

RESULT 84  
 AC121358/c  
 LOCUS  
 DEFINITION Mus musculus clone RP23-56M19, WORKING DRAFT SEQUENCE, 8 unordered pieces.  
 AC121358  
 AC121358.7 GI:28975047  
 HTG: HTGS PHASE1; HTGS\_DRAFT:  
 KEYSWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS Birren, B., Linton, L., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choquel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Deatellano, K., Dewar, K., Diaz, J. S., Dodge, S., Galagan, J., Gardina, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroque, K., Lamazares, R., Landers, T., Lebockzy, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneses, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strause, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triggioni, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE  
 JOURNAL Direct Submission (17-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 AUTHORS 3 (bases 1 to 188931)

REFERENCE  
 AUTHORS Birren, B., Nussbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choquel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Deatellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardina, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C., MacDonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneses, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schnupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE  
 JOURNAL Submitted (16-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 COMMENT On Mar 16, 2003 this sequence version replaced gi:28467251.

All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: MIBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L23278  
 Center clone name: 56 M 19  
 ----- Summary Statistics  
 Sequencing vector: Plasmid, n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 186993 bases at least Q40  
 Consensus quality: 187764 bases at least Q30  
 Consensus quality: 188102 bases at least Q20  
 Insert size: 19400; agarose-fp  
 Insert size: 18831; sum-of-contigs  
 Quality coverage: 12.4 in Q20 bases; agarose-fp  
 Quality coverage: 12.8 in Q20 bases; sum-of-contigs  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 8 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 48626: contig of 48626 bp in length  
 \* 48627 48726: gap of 100 bp  
 \* 48727 49589: contig of 863 bp in length  
 \* 49590 49689: gap of 100 bp  
 \* 49690 50333: contig of 644 bp in length  
 \* 50334 50433: gap of 100 bp  
 \* 50434 54738: contig of 4305 bp in length  
 \* 54739 54838: gap of 100 bp  
 \* 54839 6651: contig of 11813 bp in length  
 \* 6652 116345: contig of 49594 bp in length  
 \* 116346 116445: gap of 100 bp  
 \* 116446 177221: contig of 60776 bp in length  
 \* 177222 177321: gap of 100 bp  
 \* 177322 188931: contig of 11610 bp in length.

FEATURES  
 source  
 1..188931  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /clone="RP23-56M19"  
 /clone\_11b="RPci-23 Female Mouse BAC"  
 1..48626  
 /note="assembly\_fragment  
 clone end:SP6  
 vector\_side:left"  
 48727..49589  
 /note="assembly\_fragment"  
 49690..50333  
 /note="assembly\_fragment"  
 50434..54738  
 /note="assembly\_fragment"  
 54839..6651  
 /note="assembly\_fragment"  
 6652..116345  
 /note="assembly\_fragment"  
 116446..177221  
 /note="assembly\_fragment"  
 177322..188931  
 /note="assembly\_fragment  
 clone end:17  
 vector\_side:right"



ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 188931;  
 Best Local Similarity 85.7%; Pred. No. 1e+02;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 UCCUGAGNNNNNN 18  
 :||:|||||  
 Db 66759 TCCTGAGNNNNNN 66746

RESULT 85  
 CR356244 189756 bp DNA linear HTG 29-MAR-2004  
 LOCUS Dario rerio clone DKEX-149J12, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 8  
 DEFINITION Dario rerio clone DKEX-149J12, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 8  
 unorderd pieces.  
 ACCESSION CR356244  
 VERSION CR356244.4 GI:45824946  
 HTG: HTGS PHASE1.  
 KEYWORDS Dario rerio (zebrafish)  
 SOURCE Dario rerio  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 189756)  
 McIay, K.  
 Direct Submission  
 Submitted (28-MAR-2004) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
 On Mar 29, 2004 this sequence version replaced gi:45772257.  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: zfish-help@sanger.ac.uk  
 ----- Project Information  
 Center project name: zK149J12  
 ----- Summary Statistics  
 Assembly program: XGAP4; version 4.5  
 Chemistry: Dye-terminator; 100% of reads  
 Consensus quality: 186149 bases at least Q40  
 Consensus quality: 186609 bases at least Q30  
 Consensus quality: 187115 bases at least Q20  
 Insert size: 189056; sum-of-contigs  
 Insert size: 166597; 3.0% error; agarose-fp  
 Quality coverage: 8.42x in Q20 bases; sum-of-contigs Quality  
 coverage: 9.70x in Q20 bases; agarose-fp  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 8 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1  
 \* 3426: contig of 3426 bp in length  
 \* 3427 3526: gap of 100 bp  
 \* 3527 14421: contig of 10895 bp in length  
 \* 14422 14521: gap of 100 bp  
 \* 14522 35714: contig of 22193 bp in length  
 \* 35715 36815: gap of 100 bp  
 \* 36816 41106: contig of 4292 bp in length  
 \* 41107 41207: gap of 100 bp  
 \* 41208 50698: contig of 9492 bp in length  
 \* 50699 50798: gap of 100 bp  
 \* 50799 113926: contig of 6128 bp in length  
 \* 113927 114026: gap of 100 bp  
 \* 114027 121029: contig of 7003 bp in length  
 \* 121030 121129: gap of 100 bp  
 \* 121130 189756: contig of 68627 bp in length.  
 \* Location/Qualifiers

source 1..189756  
 /organism="Dario rerio"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7955"  
 /clone="DKEX-149J12"  
 /clone\_1id="DanioKey"

misc\_feature 1..3426  
 /note="assembly fragment:00068  
 fragment\_chain:1"  
 misc\_feature 3527..14421  
 /note="assembly fragment:00313  
 fragment\_chain:1"  
 misc\_feature 14522..35714  
 /note="assembly fragment:00434  
 fragment\_chain:1"  
 misc\_feature 36815..41106  
 /note="assembly fragment:00033  
 fragment\_chain:1"  
 misc\_feature 41207..50698  
 /note="assembly fragment:00212  
 fragment\_chain:1"  
 misc\_feature 50799..113926  
 /note="assembly fragment:00697  
 fragment\_chain:1"  
 misc\_feature 114027..121029  
 /note="assembly fragment:00118"  
 121130..189756  
 /note="assembly fragment:01588.0"

ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 189756;  
 Best Local Similarity 85.7%; Pred. No. 1e+02;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 UCCUGAGNNNNNN 18  
 :||:|||||  
 Db 113919 TCCTGAGNNNNNN 113932

RESULT 86  
 CR293534 189787 bp DNA linear HTG 01-MAR-2004  
 LOCUS CR293534  
 DEFINITION Dario rerio clone CH211-13J1, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 10  
 unorderd pieces.  
 ACCESSION CR293534.2 GI:44850216  
 VERSION CR293534.2  
 HTG: HTGS PHASE1.  
 KEYWORDS Dario rerio (zebrafish)  
 SOURCE Dario rerio  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 189787)  
 Sims, S.  
 Direct Submission  
 Submitted (26-FEB-2004) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
 On Mar 1, 2004 this sequence version replaced gi:42821021.  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: zfish-help@sanger.ac.uk  
 ----- Project Information  
 Center project name: zC13J1  
 ----- Summary Statistics  
 Assembly program: XGAP4; version 4.5  
 Chemistry: Dye-terminator; 100% of reads  
 Consensus quality: 187978 bases at least Q40  
 Consensus quality: 188341 bases at least Q30  
 Consensus quality: 188615 bases at least Q20  
 Insert size: 188887; sum-of-contigs

Insert size: 194889; 4.2% error; agarose-fp  
Quality coverage: 5.95x in Q20 bases; sum-of-coverage  
coverage: 5.91x in Q20 bases; agarose-fp

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 10 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 3558: contig of 3558 bp in length  
\* 3559 3658: gap of 100 bp  
\* 3659 30588: contig of 26931 bp in length  
\* 30590 30689: gap of 100 bp  
\* 30690 36897: contig of 6208 bp in length  
\* 36898 36997: gap of 100 bp  
\* 36998 100041: contig of 63044 bp in length  
\* 100042 100141: gap of 100 bp  
\* 100142 123838: contig of 23697 bp in length  
\* 123839 123938: gap of 100 bp  
\* 123939 129786: contig of 5848 bp in length  
\* 129787 129886: gap of 100 bp  
\* 129887 142544: contig of 12658 bp in length  
\* 142545 142644: gap of 100 bp  
\* 142645 169905: contig of 27261 bp in length  
\* 169906 170005: gap of 100 bp  
\* 170006 187172: contig of 17167 bp in length  
\* 187173 187272: gap of 100 bp  
\* 187273 189787: contig of 2515 bp in length.

## FEATURES

source

1.189787  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="CH211-13J1"  
/clone\_1b="CHORI-211"  
1.3558  
/note="assembly\_fragment:00065  
fragment\_chain:1  
clone\_end:SP6  
vector\_side:left"  
3659.30589  
/note="assembly\_fragment:00712  
fragment\_chain:1"  
30690.36897  
/note="assembly\_fragment:00112  
fragment\_chain:1"  
36998.100041  
/note="assembly\_fragment:01246  
fragment\_chain:1"  
100142.123838  
/note="assembly\_fragment:00510  
fragment\_chain:1"  
123939.129786  
/note="assembly\_fragment:00166  
fragment\_chain:1"  
129887.142544  
/note="assembly\_fragment:00236  
fragment\_chain:1"  
142645.169905  
/note="assembly\_fragment:00978  
fragment\_chain:1"  
170006.187172  
/note="assembly\_fragment:00367  
fragment\_chain:1"  
187273.189787  
/note="assembly\_fragment:00043"

## ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 189787;  
Best Local Similarity 85.7%; Pred. No. 1e+02;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGNNNNNN 18

Db 100034 TCCTGGAGNNNNNN 100047

## RESULT 87

AC068920

LOCUS

DEFINITION

AC068920

AC068920

AC068920

AC068920

AC068920

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## COMMENT

Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu/gsc/index.shtml  
Project Information  
Center project name: H NH0520F07  
Summary Statistics  
Sequencing vector: M13; 100%  
Sequencing vector: plasmid; 0%  
Chemistry: Dye-terminator Big Dye; 0% of reads  
Chemistry: Dye-terminator Big Dye; 0% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 178105 bases at least Q40  
Consensus quality: 182135 bases at least Q30  
Consensus quality: 184620 bases at least Q20  
Insert size: 182000; agarose-fp  
Insert size: 189102; sum-of-coverage  
Quality coverage: 4.18 in Q20 bases; agarose-fp  
Quality coverage: 3.94 in Q20 bases; sum-of-coverage

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 26 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1797: contig of 1797 bp in length  
\* 1798 1897: gap of unknown length  
\* 1898 3447: contig of 1550 bp in length  
\* 3448 3547: gap of unknown length  
\* 3548 5261: contig of 1714 bp in length  
\* 5262 5361: gap of unknown length  
\* 5362 7030: contig of 1669 bp in length  
\* 7031 7130: gap of unknown length  
\* 7131 9374: contig of 2244 bp in length  
\* 9375 9474: gap of unknown length  
\* 9475 11907: contig of 2433 bp in length  
\* 11908 12007: gap of unknown length  
\* 12008 14972: contig of 2965 bp in length  
\* 14973 15072: gap of unknown length

```
* 15073 17812: contig of 2740 bp in length
* 17813 17912: gap of unknown length
* 17913 20959: contig of 3047 bp in length
* 20960 21059: gap of unknown length
* 21060 26055: contig of 4996 bp in length
* 26056 30231: gap of unknown length
* 26156 30231: contig of 4076 bp in length
* 30232 30331: gap of unknown length
* 30332 34743: contig of 4412 bp in length
* 34744 34843: gap of unknown length
* 34844 39428: contig of 4585 bp in length
* 39429 39528: gap of unknown length
* 39529 45797: contig of 6269 bp in length
* 45798 45897: gap of unknown length
* 45898 51353: contig of 5456 bp in length
* 51354 51453: gap of unknown length
* 51454 57595: contig of 6142 bp in length
* 57596 57695: gap of unknown length
* 57696 64225: contig of 6530 bp in length
* 64226 64325: gap of unknown length
* 64326 71971: contig of 7646 bp in length
* 71972 80420: contig of 8349 bp in length
* 80421 80520: gap of unknown length
* 80521 88981: contig of 8461 bp in length
* 88982 89081: gap of unknown length
* 89082 96199: contig of 7118 bp in length
* 96200 96299: gap of unknown length
* 96300 108298: contig of 11999 bp in length
* 108299 121805: gap of unknown length
* 108306 121905: contig of 13407 bp in length
* 121806 121905: gap of unknown length
* 121906 138416: contig of 16511 bp in length
* 138417 138516: gap of unknown length
* 138517 163957: contig of 25440 bp in length
* 163957 164057: gap of unknown length
* 164057 191602: contig of 27546 bp in length.
```

## FEATURES

## SOURCE

```
1. .191602
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
/clone="RP11-520F7"
1. .11797
/note="assembly_name:Contig10"
1898. .3447
/note="assembly_name:Contig11"
3548. .5261
/note="assembly_name:Contig12"
5362. .7030
/note="assembly_name:Contig13"
7131. .9374
/note="assembly_name:Contig14"
9475. .11907
/note="assembly_name:Contig15"
12008. .14972
/note="assembly_name:Contig16"
15073. .17812
/note="assembly_name:Contig17"
17913. .20959
/note="assembly_name:Contig18"
21060. .26055
/note="assembly_name:Contig19"
26156. .30231
/note="assembly_name:Contig20"
30332. .34743
/note="assembly_name:Contig21"
34844. .39428
/note="assembly_name:Contig22
clone end:77
vector_side:right"
39529. .45797
misc_feature
```

```
misc_feature /note="assembly_name:Contig23"
45898. .51353
/note="assembly_name:Contig24"
51454. .57595
/note="assembly_name:Contig25"
57696. .64225
/note="assembly_name:Contig26
clone_end:SP6
vector_side:left"
64326. .71971
/note="assembly_name:Contig27"
72072. .80420
/note="assembly_name:Contig28"
80521. .88981
/note="assembly_name:Contig29"
89082. .96199
/note="assembly_name:Contig30"
96300. .108298
/note="assembly_name:Contig31"
108399. .121805
/note="assembly_name:Contig32"
121906. .138416
/note="assembly_name:Contig33"
138517. .163956
/note="assembly_name:Contig34"
164057. .191602
/note="assembly_name:Contig35"
```

## ORIGIN

```
Query Match 77.8% Score 14; DB 2; Length 191602;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 UCCUGAGAGNNNNNN 18
:|||||
Db 5254 TCCGAGAGNNNNN 5267
```

## RESULT 88

## CRS24482

LOCUS CRS24482 194513 bp DNA linear HTG 19-AUG-2004  
DEFINITION Danio rerio clone DKEX-109F24, WORKING DRAFT SEQUENCE, 15 unordered  
pieces.

## ACCESSION

CRS24482 GI:51470689

## VERSION

HTG; HTGS PHASRI; HTGS DRAFT; HTGS\_FULUTOP.

## KEYWORDS

Danio rerio (zebrafish)

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Submitted (16-AUG-2004) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
On Aug 20, 2004 this sequence version replaced gi:51242031.  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: zfish-help@sanger.ac.uk  
----- Project Information  
Center project name: ZK109F24  
----- Summary Statistics  
Assembly program: XGAP4, version 4.5  
Chemistry: Dye-terminator; 100% of reads  
Consensus quality: 188805 bases at least Q40  
Consensus quality: 189699 bases at least Q30  
Consensus quality: 190483 bases at least Q20  
Insert size: 19313; sum-of-contigs  
Insert size: 203739; 6.5% error; agarose-tp

Quality coverage: 6.93x in Q20 bases; sum-of-contigs Quality coverage: 6.71x in Q20 bases; agarose-ftp

\*\*\*\*\* NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

```
1 38721: contig of 38721 bp in length
* 38722 38821: gap of 100 bp
* 38822 59895: contig of 21074 bp in length
* 59895 59995: gap of 100 bp
* 59995 65918: contig of 5923 bp in length
* 65918 66019: gap of 100 bp
* 66019 74644: contig of 8626 bp in length
* 74644 74744: gap of 100 bp
* 74744 89717: contig of 14973 bp in length
* 89717 89817: gap of 100 bp
* 89817 98513: contig of 8696 bp in length
* 98513 98614: gap of 100 bp
* 98614 100848: contig of 2235 bp in length
* 100848 100949: gap of 100 bp
* 100949 108230: contig of 7282 bp in length
* 108230 108330: gap of 100 bp
* 108330 120926: contig of 12596 bp in length
* 120926 121027: gap of 100 bp
* 121027 129164: contig of 8138 bp in length
* 129164 129264: gap of 100 bp
* 129264 162822: contig of 33558 bp in length
* 162822 162922: gap of 100 bp
* 162922 170558: contig of 7636 bp in length
* 170558 170659: gap of 100 bp
* 170659 188732: contig of 18074 bp in length
* 188732 188832: gap of 100 bp
* 188832 191673: contig of 2841 bp in length
* 191673 191774: gap of 100 bp
* 191774 194513: contig of 2740 bp in length.
```

## FEATURES

source

```
1. 194513
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKF1-109F24"
/clone_lib="DanioKey"
1. 38721
/note="assembly fragment: 01832
fragment chain: 1"
misc_feature
38822..59895
/note="assembly fragment: 01070
fragment chain: 1"
misc_feature
59996..65918
/note="assembly fragment: 00149
fragment chain: 1"
misc_feature
66019..74644
/note="assembly fragment: 00417
fragment chain: 1"
misc_feature
74745..89717
/note="assembly fragment: 00739
fragment chain: 1"
misc_feature
89818..98513
/note="assembly fragment: 00331
fragment chain: 1"
misc_feature
98614..100848
/note="assembly fragment: 00067
fragment chain: 2"
misc_feature
100949..108230
/note="assembly fragment: 00185
fragment chain: 2"
misc_feature
108331..120926
/note="assembly fragment: 00618
```

```
misc_feature      fragment chain: 2"
121027..129164
/note="assembly fragment: 00504
fragment chain: 2"
misc_feature      129265..162822
/note="assembly fragment: 01355
fragment chain: 2"
misc_feature      162923..170558
/note="assembly fragment: 00253
fragment chain: 3"
170659..188732
/note="assembly fragment: 00889
fragment chain: 3"
188833..191673
/note="assembly fragment: 00089"
191774..194513
/note="assembly fragment: 00116.0"
```

## ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 194513;  
Best Local Similarity 85.7%; Pred. No. 16+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy      5 UCCUGAGNNNNNN 18
          |||:|||||
Db      191666 TCCTGGAGNNNNNN 191679
```

## RESULT 89

AC150020/c  
LOCUS  
DEFINITION Papio anubis clone RP41-380L14, WORKING DRAFT SEQUENCE, 11 ordered pieces.

AC150020  
AC150020.2 GI:51241824  
VERSION HTG; HTGS PHASE2; HTGS DRAFT.  
KEYWORDS Papio anubis (olive baboon)  
SOURCE Papio anubis  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Papio.

## REFERENCE

AUTHORS Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, B., Coleman, H., Daki, N., Engle, J., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P., Hurler, B., Idol, J.R., Jones, C., Karlins, E., Kim, H., Kwong, P., Latic, P., Larson, S., Lee-Lin, S.-O., Legaspi, R., Madden, M., Maduro, Q.L., Maduro, Y.B., Margulies, E.H., Mastaglio, C., Maskeri, B., McDowell, J., Mullikin, J.C., Paguirigan, C., Park, M., Portnoy, M.E., Prasad, A., Puri, O., Reddix-Dugue, N., Schandler, K., Schneider, M.G., Shah, K., Sison, C., Stantipoy, S., Thomas, J.W., Thomas, P.J., Tsipouri, V., Vogt, J.L., Wetherby, K.D., Young, A. and Green, E.D.  
NISC Comparative Sequencing Initiative  
2. (bases 1 to 202456)  
Green, E.D.  
Direct Submission  
Submitted (30-JUN-2004) NIH Intramural Sequencing Center, 8717  
JOURNAL  
Groveomont Circle, Gaithersburg, MD 20877, USA  
3 (bases 1 to 202456)  
Green, E.D.  
Direct Submission  
Submitted (14-AUG-2004) NIH Intramural Sequencing Center, 8717  
JOURNAL  
Groveomont Circle, Gaithersburg, MD 20877, USA  
On Aug 14, 2004 this sequence version replaced gi:49457902.  
COMMENT  
Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: http://www.nisc.nih.gov  
Contact: nisc\_zoo@nhgri.nih.gov  
Project Information  
Center project name: hot

Center clone name: 380L14

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics -----

Sequencing Vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 200278 bases at least Q40  
Consensus quality: 201061 bases at least Q30  
Consensus quality: 201319 bases at least Q20  
Insert size: 199000; agarose-fp  
Quality coverage: 11.29x in Q20 bases; sum-of-contigs  
Quality coverage: 11.16x in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

\* This sequence will be replaced by the finished sequence as soon as it is available and by the finished sequence will be preserved.

1 491: contig of 491 bp in length  
\* 492 591: gap of unknown length  
\* 592 15469: contig of 14878 bp in length  
\* 15470 15569: gap of unknown length  
\* 15570 27004: contig of 11435 bp in length  
\* 27005 27104: gap of unknown length  
\* 27105 54767: contig of 27663 bp in length  
\* 54768 54867: gap of unknown length  
\* 54868 68611: contig of 13744 bp in length  
\* 68612 68711: gap of unknown length  
\* 68712 80967: contig of 12256 bp in length  
\* 80968 81067: gap of unknown length  
\* 81068 89969: contig of 8902 bp in length  
\* 89970 90069: gap of unknown length  
\* 90070 124231: contig of 34162 bp in length  
\* 124232 124331: gap of unknown length  
\* 124332 163717: contig of 33386 bp in length  
\* 163718 163817: gap of unknown length  
\* 163818 174752: contig of 10935 bp in length  
\* 174753 174853: gap of unknown length  
\* 174853 202456: contig of 27604 bp in length.

FEATURES

SOURCE

1. 202456  
/organism="Papio anubis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9555"  
/clone="RP41-380L14"  
/clone\_id="RP41"  
/note="BAC resource: http://bacpac.chori.org/"  
1. 80967  
/note="clone overlaps with GenBank Accession Number AC149866 clone RP41-475C15 (center project name hos)"  
misc\_feature  
1. 491  
/note="assembly\_fragment"  
clone\_end:sp6  
vector\_side:left  
592. 15469  
misc\_feature  
/note="assembly\_fragment"

misc\_feature 15570..27004  
/note="assembly\_fragment"  
misc\_feature 27105..54767  
/note="assembly\_fragment"  
misc\_feature 54868..68611  
/note="assembly\_fragment"  
misc\_feature 68712..80967  
/note="assembly\_fragment"  
misc\_feature 81068..89969  
/note="assembly\_fragment"  
misc\_feature 90070..124231  
/note="assembly\_fragment"  
misc\_feature 124332..163717  
/note="assembly\_fragment"  
misc\_feature 152381..202456  
/note="clone overlaps with GenBank Accession Number AC149852 clone RP41-253C23 (center project name hos)"  
misc\_feature 163818..174752  
misc\_feature 174853..202456  
/note="assembly\_fragment"  
clone\_end:T7  
vector\_side:right

ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 202456;  
Best Local Similarity 85.7%; Pred. No. 1e+02;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Oy 5 UCCUGAGAGNNNNN 18  
Db 81075 TCCTGAGNNNNN 81062

RESULT 90  
CR749177  
LOCUS 210310 bp DNA linear HTG 23-AUG-2004  
DEFINITION Danio rerio clone DKXP-85E10, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 6  
unordered pieces.  
ACCESSION CR749177  
VERSION CR749177.5 GI:51510883  
KEYWORDS HTG; HTGS PHASE1.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
REFERENCE 1 (bases 1 to 210310)  
Mclay, K.  
AUTHORS Direct Submission  
TITLE Submitted (22-AUG-2004) Wellcome Trust Sanger Institute, Hinxton,  
JOURNAL Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
zfish-help@sanger.ac.uk  
COMMENT On Aug 23, 2004 this sequence version replaced gi:51491341.  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: zfish-help@sanger.ac.uk  
----- Project Information  
Center project name: zkp85E10  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 100% of reads  
Consensus quality: 208982 bases at least Q40  
Consensus quality: 209266 bases at least Q30  
Consensus quality: 209525 bases at least Q20  
Insert size: 209810; sum-of-contigs  
Insert size: 208739; 3.5% error; agarose-fp  
Quality coverage: 8.69x in Q20 bases; sum-of-contigs Quality  
Coverage: 8.73x in Q20 bases; agarose-fp

\* NOTE: This is a 'working draft' sequence. It currently

```

* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 37505: contig of 37505 bp in length
* 37506: gap of 100 bp
* 37606: contig of 18649 bp in length
* 56354: gap of 100 bp
* 56355: contig of 35547 bp in length
* 91901: gap of 100 bp
* 92001: contig of 26216 bp in length
* 118217: gap of 100 bp
* 118318: contig of 42865 bp in length
* 16182: gap of 100 bp
* 16183: contig of 49028 bp in length.
161283 Location/Qualifiers
1..210310
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone_id="DKEXP-85E10"
/clone_lib="DanioKeyPilot"
1..37505
/note="assembly_fragment:01090
fragment_chain:1"
37606..56254
/note="assembly_fragment:00006
fragment_chain:1"
56355..91901
/note="assembly_fragment:00639
fragment_chain:1"
92002..118217
/note="assembly_fragment:00271"
118318..161182
/note="assembly_fragment:01599"
161283..210310
/note="assembly_fragment:02149.0"

ORIGIN
Query Match 77.8%; Score 14; DB 2; Length 210310;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGNNNNNN 18
Db 37498 TCCTGGAGNNNNNN 37511

RESULT 91
CR376743/ 210481 bp DNA linear HTG 21-MAR-2004
LOCUS Danio rerio clone CH211-215N20, *** SEQUENCING IN PROGRESS ***, 14
DEFINITION unordered pieces.
ACCESSION CR376743
VERSION CR376743.2 GI:45598670
KEYWORDS HTG; HTGS PHASE1.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 210481)
Sims,S.
Direct Submission
Submitted (20-MAR-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zf1th-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 21, 2004 this sequence version replaced gi:455986211.
----- Genome Center
Center: Wellcome Trust Sanger Institute

```

```

Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zf1th-help@sanger.ac.uk
----- Project Information
Center project name: ZC215N20
----- Summary Statistics
Assembly program: XGAP4, version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 204148 bases at least Q40
Consensus quality: 205280 bases at least Q30
Consensus quality: 206024 bases at least Q20
Insert size: 209181; sum-of-contigs
Insert size: 187345; 2.5% error; agarose-fp
Quality coverage: 5.75x in Q20 bases; sum-of-contigs Quality
coverage: 6.45x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 5312: contig of 5312 bp in length
* 5313: gap of 100 bp
* 5412: gap of 100 bp
* 5413: contig of 4983 bp in length
* 10395: gap of 100 bp
* 10396: contig of 5873 bp in length
* 16369: gap of 100 bp
* 16468: contig of 41569 bp in length
* 58037: gap of 100 bp
* 58038: contig of 14863 bp in length
* 58138: gap of 100 bp
* 73001: gap of 100 bp
* 73100: gap of 100 bp
* 92512: contig of 19412 bp in length
* 92613: gap of 100 bp
* 92613: contig of 2381 bp in length
* 116193: gap of 100 bp
* 116294: gap of 100 bp
* 116294: contig of 14669 bp in length
* 130963: gap of 100 bp
* 131062: gap of 100 bp
* 131063: contig of 40897 bp in length
* 171959: gap of 100 bp
* 172059: gap of 100 bp
* 172060: contig of 9000 bp in length
* 181059: gap of 100 bp
* 181060: contig of 3058 bp in length
* 181160: gap of 100 bp
* 184217: contig of 4758 bp in length
* 184218: gap of 100 bp
* 184318: contig of 4758 bp in length
* 189075: gap of 100 bp
* 189175: gap of 100 bp
* 189176: contig of 7734 bp in length
* 196909: gap of 100 bp
* 196910: contig of 13472 bp in length.
197010 Location/Qualifiers
1..210481
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone_id="CH211-215N20"
/clone_lib="CHOR1-211"
1..5312
/note="assembly_fragment:00187
clone_end:SP6
vector_side:left"
5413..10395
/note="assembly_fragment:00136
fragment_chain:1"
10496..16368
/note="assembly_fragment:00092
fragment_chain:1"
16469..58037
/note="assembly_fragment:01222
fragment_chain:1"
58138..73000
/note="assembly_fragment:00496

```

```

misc_feature      73101..52512      fragment chain:1"
                    /note="assembly_fragment:00766
                    fragment chain:1"
misc_feature      92613..116193   /note="assembly_fragment:00962
                    fragment chain:1"
misc_feature      116294..110962   /note="assembly_fragment:00628
                    fragment chain:1"
misc_feature      131063..171959   /note="assembly_fragment:01601
                    fragment chain:1"
misc_feature      172060..181059   /note="assembly_fragment:00245
                    fragment chain:1"
misc_feature      181160..184217   /note="assembly_fragment:00029
                    fragment chain:1"
misc_feature      184318..189075   /note="assembly_fragment:00052
                    fragment chain:1"
misc_feature      189176..196909   /note="assembly_fragment:00309
                    fragment chain:1"
misc_feature      197010..210481   /note="assembly_fragment:00376
                    fragment chain:1"

ORIGIN

Query Match      77.8% Score 14; DB 2; Length 210481;
Best Local Similarity 85.7% Pred. NO. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      5 UCCUGAGAGNNNNNN 18
Db      58145 TCCGCGAGNNNNNN 58132

RESULT 92
AC122949
LOCUS      AC122949      213181 bp      DNA      linear      HTG 19-NOV-2002
DEFINITION      Rattus norvegicus clone CH230-290B6, *** SEQUENCING IN PROGRESS
ACCESSION      AC122949
VERSION      AC122949.5 GI:25089514
KEYWORDS      HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM      Rattus norvegicus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE      1 (bases 1 to 213181)
AUTHORS      Muzny D,Marie, Metzker M, Lee, Abramzon S, Adams C, Alder J,
            Allen C, Allen H, Albrooks S, Amin A, Angiano D,
            Anyaldebechi V, Aoyagi A, Ayodeji M, Baca E, Baden H,
            Baldwin D, Bandaramaiki D, Barber M, Barnstead M, Benahmed F,
            Biewald K, Blair J, Blankenburg K, Blyth P, Brown M,
            Bryant N, Buhay C, Burch P, Burrell K, Calderon E,
            Cardenas V, Carter K, Cavazos I, Ceasar H, Center A,
            Chacko J, Chavez D, Chen G, Chen R, Chen Y, Chen Z, Chu J,
            Cleveland C, Cockrell R, Cox C, Coyle M, Cree A, D'Souza L,
            Devilla M, L, Davis C, Davy-Carroll L, De Anda C, Dederich D,
            Delgado O, Denison S, Deramo C, Ding Y, Dinh H, Divya K,
            Draper H, Dugan-Rocha S, Dunn A, Durbin K, Duval B, Eaves K,
            Egan A, Escotto M, Eugene C, Evans C, A, Falls T, Fan G,
            Fernandez S, Finley M, Flagg N, Forbes L, Foster M, Foster P,
            Frazer C, M, Gabisi A, Ganta R, Garcia A, Garner J, Garza M,
            Gebregiorgis E, Geer K, Gill R, Grady M, Guerra W, Guevara W,
            Gunaratne P, Haaland W, Hamill C, Hamilton C, Hamilton K,
            Harvey Y, Havlak P, Hawes A, Henderson N, Hernandez J,
            Hernandez R, Hines S, Hladun S, L, Hodgson A, Hogues M,
            Hollins B, Howells S, Hulys S, Hume J, Idlebird D, Jackson A,

```

```

TITLE      JOURNAL
AUTHORS      Karpachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
            Kowis, C., Kraf, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
            Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
            Lorenuhewa, L., Loulesged, H., Lozano, R. J., Lu, X., Ma, J.,
            Maheshwari, M., Mahindartine, M., Mahmood, M., Malloy, K., Mangum, A.,
            Mangum, B., Mapa, P., Martin, K., Martin, K., Martinez, E.,
            Mawhney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,
            Milosavljevic, A., Miner, G., Ming, E., Montemayor, J., Moore, S.,
            Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Naik, L.,
            Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
            Nwokeneme, O., Okunolu, G., Olarinpoju, A., Pal, S., Parks, K.,
            Paaternek, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,
            Plopper, F., Poindester, A., Popovic, D., Primus, E., Pu, L., L.,
            Piazzi, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R.,
            Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
            Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J.,
            Sanders, M., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
            Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C. D., Smajic, D.,
            Sneed, A., Sodergren, E., Song, X. Z., Sorelle, R., Sosa, J.,
            Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
            Taylor, T., Thomas, N., Thomas, S., Tangey, A., Trejos, Z., Usmani, K.,
            Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J.,
            Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
            Williams, G., Willson, R., Wleczek, R., Wooden, H., Worley, K.,
            Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
            Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
            Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
            Weinstock, G. and Gibbs, R. A.
            Direct Submission
            Unpublished
            2 (bases 1 to 213181)
            Worley, K. C.
            Direct Submission
            Submitted (26-MAY-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            3 (bases 1 to 213181)
            Rat Genome Sequencing Consortium.
            Direct Submission
            Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            On Nov 19, 2002 this sequence version replaced gi:22907669.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.

            ----- Genome Center
            Center: Baylor College of Medicine
            Center code: BCM
            Web site: http://www.hgsc.bcm.tmc.edu/
            Contact: hgsc-help@bcm.tmc.edu
            ----- Project Information
            Center project name: CH230-290B6
            Center clone name: GW2W
            ----- Summary Statistics
            Assembly program: Phrap; version 0.990329
            Consensus quality: 187583 bases at least Q40
            Consensus quality: 189673 bases at least Q30
            Consensus quality: 191228 bases at least Q20
            Estimated insert size: 184726; sum-of-contigs estimation
            Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

            * NOTE: Estimated insert size may differ from sequence length

```





TITLE Direct Submission  
JOURNAL Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One

## COMMENT

Baylor Plaza, Houston, TX 77030, USA  
On May 10, 2003 this sequence version replaced gi:23269275.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

## ----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: GFTL

Center clone name: CH230-137022

## ----- Summary Statistics

Assembly program: Atlas 3.0;  
Consensus quality: 204318 bases at least Q40  
Consensus quality: 205839 bases at least Q30  
Consensus quality: 206762 bases at least Q20  
Estimated insert size: 213544; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 5 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 89642: contig of 89642 bp in length  
1 89643 89742: gap of unknown length  
1 89743 107775: contig of 18033 bp in length  
1 107776 107875: gap of unknown length  
1 107876 120148: contig of 12273 bp in length  
1 120149 120248: gap of unknown length  
1 120249 214156: contig of 93908 bp in length  
1 214157 214256: gap of unknown length  
1 214257 215479: contig of 1223 bp in length.

## Location/Qualifiers

1. 215479  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-137022"  
1. 1132  
/note="wgs\_contig"

## ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 215479;  
Best Local Similarity 85.7%; Pred. No. 99;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 5 UCCUGAGANNNNN 18  
Db 126882 TCCTGAGANNNNN 126865

RESULT 94  
CR376804/c

## LOCUS

CR376804 215604 bp DNA linear HTG 27-MAR-2004

DEFINITION Danio rerio clone DKEX-42P14, \*\*\* SEQUENCING IN PROGRESS \*\*\*. 18.

UNORDERED PIECES.

ACCESSION CR376804.2 GI:45772275

VERSION HTG; HTGS PHASE1.

KEYWORDS Danio rerio (zebrafish)

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 215604)

McLay, K.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Direct Submission

Submitted (26-MAR-2004) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

fish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Mar 27, 2004 this sequence version replaced gi:45598604.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: zfish-help@sanger.ac.uk

Project Information

Center project name: ZK42P14

## ----- Summary Statistics

Assembly program: XGAP4; version 4.5

Chemistry: Dye-terminator; 100% of reads

Consensus quality: 210686 bases at least Q40

Consensus quality: 211687 bases at least Q30

Consensus quality: 212503 bases at least Q20

Insert size: 213904; sum-of-contigs

Insert size: 207062; 4.5% error; agarose-gel

Quality coverage: 6.90x in Q20 bases; sum-of-contigs Quality

coverage: 7.33x in Q20 bases; agarose-gel

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 18 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

1 2616: contig of 2616 bp in length

1 2617 2716: gap of 100 bp

1 2717 17493: contig of 14776 bp in length

1 17493 17593: gap of 100 bp

1 17593 47621: contig of 30029 bp in length

1 47622 47721: gap of 100 bp

1 47722 54207: contig of 6486 bp in length

1 54208 54307: gap of 100 bp

1 54308 60090: contig of 5783 bp in length

1 60091 60190: gap of 100 bp

1 60191 64267: contig of 4077 bp in length

1 64268 64367: gap of 100 bp

1 64368 80144: contig of 15777 bp in length

1 80145 80244: gap of 100 bp

1 80244 93958: contig of 13714 bp in length

1 93959 94058: gap of 100 bp

1 94059 121790: contig of 27732 bp in length

1 121791 121890: gap of 100 bp

1 121891 144599: contig of 22709 bp in length

1 144600 144699: gap of 100 bp

1 144700 151660: contig of 6961 bp in length

1 151661 151760: gap of 100 bp

1 151761 163632: contig of 11872 bp in length

1 163633 163732: gap of 100 bp

1 163733 177690: contig of 13558 bp in length

1 177691 177790: gap of 100 bp

1 177791 183034: contig of 5244 bp in length

1 183035 183134: gap of 100 bp

1 183135 187729: contig of 4595 bp in length

FEATURES  
source  
misc\_feature 187730 187829: gap of 100 bp  
\* 187830 209233: contig of 21404 bp in length  
\* 209234 209333: gap of 100 bp  
\* 209334 211603: contig of 2270 bp in length  
\* 211604 211703: gap of 100 bp  
\* 211704 215604: contig of 3901 bp in length.  
Location/Qualifiers  
1. .215604  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKEX-42P14"  
/clone\_lib="DanioKey"  
1. .2616  
/note="assembly\_fragment:00053  
fragment\_chain:1"  
2717. .17492  
/note="assembly\_fragment:01151  
fragment\_chain:1"  
17593. .47621  
/note="assembly\_fragment:02225  
fragment\_chain:1"  
47722. .54207  
/note="assembly\_fragment:00295  
fragment\_chain:1"  
54308. .60090  
/note="assembly\_fragment:00433  
fragment\_chain:1"  
60191. .64267  
/note="assembly\_fragment:00141  
fragment\_chain:1"  
64368. .80144  
/note="assembly\_fragment:00825  
fragment\_chain:1"  
80245. .93958  
/note="assembly\_fragment:00510  
fragment\_chain:1"  
94059. .121790  
/note="assembly\_fragment:01844  
fragment\_chain:1"  
121891. .144599  
/note="assembly\_fragment:01579  
fragment\_chain:1"  
144700. .151660  
/note="assembly\_fragment:00360  
fragment\_chain:2"  
151761. .163632  
/note="assembly\_fragment:00667  
fragment\_chain:2"  
163733. .177690  
/note="assembly\_fragment:00986  
fragment\_chain:2"  
177791. .183034  
/note="assembly\_fragment:00186  
fragment\_chain:2"  
183135. .187729  
/note="assembly\_fragment:00097  
fragment\_chain:3"  
187830. .209233  
/note="assembly\_fragment:01336  
fragment\_chain:3"  
209334. .211603  
/note="assembly\_fragment:00033"  
211704. .215604  
/note="assembly\_fragment:00231.0"  
ORIGIN  
Query Match 77.8%; Score 14; DB 2; Length 215604;  
Best Local Similarity 85.7%; Pred. No. 99;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 5 UCCUGAGAGNNNNN 18  
:|||||

Db 187837 TCCTGAGAGNNNNN 187824  
RESULT 95  
BX927238  
LOCUS  
DEFINITION  
BX927238 216013 bp DNA linear HTG 26-JAN-2004  
Danio rerio clone DKEX-98N4, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 9  
unordered pieces.  
BX927238  
VERSION  
BX927238.2 GI:41349671  
HTG; HTGS PHASE1.  
SOURCE  
Danio rerio (zebrafish)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 216013)  
McLay, K.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Submitted (25-JAN-2004) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
fish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
On Jan 26, 2004 this sequence version replaced gi:4133245.  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: zfish-help@sanger.ac.uk  
----- Project Information  
Center project name: ZK98N4  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 100% of reads  
Consensus quality: 21413 bases at least Q40  
Consensus quality: 214460 bases at least Q30  
Consensus quality: 214760 bases at least Q20  
Insert size: 215213; sum-of-contigs  
Insert size: 205178; 6.6% error; agarose-fp  
Quality coverage: 8.34x in Q20 bases; sum-of-contigs Quality  
coverage: 8.94x in Q20 bases; agarose-fp  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 9 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1 40662: contig of 40662 bp in length  
\* 40663 40762: gap of 100 bp  
\* 40763 70874: contig of 30112 bp in length  
\* 70875 70974: gap of 100 bp  
\* 70975 75647: contig of 4673 bp in length  
\* 75648 75747: gap of 100 bp  
\* 75748 80091: contig of 434 bp in length  
\* 80092 80191: gap of 100 bp  
\* 80192 94544: contig of 14353 bp in length  
\* 94545 94644: gap of 100 bp  
\* 94645 163221: contig of 68477 bp in length  
\* 163222 163221: gap of 100 bp  
\* 163222 174523: contig of 11302 bp in length  
\* 174524 174623: gap of 100 bp  
\* 174624 204483: contig of 29860 bp in length  
\* 204484 204583: gap of 100 bp  
\* 204584 216013: contig of 11430 bp in length.  
Location/Qualifiers  
1. .216013  
/organism="Danio rerio"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7955"  
/clone="DKEX-98N4"  
/clone\_lib="DanioKey"

```
misc_feature 1..40662
/note="assembly_fragment:01484
fragment_chain:1"
misc_feature 40763..70874
/note="assembly_fragment:01075
fragment_chain:1"
misc_feature 70975..75647
/note="assembly_fragment:00094
fragment_chain:1"
misc_feature 75748..80091
/note="assembly_fragment:00038
fragment_chain:1"
misc_feature 80192..94544
/note="assembly_fragment:00458
fragment_chain:1"
misc_feature 94645..163121
/note="assembly_fragment:01993
fragment_chain:1"
misc_feature 163322..174523
/note="assembly_fragment:00157
fragment_chain:1"
misc_feature 174624..204483
/note="assembly_fragment:00687
fragment_chain:1"
misc_feature 204584..216013
/note="assembly_fragment:00285.0"

ORIGIN
Query Match 77.8%; Score 14; DB 2; Length 216013;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGANNNNN 18
Db 94537 TCCTGAGANNNNN 94550

RESULT 96
BX901905/c 217309 bp DNA linear HTG 04-JAN-2004
LOCUS Danio rerio clone CH211-208N20, ** SEQUENCING IN PROGRESS ***, 14
DEFINITION unorderd piecec.
ACCESSION BX901905
VERSION BX901905.1 GI:40556537
KEYWORDS HTG; HTGS PHASE1.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 217309)
Sim8.S.
Direct Submission
Submitted (03-JAN-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: zc208N20
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 213096 bases at least Q40
Consensus quality: 213787 bases at least Q20
Consensus quality: 214425 bases at least Q20
Insert size: 216009; sum-of-contigs
Insert size: 210494; 5.9% error; agarose-fp
Quality coverage: 8.71x in Q20 bases; sum-of-contigs Quality
coverage: 9.06x in Q20 bases; agarose-fp
```

```
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
9698: contig of 9698 bp in length
9699: gap of 100 bp
9798: contig of 6750 bp in length
16548: gap of 100 bp
16549: gap of 100 bp
16649: contig of 5309 bp in length
21957: gap of 100 bp
22058: contig of 22103 bp in length
44160: gap of 100 bp
44261: contig of 7879 bp in length
52140: gap of 100 bp
52240: contig of 4918 bp in length
57158: gap of 100 bp
57257: contig of 19348 bp in length
57258: gap of 100 bp
76605: contig of 8958 bp in length
76706: gap of 100 bp
85664: contig of 58923 bp in length
85764: gap of 100 bp
144687: contig of 5468 bp in length
144787: gap of 100 bp
150254: contig of 21537 bp in length
150255: gap of 100 bp
171892: contig of 7461 bp in length
171991: gap of 100 bp
179453: contig of 100 bp
179552: gap of 100 bp
207095: contig of 27543 bp in length
207096: gap of 100 bp
207196: contig of 10114 bp in length.

FEATURES
source
1..217309
location/Qualifiers
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-208N20"
/clone_1bp="CHOR1-211"
1..9658
/note="assembly_fragment:00393
fragment_chain:1
clone_end:T7
vector_side:left"
9799..16548
/note="assembly_fragment:00151
fragment_chain:1"
16649..21957
/note="assembly_fragment:00110
fragment_chain:1"
22058..44160
/note="assembly_fragment:00952
fragment_chain:1"
44261..52139
/note="assembly_fragment:00249
fragment_chain:1"
52240..57157
/note="assembly_fragment:00072.0"
57258..76605
/note="assembly_fragment:00772
fragment_chain:2"
76706..85663
/note="assembly_fragment:00638
fragment_chain:2"
85764..144686
/note="assembly_fragment:01937
fragment_chain:2"
144787..150254
/note="assembly_fragment:00194
```

```

misc_feature      150355..171891
                    /note="assembly_fragment:01196
                    fragment_chain:2"
misc_feature      171992..179452
                    /note="assembly_fragment:00318
                    fragment_chain:2"
misc_feature      179553..207095
                    /note="assembly_fragment:01531
                    fragment_chain:2"
misc_feature      207196..217309
                    /note="assembly_fragment:00504
                    fragment_chain:2
                    clone_end:SP6
                    vector_side:right"

ORIGIN
Query Match      77.8%; Score 14; DB 2; Length 217309;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      5 UCCUGGAGNNNNNN 18
        :||:|||||||
Db      171999 TCCTGGAGNNNNNN 171986

RESULT 97
AC106115/c      222632 bp      DNA      linear      HTG 10-MAY-2003
LOCUS      Rattus norvegicus clone CH230-137L21, *** SEQUENCING IN PROGRESS
DEFINITION
ACCESSION      AC106115
VERSION      AC106115.6 GI:30521579
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus
ORGANISM      Rattus norvegicus
                    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
                    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                    Rattus.
REFERENCE      1 (bases 1 to 222632)
AUTHORS      Muzny, D., Maric, M., Metzker, M., Lee, A., Abramson, S., Adams, C., Alder, J.,
                    Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
                    Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
                    Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
                    Bismalo, K., Blair, J., Blankenburg, K., Blych, P., Brown, M.,
                    Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
                    Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
                    Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
                    Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
                    Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
                    Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diya, K.,
                    Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
                    Egan, A., Escotto, M., Eugene, C., Evans, C., Falls, T., Fan, G.,
                    Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
                    Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
                    Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
                    Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
                    Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
                    Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogue, M.,
                    Hollins, B., Howells, S., Hu, Y., Hume, J., Idlebird, D., Jackson, A.,
                    Jackson, J., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
                    Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
                    Kowitz, C., Kraft, C. L., Lebow, H., Levay, J., Lewis, L., Li, Z., Liu, J.,
                    Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
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                    Maheshwari, M., Mahndarine, M., Mahmoud, M., Mallory, K., Mangum, A.,
                    Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
                    Mawney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,
                    Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
                    Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
                    Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
                    Nwackelmen, O., Okunom, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
                    Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,

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TITLE      JOURNAL
REFERENCE   JOURNAL
AUTHORS     JOURNAL
TITLE      JOURNAL
REFERENCE   JOURNAL
AUTHORS     JOURNAL
TITLE      JOURNAL
COMMENT     JOURNAL

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Plopper, F., Polindexter, A., Popovic, D., Primus, E., Pu, L., L.,
Pruzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reish, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
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Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umanan, K.,
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
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Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
Weinstock, G. and Gibbs, R. A.
Direct Submission
Unpublished
2 (bases 1 to 222632)
Mortley, K. C.
Direct Submission
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 222632)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:24953991.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GHKJ
Center clone name: CH230-137L21
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 182183 bases at least Q40
Consensus quality: 186060 bases at least Q30
Consensus quality: 189005 bases at least Q20
Estimated insert size: 191530; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_diff_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 202667: contig of 202667 bp in length
* 202668 202767: gap of unknown length
* 202768 221218: contig of 18451 bp in length
* 221219 221318: gap of unknown length

```

```

FEATURES      * 221319 222632: contig of 1314 bp in length.
SOURCE
  1..222632
    /organism="Rattus norvegicus"
    /mol_type="genomic DNA"
    /db_xref="taxon:10116"
    /clone="CH230-137L21"
  misc_feature 4877..7300
    /note="wgs_contig"
  misc_feature 48572..50625
    /note="wgs_contig"
  misc_feature 152768..154725
    /note="wgs_contig"
  misc_feature 155213..156643
    /note="wgs_contig"
ORIGIN
Query Match 77.8%; Score 14; DB 2; Length 222632;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 5 UCCUGAGAGNNNNN 18
Db 72066 TCCTGAGAGNNNNN 72053

RESULT 98
CR382363/c CR382363 222961 bp DNA linear HTG 03-APR-2004
DEFINITION Danio rerio clone DKEX-23p11, *** SEQUENCING IN PROGRESS ***, 22
unordered pieces.
ACCESSION CR382363
VERSION CR382363.2 GI:46194580
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Danio rerio (zebrafish)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 222961)
REFERENCE 1
AUTHORS McIay, K.
JOURNAL Direct Submission
Submitted (01-APR-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clonerequests@sanger.ac.uk
zf1sh-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Apr 3, 2004 this sequence version replaced gi:46019166.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zf1sh-help@sanger.ac.uk
----- Project Information
Center project name: zK23p11
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 21673 bases at least Q40
Consensus quality: 21736 bases at least Q30
Consensus quality: 218438 bases at least Q20
Insert size: 220861; sum-of-contigs
Insert size: 207717; 1.0% error; agarose-fp
Quality coverage: 6.70x in Q20 bases; sum-of-contigs Quality
coverage: 7.25x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 5743: contig of 5743 bp in length

```

```

FEATURES
SOURCE
  1..222961
    /organism="Danio rerio"
    /mol_type="genomic DNA"
    /db_xref="taxon:7955"
    /clone="DKEX-23p11"
    /clone_1fb="DanioKey"
  1..5743
    /note="assembly_fragment:00234
    fragment_chain:1"
  misc_feature 5844..8760
    /note="assembly_fragment:00065
    fragment_chain:1"
  misc_feature 8861..38667
    /note="assembly_fragment:01842
    fragment_chain:1"
  misc_feature 38768..46216
    /note="assembly_fragment:00330
    fragment_chain:1"
  misc_feature 46317..49904
    /note="assembly_fragment:00196
    fragment_chain:1"
  misc_feature 50005..80575
    /note="assembly_fragment:02173
    fragment_chain:1"
  misc_feature 80676..83226
    /note="assembly_fragment:00047
    fragment_chain:1"
  misc_feature 83327..101361
    /note="assembly_fragment:01036
    fragment_chain:1"
  5744 5843: gap of 100 bp
  * 5844 8760: contig of 2917 bp in length
  * 8761 8860: gap of 100 bp
  * 8861 38667: contig of 29807 bp in length
  * 38668 38767: gap of 100 bp
  * 38768 46216: contig of 7449 bp in length
  * 46217 46315: gap of 100 bp
  * 46317 49904: contig of 3588 bp in length
  * 49905 50004: gap of 100 bp
  * 50005 80575: contig of 30571 bp in length
  * 80576 80675: gap of 100 bp
  * 80676 83226: contig of 2551 bp in length
  * 83227 83325: gap of 100 bp
  * 83327 101361: contig of 18035 bp in length
  * 101362 101461: gap of 100 bp
  * 101462 108527: contig of 7066 bp in length
  * 108528 108627: gap of 100 bp
  * 108628 110978: contig of 2351 bp in length
  * 110979 11078: gap of 100 bp
  * 11079 113982: contig of 2904 bp in length
  * 113983 114082: gap of 100 bp
  * 114083 116877: contig of 2795 bp in length
  * 116878 116977: gap of 100 bp
  * 116978 121962: contig of 4985 bp in length
  * 121963 122062: gap of 100 bp
  * 122063 128775: contig of 7713 bp in length
  * 128776 129875: gap of 100 bp
  * 129876 133929: contig of 4054 bp in length
  * 133930 134029: gap of 100 bp
  * 134030 138068: contig of 4039 bp in length
  * 138069 138168: gap of 100 bp
  * 138169 143235: contig of 5067 bp in length
  * 143236 143335: gap of 100 bp
  * 143336 151982: contig of 8647 bp in length
  * 151983 152082: gap of 100 bp
  * 152083 161834: contig of 9752 bp in length
  * 161835 161934: gap of 100 bp
  * 161935 174485: contig of 12351 bp in length
  * 174486 174585: gap of 100 bp
  * 174586 200738: contig of 26153 bp in length
  * 200739 200839: gap of 100 bp
  * 200839 222961: contig of 22123 bp in length.
Location/Qualifiers
  1..222961
    /organism="Danio rerio"
    /mol_type="genomic DNA"
    /db_xref="taxon:7955"
    /clone="DKEX-23p11"
    /clone_1fb="DanioKey"
  1..5743
    /note="assembly_fragment:00234
    fragment_chain:1"
  misc_feature 5844..8760
    /note="assembly_fragment:00065
    fragment_chain:1"
  misc_feature 8861..38667
    /note="assembly_fragment:01842
    fragment_chain:1"
  misc_feature 38768..46216
    /note="assembly_fragment:00330
    fragment_chain:1"
  misc_feature 46317..49904
    /note="assembly_fragment:00196
    fragment_chain:1"
  misc_feature 50005..80575
    /note="assembly_fragment:02173
    fragment_chain:1"
  misc_feature 80676..83226
    /note="assembly_fragment:00047
    fragment_chain:1"
  misc_feature 83327..101361
    /note="assembly_fragment:01036
    fragment_chain:1"

```

```

misc_feature      101462..108527
                    /note="assembly_fragment:00453
                    fragment_chain:1"
misc_feature      108628..110978
                    /note="assembly_fragment:00084
                    fragment_chain:1"
misc_feature      111079..113982
                    /note="assembly_fragment:00165
                    fragment_chain:1"
misc_feature      114083..116877
                    /note="assembly_fragment:00134
                    fragment_chain:1"
misc_feature      116978..121962
                    /note="assembly_fragment:00389
                    fragment_chain:1"
misc_feature      122063..129775
                    /note="assembly_fragment:00594
                    fragment_chain:1"
misc_feature      129876..133929
                    /note="assembly_fragment:00106
                    fragment_chain:1"
misc_feature      134030..138068
                    /note="assembly_fragment:00281
                    fragment_chain:2"
misc_feature      138169..143335
                    /note="assembly_fragment:00522
                    fragment_chain:2"
misc_feature      143336..151982
                    /note="assembly_fragment:00909
                    fragment_chain:2"
misc_feature      152083..161834
                    /note="assembly_fragment:00685
                    fragment_chain:3"
misc_feature      161935..174485
                    /note="assembly_fragment:00792
                    fragment_chain:3"
misc_feature      174586..200738
                    /note="assembly_fragment:01223
                    fragment_chain:3"
misc_feature      200839..222961
                    /note="assembly_fragment:01522.0"
ORIGIN

```

```

Query Match      77.8% Score 14; DB 2; Length 222961;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 5 UCCUGAGAGNNNNN 18
Db 174593 TCCTGGAGNNNNN 174580

```

```

RESULT 99
AC097049
LOCUS
DEFINITION
AC097049 224370 bp DNA linear HTG 10-MAY-2003
***, 9 unordered pieces.
AC097049.7 GI:30521039
VERSION
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 224370)
REFERENCE
AUTHORS
Muzny,D.,Marle.,Metzker,M.,Lee.,Abramson,S.,Adams,C.,Alder,J.,
Allen,C.,Allen,H.,Alsbrooks,S.,Amin,A.,Angiano,D.,
Anyalebechi,V.,Aoyagi,A.,Ayodeji,M.,Baca,E.,Baden,H.,
Baldwin,D.,Bandaranaike,D.,Barber,M.,Barnstead,M.,Benahmed,F.,
Biswal,K.,Blair,J.,Blankenburg,K.,Blyth,P.,Brown,M.,
Bryant,N.,Buhay,C.,Burch,P.,Burrell,K.,Calderson,E.,
Cardenas,V.,Carter,K.,Cavazos,I.,Caesar,H.,Center,A.,

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL
COMMENT

```

```

REFERENCE
AUTHORS
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 224370)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (06-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:25188677.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/

```

```

Contact: hgsc-help@bcm.tmc.edu
----- Project Information -----
Center project name: G1DT
Center clone name: CH230-204423
----- Summary Statistics -----
Assembly program: AClas 3.0;
Consensus quality: 189343 bases at least Q40
Consensus quality: 194891 bases at least Q30
Consensus quality: 198424 bases at least Q20
Estimated insert size: 212744; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
  (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
* NOTE: This is a "working draft" sequence. It currently
  consists of 9 contigs. The true order of the pieces
  is not known and their order in this sequence record is
  arbitrary. Gaps between the contigs are represented as
  runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
  as soon as it is available and the accession number will
  be preserved.
*
  1 206236: contig of 206236 bp in length
*
  * 206237 206336: gap of unknown length
*
  * 206337 207904: contig of 1568 bp in length
*
  * 207905 208004: gap of unknown length
*
  * 208005 209107: contig of 1103 bp in length
*
  * 209108 209207: gap of unknown length
*
  * 209208 210423: contig of 1216 bp in length
*
  * 210424 210523: gap of unknown length
*
  * 210524 212598: contig of 2075 bp in length
*
  * 212599 212698: gap of unknown length
*
  * 212699 214371: contig of 1573 bp in length
*
  * 214372 217564: gap of unknown length
*
  * 217565 217664: contig of 3193 bp in length
*
  * 217665 222371: gap of unknown length
*
  * 222372 222371: contig of 4667 bp in length
*
  * 222372 224370: gap of unknown length
*
  * 224370 224370: contig of 1999 bp in length.
  Location/Qualifiers
    1..224370
      /organism="Rattus norvegicus"
      /mol_type="genomic DNA"
      /db_xref="taxon:10116"
      /clone="CH230-204423"
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        clone_end=T7
        site:EcoRI
      end_sequence=B2106407"
      133012..135520
        /note="wgs_contig"
      139324..151199
        /note="clone_boundary"
        clone_end=SP6
        site:EcoRI
      end_sequence=B2106411"
ORIGIN
Query Match 77.8%; Score 14; DB 2; Length 224370;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 5 UCCUGAGAGNNNNNN 18
DB 143235 TCCTGAGAGNNNNN 143248
-----
RESULT 100
BX927188/c 228022 bp DNA linear HTG 10-OCT-2004
DEFINITION Dario Perio clone DKEX-264N13, WORKING DRAFT SEQUENCE, 9 unordered
pieces.

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ACCESSION      BX927188.4 GI:41630180
VERSION        HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS
SOURCE         Danio rerio (zebrafish)
ORGANISM       Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
               Cypriniformes; Cyprinidae; Danio.
               1 (bases 1 to 228022)
REFERENCE      McLaren,S.
               Direct Submission
               Submitted (08-OCT-2004) Wellcome Trust Sanger Institute, Hinxton,
               Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
               zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
               On Feb 2, 2004 this sequence version replaced gi:4132817.
COMMENT
               -----
               Center: Wellcome Trust Sanger Institute
               Genome Center
               Center code: SC
               Web site: http://www.sanger.ac.uk
               Contact: zfish-help@sanger.ac.uk
               -----
               Project Information
               Center project name: ZK264N13
               -----
               Summary Statistics
               Assembly program: XGAP4; version 4.5
               Chemistry: Dye-terminator; 100% of reads
               Consensus quality: 225138 bases at least Q40
               Consensus quality: 225502 bases at least Q30
               Consensus quality: 225841 bases at least Q20
               Insert size: 227222; sum-of-contigs
               Insert size: 221727; 4.7% error; agarose-fp
               Quality coverage: 8.04x in Q20 bases; sum-of-contigs Quality
               coverage: 8.28x in Q20 bases; agarose-fp
               -----
               * NOTE: This is a 'working draft' sequence. It currently
               * consists of 9 contigs. The true order of the pieces
               * is not known and their order in this sequence record is
               * arbitrary. Gaps between the contigs are represented as
               * runs of N, but the exact sizes of the gaps are unknown.
               * This record will be updated with the finished sequence
               * as soon as it is available and the accession number will
               * be preserved.
               -----
               1      16758: contig of 16758 bp in length
               *      16759      16858: gap of 100 bp
               *      16859      20882: contig of 4024 bp in length
               *      20883      20982: gap of 100 bp
               *      20983      75976: contig of 54994 bp in length
               *      75977      76076: gap of 100 bp
               *      76077      82135: contig of 6055 bp in length
               *      82136      82235: gap of 100 bp
               *      82236      89536: contig of 7301 bp in length
               *      89537      89636: gap of 100 bp
               *      89637      101310: contig of 11674 bp in length
               *      101311      101410: gap of 100 bp
               *      101411      120443: contig of 19053 bp in length
               *      120444      120543: gap of 100 bp
               *      120544      168466: contig of 47923 bp in length
               *      168467      168566: gap of 100 bp
               *      168567      228022: contig of 59456 bp in length.
               -----
               Location/Qualifiers
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               /mol_type="genomic DNA"
               /db_xref="taxon:7955"
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               /clone_1lb="DantioKey"
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               /note="assembly_fragment:00009
               fragment_chain:1"
               20983..75976
               /note="assembly_fragment:02092

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misc_feature      fragment chain:1"
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                    /note="assembly: fragment:00113
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misc_feature      89637..101310
                    /note="assembly: fragment:00225
                    fragment chain:2"
misc_feature      101411..120443
                    /note="assembly: fragment:00552
                    fragment chain:2"
misc_feature      120544..168466
                    /note="assembly: fragment:00801.0"
misc_feature      168567..228022
                    /note="assembly: fragment:01385"

ORIGIN
Query Match      77.8%; Score 14; DB 2; Length 228022;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy      5 UCCUGAGAGNNNNNN 18
        |||:|||||
Db      82243 TCCGAGGNNNNNN 82230

RESULT 101
AC107590/c      232490 bp DNA linear HTG 13-NOV-2002
LOCUS           *** 8 unordered pieces.
DEFINITION      Rattus norvegicus clone CH230-99F11. *** SEQUENCING IN PROGRESS
ACCESSION       AC107590
VERSION         AC107590.4 GI:24941933
KEYWORDS        HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
SOURCE          Rattus norvegicus (Norway rat)
ORGANISM        Rattus norvegicus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                Rattus.
                1 (bases 1 to 232490)
REFERENCE
AUTHORS        Muzny,D.,Marie,,Metzker,M.,Lee,,Abramzon,S.,Adams,C.,Alder,J.,
                Allen,C.,Allen,H.,Aisbrooks,S.,Amin,A.,Anguiano,D.,
                Anyalebechi,V.,Aoyagi,A.,Ayodeji,M.,Baca,E.,Baden,H.,
                Baldwin,D.,Bandaranaik,D.,Barber,M.,Barnstead,M.,Benahmed,F.,
                Biswalio,K.,Blair,J.,Blankenburg,K.,Blych,P.,Brown,M.,
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                Cleveland,C.,Cockrell,R.,Cox,C.,Coyle,M.,Cree,A.,D'Souza,L.,
                Davila,M.L.,Davis,C.,Davy-Carroll,L.,De Anda,C.,Dederich,D.,
                Delgado,O.,Denson,S.,Derramo,C.,Ding,Y.,Dinh,H.,Diyak,K.,
                Draper,H.,Dugan-Rocha,S.,Dunn,A.,Durbin,K.,Duvall,B.,Eaves,K.,
                Egan,A.,Escotto,M.,Eugene,C.,Evans,C.A.,Falls,T.,Fan,G.,
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                Fraser,C.M.,Gabisi,A.,Ganta,R.,Garcia,A.,Garner,T.,Garza,M.,
                Gebregergis,B.,Geer,K.,Gill,R.,Grady,M.,Guerra,M.,Guevara,W.,
                Gunaratne,P.,Haaland,W.,Hamill,C.,Hamilton,C.,Hamilton,K.,
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                Jackson,B.,Jacob,L.,Jiang,H.,Johnson,B.,Johnson,R.,Jolivet,A.,
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                Mangum,B.,Mapua,P.,Martin,K.,Martin,R.,Martinez,E.,
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                Morgan,M.,Morris,K.,Morris,S.,Munidasa,M.,Murphy,M.,Nair,L.,
                Nankervis,C.,Neal,D.,Newton,N.,Nguyen,N.,Norris,S.,

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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Nwaokelemeh,O., Okunnu,G., Olarunpasegun,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C.,
Plopper,F., Polindexter,A., Popovic,D., Prims,E., Pu,L.-L.,
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Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wlezyk,R., Wooden,H., Worley,K.,
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Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., Von
Niederhausem,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 232490)
Worley,K.C.
Direct Submission
Submitted (23-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 232490)
Rat Genome Sequencing Consortium.
Submitted (13-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 13, 2002 this sequence version replaced gi:23267838.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GOPW
Center clone name: CH230-99F11
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 199275 bases at least Q40
Consensus quality: 203573 bases at least Q20
Consensus quality: 206713 bases at least Q20
Estimated insert size: 201384; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 6116: contig of 6116 bp in length
* 6117 6216: gap of unknown length

```



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*      6217      62242: contig of 56026 bp in length
*      62342: 62342: gap of unknown length
*      62343      135755: contig of 73413 bp in length
*      135756      135855: gap of unknown length
*      135856      227081: contig of 91226 bp in length
*      227082      227181: gap of unknown length
*      227182      226618: contig of 1437 bp in length
*      228619      228718: gap of unknown length
*      228719      230002: contig of 1284 bp in length
*      230003      230102: gap of unknown length
*      231003      231206: contig of 1104 bp in length
*      231207      231306: gap of unknown length
*      231307      232490: contig of 1184 bp in length.
*
FEATURES
  source
    1..232490
    /organism="Rattus norvegicus"
    /mol_type="genomic DNA"
    /db_xref="taxon:10116"
    /clone="CH230-99F11"
    874..1283
    /note="clone_boundary"
    clone_end:5p6
    site:
    end_sequence:BH334967"
    6217..7733
    /note="wgs_contig"
    189472..151092
    /note="wgs_contig"
    200912..202317
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ORIGIN
Query Match      77.8%  Score 14; DB 2; Length 232490;
Best Local Similarity 85.7%: Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      5 UCCUGAGANNNNNN 18
Db      228726 TCCTGAGANNNNNN 228713

RESULT 102
BX950179      239166 bp  DNA  linear  HTG-18-FEB-2004
LOCUS      Danio rerio clone DKEX-27P23, *** SEQUENCING IN PROGRESS ***, 14
DEFINITION      Unordered pieces.
ACCESSION      BX950179
VERSION      BX950179.3 GI:42627395
KEYWORDS      HTG: HTGS PHASE1.
SOURCE      Danio rerio (zebrafish)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
      Cypriniformes; Cyprinidae; Danio.
      1 (bases 1 to 239166)
      Sime.S.
REFERENCE      Direct Submission
      Submitted (17-FEB-2004) Wellcome Trust Sanger Institute, Hinxton,
      Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
      zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
      On Feb 18, 2004 this sequence version replaced gi:42600214.
      ----- Genome Center
      Center: Wellcome Trust Sanger Institute
      Center code: SC
      Web site: http://www.sanger.ac.uk
      Contact: zfish-help@sanger.ac.uk
      ----- Project Information
      Center project name: ZK27P23
      ----- Summary Statistics
      Assembly program: XGAP4; version 4.5
      Chemistry: Dye-terminator; 100% of reads
      Consensus quality: 234745 bases at least Q40
      Consensus quality: 235466 bases at least Q30

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Consensus quality: 236100 bases at least Q20
Insert size: 237866; sum-of-contigs
Insert size: 235442; 3.9% error; agarose-fp
Quality coverage: 9.54x in Q20 bases; sum-of-contigs Quality
coverage: 9.64x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1..11014: contig of 11014 bp in length
*      11015      11114: gap of 100 bp
*      11115      15181: contig of 4067 bp in length
*      15182      15281: gap of 100 bp
*      15282      84366: contig of 69085 bp in length
*      84367      84466: gap of 100 bp
*      84467      97522: contig of 13056 bp in length
*      97523      97622: gap of 100 bp
*      97623      109674: contig of 12052 bp in length
*      109675      109774: gap of 100 bp
*      109775      139344: contig of 29570 bp in length
*      139345      139444: gap of 100 bp
*      139445      145157: contig of 5713 bp in length
*      145158      145257: gap of 100 bp
*      145258      163330: contig of 18073 bp in length
*      163331      163430: gap of 100 bp
*      163431      175658: contig of 12228 bp in length
*      175659      175758: gap of 100 bp
*      175759      192348: contig of 16590 bp in length
*      192349      192448: gap of 100 bp
*      192449      198785: contig of 6337 bp in length
*      198786      198885: gap of 100 bp
*      198886      216179: contig of 17294 bp in length
*      216180      216279: gap of 100 bp
*      216280      219430: contig of 3151 bp in length
*      219431      219530: gap of 100 bp
*      219531      239166: contig of 19636 bp in length.
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    /mol_type="genomic DNA"
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    /clone="DKEX-27P23"
    /clone_1fb="DanioKey"
    1..11014
    /note="assembly_fragment:00357"
    fragment_chain:1
    1115..15181
    /note="assembly_fragment:00012"
    fragment_chain:1
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    /note="assembly_fragment:02441"
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    /note="assembly_fragment:00496"
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    /note="assembly_fragment:00146"
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/notes="assembly_fragment:00233
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216280..219430
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219531..239166
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ORIGIN

Query Match      77.8% Score 14; DB 2; Length 239166;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      5 UCCUGAGANNNNNN 18
Db      139337 TCCTGAGANNNNNN 139350.

RESULT 103
AC110826
LOCUS
DEFINITION
Rattus norvegicus clone CH230-19912, *** SEQUENCING IN PROGRESS
***, 7 unordered pieces.
AC110826
AC110826.5 GI:24818668
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 241934)
Muzny,D,Marle, Metzker,M, Lee, Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, N., Blais, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Carnadas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
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Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
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Hollins, B., Howells, S., Hu, Y. S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowls, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorenshuwa, L., Loulsegue, H., Lozada, R. J., Lu, X., Ma, U.,
Maheshwari, M., Mahindaratne, M., Mahmoud, M., Mallory, K., Mangum, A.,
Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E.,
Mawhinney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Muniasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwachukwu, O., Okwuonu, G., Olarinmoye, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,

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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GCGI
Center clone name: CH230-19912
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 217093 bases at least Q40
Consensus quality: 221891 bases at least Q30
Consensus quality: 225435 bases at least Q20
Estimated insert size: 2277851 sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbankdraft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order in this sequence record is
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 10980: contig of 10980 bp in length
* 10981 11080: gap of unknown length
* 11081 20228: contig of 9148 bp in length
* 20229 20328: gap of unknown length

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*      20329      98047: contig of 77719 bp in length
*      98048      98147: gap of unknown length
*      98148      179247: contig of 81100 bp in length
*      179248      179347: gap of unknown length
*      179348      239002: contig of 59655 bp in length
*      239003      239102: gap of unknown length
*      239103      240128: contig of 1026 bp in length
*      240129      240228: gap of unknown length
*      240229      241934: contig of 1706 bp in length.
*      Location/Qualifiers
*          source
*              1..241934
*                  /organism="Rattus norvegicus"
*                  /mol_type="genomic DNA"
*                  /db_xref="taxon:10116"
*                  /clone="CH230-19912"
*                  1..1019
*                      /note="wgs_contig"
*                      11081..13112
*                          /note="wgs_contig"
*                          32300..33356
*                              /note="wgs_contig"
*                              102325..103591
*                                  /note="wgs_contig"
*                                  179348..181311
*                                      /note="wgs_contig"
*                                      181504..183523
*                                          /note="wgs_contig"
*                                          201369..203099
*                                              /note="wgs_contig"

ORIGIN
Query Match      77.8%; Score 14; DB 2; Length 241934;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy      5      UCCUGAGNNNNNN 18
Db      103584      TCCTGAGNNNNNN 103597

RESULT 104
AC131536      243490 bp      DNA      linear      HTG 10-MAY-2003
LOCUS      AC131536
DEFINITION      Rattus norvegicus clone CH230-49E2, *** SEQUENCING IN PROGRESS ***
ACCESSION      AC131536
VERSION      AC131536.4 GI:30520641
KEYWORDS      HTG; HTGS PHASE2; HTGS DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM      Rattus norvegicus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
            1 (bases 1 to 243490)
            Mueny,D,Marley, Metzker,M, Lee, Abramson,S, Adams,C, Alder,J,
            Allen,C, Allen,H, Alebrooke,S, Amin,A, Anguiano,D,
            Anyalbechi,V, Aoyagi,A, Ayodeji,M, Baca,E, Baden,H,
            Baldwin,D, Bandaranaike,D, Barber,M, Barnstead,M, Benahmed,F,
            Bismato,K, Blair,J, Blankenburg,K, Blyth,P, Brown,M,
            Bryant,N, Buhay,C, Burch,P, Burrell,K, Calderon,E,
            Cardenas,V, Carter,K, Cavazos,I, Ceasar,H, Center,A,
            Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J,
            Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L,
            Davila,M,L, Davis,C, Davy-Carroll,L, De Anda,C, Dederick,D,
            Delgado,O, Denison,S, Deramo,C, Ding,Y, Dinh,H, Divya,K,
            Draper,H, Dugan-Rocha,S, Dunn,A, Durbin,K, Duval,B, Eaves,K,
            Egan,A, Escotto,M, Eugene,C, Evans,C,A, Falle,T, Fan,G,
            Fernandez,S, Finley,M, Flagg,N, Forbes,L, Foster,M, Foster,P,
            Frasee,C,M, Gabisi,A, Gantey,R, Garcia,A, Garner,F, Garza,M,
            Gebregeorgis,E, Geer,K, Gill,R, Grady,M, Guerra,W, Guevara,W,
            Gunaratne,P, Haaland,W, Hamli,C, Hamilton,C, Hamilton,K,
            Hanvey,Y, Havlak,P, Hawes,A, Henderson,N, Hernandez,J,
            Hernandez,R, Hines,S, Hladun,S,L, Hodgson,A, Hogues,M,
            Hollins,B, Howells,S, Hulik,S, Hume,J, Idlebird,D, Jackson,A,

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            Jackson,L, Jacob,L, Jiang,H, Johnson,B, Johnson,R, Jollivet,A,
            Karpachy,S, Kelly,S, Kelly,S, Khan,Z, King,L, Kovac,C,
            Komis,C, Kraft,C,L, Lebow,H, Levan,J, Lewis,L, Li,Z, Liu,J,
            Liu,J, Liu,W, Liu,Y, London,P, Longacre,S, Lopez,J,
            Lorenshewa,L, Louised,H, Lozano,R,J, Lu,X, Ma,J,
            Maheshwari,M, Mahindartine,M, Mahmud,M, Malloy,K, Martinez,B,
            Mangun,B, Mapa,P, Martin,K, Martin,R, Martinez,B,
            Mawhinney,S, McLeod,M,P, McNeill,T,Z, Meenen,E,
            Mitosavljevic,A, Miner,G, Minja,E, Montemayor,J, Moore,S,
            Morgan,M, Morris,K, Morris,S, Munidasa,M, Murphy,M, Nair,L,
            Nankervis,C, Neal,D, Newton,N, Nguyen,N, Norris,S,
            Nwaelekeh,O, Okwunonu,G, Olanpursagoon,A, Pal,S, Parke,K,
            Pasternak,S, Paul,H, Perez,A, Perez,L, Pfannkuch,C,
            Plopper,F, Polidexter,A, Popovic,D, Primus,E, Pu,L,L,
            Puzo,M, Quiroz,J, Rachlin,E, Reeves,K, Regier,M,A, Reigh,R,
            Reilly,B, Reilly,M, Ren,Y, Reuter,M, Richards,S, Riggs,F,
            Rivers,C, Rodkey,T, Rojas,A, Rose,M, Rose,R, Ruiz,S,J,
            Sanders,W, Savary,G, Scherer,S, Scott,G, Shatsman,S, Shen,H,
            Shetty,J, Shvartsbeyn,A, Sisson,I, Sitter,C,D, Smajic,D,
            Sneed,A, Sodergren,E, Song,X,Z, Sorelle,R, Sosa,J,
            Steimle,M, Strong,R, Sutton,A, Svatek,A, Tabor,P, Taylor,C,
            Taylor,T, Thomas,N, Thomas,S, Tingey,A, Trejos,Z, Usmani,K,
            Valas,R, Vera,V, Villaseana,D, Waldron,L, Walker,B, Wang,J,
            Wang,O, Wang,S, Warren,J, Warren,R, Wei,X, White,F,
            Williams,G, Willson,R, Wleczek,R, Wooden,H, Worley,K,
            Wright,D, Wright,R, Wu,J, Yakub,S, Yen,J, Yoon,L, Yoon,V,
            Yu,F, Zhang,J, Zhou,J, Zhou,X, Zhao,S, Dunn,D, von
            Niederhausen,A, Weiss,R, Smith,D,R, Holt,R,A, Smith,H,O,
            Weinstein,G, and Gibbs,R,A.
            Direct Submission
            Unpublished
            2 (bases 1 to 243490)
            Rat Genome Sequencing Consortium.
            Direct Submission
            Submitted (24-AUG-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            3 (bases 1 to 243490)
            Rat Genome Sequencing Consortium.
            Direct Submission
            Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
            On May 10, 2003 this sequence version replaced gi:24819714.
            The sequence in this assembly is a combination of BAC based reads
            and whole genome shotgun sequencing reads assembled using Atlas
            (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
            in the feature table below represents a scaffold in the Atlas
            assembly (a 'contig-scaffold'). Within each contig-scaffold,
            individual sequence contigs are ordered and oriented, and separated
            by sized gaps filled with Ns to the estimated size. The sequence
            may extend beyond the ends of the clone and there may be sequence
            contigs within a contig-scaffold that consist entirely of whole
            genome shotgun sequence reads. Both end sequences and whole genome
            shotgun sequence only contigs will be indicated in the feature
            table.

            ----- Genome Center
            Center: Baylor College of Medicine
            Center code: BCM
            Web site: http://www.hgsc.bcm.tmc.edu/
            Contact: hgsc-help@bcm.tmc.edu
            ----- Project Information
            Center project name: GPCR
            Center clone name: CH230-49E2
            ----- Summary Statistics
            Assembly program: Atlas 3.0:
            Consensus quality: 214615 bases at least Q40
            Consensus quality: 219225 bases at least Q30
            Consensus quality: 222545 bases at least Q20
            Estimated insert size: 228801; sum-of-contigs estimation
            Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
            -----
            * NOTE: Estimated insert size may differ from sequence length

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* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
* NOTE: This is a working draft sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 243490: contig of 243490 bp in length.
  Location/Qualifiers
    1..243490
      /organism="Rattus norvegicus"
      /mol_type="genomic DNA"
      /db_xref="taxon:10116"
      /clone="CH230-49B2"
    1..1169
      /note="wgs end_extension
      clone_end:Sp6"
    3932..5805
      /note="wgs end_extension
      clone_end:Sp6"
      complement(6360..6720)
      /note="clone boundary
      clone_end:Sp6
      site:ECORI
      end_sequence:BH280612"
    131675..134466
      /note="wgs contig"
    172018..173754
      /note="wgs contig"
    240820..241559
      /note="clone boundary
      clone_end:T7
      site:ECORI
      end_sequence:BH280566"

```

ORIGIN

```

Query Match      77.8%; Score 14; DB 2; Length 243490;
Best Local Similarity 85.7%; Pred.No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

Qy 5 UCCUGGAGNNNNNN 18  
 13326 TCCTGCGAGNNNNNN 13339

Db 13326 TCCTGCGAGNNNNNN 13339

RESULT 105  
 AC112470/c  
 LOCUS  
 DEFINITION  
 AC112470 244594 bp DNA linear HTG 19-NOV-2002  
 Rattus norvegicus clone CH230-120K2, WORKING DRAFT SEQUENCE, 3  
 unoriented pieces.  
 AC112470  
 AC112470.5 GI:25072802  
 HTG: HTGS PHASE1; HTGS DRAFT; HTGS\_FULLTOP.  
 Rattus norvegicus (Norway rat)  
 SOURCE  
 ORGANISM  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 244594)  
 Muzny,D,Marie,,Metzker,M,Lee,,Abramson,S,,Adams,C,,Alder,J,,  
 Allen,C,,Allen,H,,Alsbrooks,S,,Amin,A,,Anguiano,D,,  
 Anyalebechi,V,,Ayogagi,A,,Ayodeji,M,,Baca,B,,Baden,H,,  
 Baldwin,D,,Bandaranaik,D,,Barber,M,,Barnstead,M,,Behamed,F,,  
 Biswal,K,,Blair,J,,Blankenburg,K,,Blyth,P,,Brown,M,,  
 Bryant,N,,Buhay,C,,Burck,P,,Burrell,K,,Calderson,E,,  
 Cardenas,V,,Carter,K,,Cavazos,I,,Cassar,H,,Center,A,,  
 Chacko,J,,Chavez,D,,Chen,G,,Chen,R,,Chen,Y,,Chen,Z,,Chu,J,,  
 Cleveland,C,,Cockrell,R,,Cox,C,,Coyle,M,,Cree,A,,D'Souza,L,,  
 Davila,M,L,,Davis,C,,Davy-Carroll,L,,De Anda,C,,Dederich,D,,  
 Delgado,O,,Denson,S,,Deramo,C,,Ding,Y,,Dinh,H,,Divya,K,,

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL

COMMENT

Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 244594)  
 Rat Genome Sequencing Consortium.  
 Direct Submission  
 Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23195038.  
 The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are oriented and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: http://www.hgsc.bcm.tmc.edu/  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: GSRF  
 Center clone name: CH230-120K2

```

----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 229883 bases at least Q40
Consensus quality: 232598 bases at least Q30
Consensus quality: 234946 bases at least Q20
Estimated insert size: 236805; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 116449: contig of 116449 bp in length
* 116450 116549: gap of unknown length
* 116550 126724: contig of 12175 bp in length
* 126725 126825 126825: gap of unknown length
* 126825 244594: contig of 115770 bp in length.
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* Location/Qualifiers
*   1. 244594
*      /organism="Rattus norvegicus"
*      /mol_type="genomic DNA"
*      /db_xref="taxon:10116"
*      /clone="CH230-120K2"
*      1. 1266
*         /note="wgs_end_extension"
*         clone_end:5p6"
*         4345..5214
*         /note="clone_boundary"
*         clone_end:5p6
*         site:
*           end_sequence:BH350437"
*         70263..70953
*         /note="clone_boundary"
*         clone_end:T7
*         site:
*           end_sequence:BH350435"
*         115434..116449
*         /note="wgs_end_extension"
*         clone_end:T7"
*         120743..121884
*         /note="wgs_end_extension"
*         clone_end:T7"
*         126191..126874
*         /note="wgs_end_extension"
*         clone_end:T7"

ORIGIN
Query Match      77.8% Score 14; DB 2; Length 244594;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      5 UCCUGAGAGNNNNNN 18
      :||:|||||
Db      148237 TCCTGAGAGNNNNN 148224

RESULT 106
AC117977      245318 bp DNA linear HTG 26-SEP-2002
LOCUS      Rattus norvegicus clone CH230-13311, *** SQUENCING IN PROGRESS
DEFINITION
AC117977      245318 bp DNA linear HTG 26-SEP-2002
VERSION      AC117977.5 GI:23322207
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE
AUTHORS
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 245318)
Muzny,D,Marle, Metzker,M, Lee, Abramson,S, Adams,C, Alder,J,
Allen,C, Allen,H, Alsbrooks,S, Amin,A, Anguiano,D,
Anyalebechi,V, Aoyagi,A, Ayodeji,M, Bacc,E, Baden,H,
Baldwin,D, Bandaranaike,D, Barber,M, Barnstead,M, Benahmed,F,
Biswalto,K, Blair,J, Blankenburg,K, Blyth,P, Brown,M,
Bryant,N, Buhay,C, Burch,P, Burrell,K, Calderon,E,
Cardenas,V, Carter,K, Cavazos,I, Caesar,H, Chen,A,
Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z,
Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L,
Devila,M,L, Davis,C, Davy-Carroll,L, De Anda,C, Dederich,D,
Delgado,O, Denson,S, Detamo,C, Ding,Y, Dinh,H, Divya,K,
Draper,H, Dugan-Rocha,S, Dunn,A, Dublin,K, Duval,B, Eaves,K,
Egan,A, Escotto,M, Eugene,C, Evans,C,A, Falls,T, Fan,G,
Fernandez,S, Finley,M, Flagg,N, Forbes,L, Foster,M, Foster,P,
Fraser,C,M, Gabisi,A, Ganta,R, Garcia,A, Garner,T, Garza,M,
Georgescu,E, Geer,K, Gill,R, Grady,M, Guerra,W, Guevara,W,
Gunnarsson,P, Haland,M, Hamill,C, Hamilton,C, Hamilton,K,
Harvey,Y, Havlak,P, Hawes,A, Henderson,N, Hernandez,J,
Hernandez,R, Hines,S, Hladun,S,L, Hodgson,A, Hogues,M,
Hollins,B, Howells,S, Huliy,S, Hume,J, Idlebird,D, Jackson,A,
Jackson,L, Jacob,L, Jiang,H, Johnson,B, Johnson,R, Joliver,A,
Karpachy,S, Kelly,S, Kelly,S, Khan,Z, King,L, Koyar,C,
Kovis,C, Kraft,C,L, Lebow,H, Levay,N, Lewis,L, Li,Z, Liu,J,
Liu,J, Liu,W, Liu,Y, London,P, Longacre,S, Lopez,J,
Lorenshuwa,L, Louisedge,H, Lozada,R,J, Lu,X, Ma,J,
Maheshwari,M, Mahindartne,M, Mahmood,M, Malloy,K, Mangum,A,
Mangum,B, Mapa,P, Martin,K, Martin,R, Martinez,E,
McWhiney,S, McLeod,M,P, McNeill,T,Z, Meenen,E,
Milosavljevic,A, Miner,G, Minja,E, Montemayor,J, Moore,S,
Morgan,M, Morris,K, Morris,S, Mundasa,M, Murphy,M, Nair,L,
Nankervill,C, Neal,D, Newton,N, Nguyen,N, Norris,S,
Nwokediemen,O, Okwuonu,G, Olarnpungoon,A, Pal,S, Parks,K,
Pasternak,S, Paul,H, Perez,A, Perez,L, Pfamnoch,C,
Plopper,F, Polidexter,A, Popovic,D, Primus,E, Pu,L-L,
Puzo,M, Quiroz,J, Rachin,E, Reeves,K, Regier,M,A, Reigh,R,
Reilly,B, Reilly,M, Ren,Y, Reuter,M, Richards,S, Riggs,F,
Rivers,C, Rodkey,T, Rojas,A, Rose,M, Rose,R, Ruiz,S,J,
Sanders,W, Savary,G, Scherer,S, Scott,G, Shatsman,S, Shen,H,
Shetty,J, Shvartbeyn,A, Sisson,I, Sitter,C,D, Smaiz,D,
Sneed,A, Sodergren,E, Song,X-Z, Sorelle,R, Sosa,J,
Steinle,M, Strong,R, Sutton,A, Swatek,A, Taber,P, Taylor,C,
Taylor,T, Thomas,N, Thomas,S, Tinney,A, Trejos,Z, Uemami,K,
Valas,R, Vera,V, Villaseana,D, Waldron,L, Walker,B, Wang,J,
Wang,Q, Wang,S, Warren,J, Warren,R, Wei,X, White,F,
Williams,G, Willson,R, Wleczky,R, Wooden,H, Worley,K,
Wright,D, Wright,R, Wu,J, Yakub,S, Yen,J, Yoon,L, Yoon,V,
Yu,F, Zhang,J, Zhou,J, Zhou,X, Zhao,S, Dunn,D, von
Niederhausen,A, Weiss,R, Smith,D,R, Holt,R,A, Smith,H,O,
Weinstock,G, and Gibbs,R,A.
Direct Submission
Unpublished
2 (bases 1 to 245318)
Worley,K.C.
Direct Submission
Submitted (12-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 245318)
Rat Genome Sequencing Consortium.
Rat Genome Sequencing Consortium.
Submitted (26-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 26, 2002 this sequence version replaced gi:21903166.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atilas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the
sequence may extend beyond the ends of the clone and there may be
contigs that consist entirely of whole genome shotgun sequence
reads. Both end sequences and whole genome shotgun sequence only

```

contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information

Center project name: GWIE

Center clone name: CH230-13311

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 207818 bases at least Q40

Consensus quality: 212673 bases at least Q30

Consensus quality: 215838 bases at least Q20

Estimated insert size: 248658; sum-of-contigs estimation

Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length

(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 12 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

```

* 1 6825: contig of 6825 bp in length
* 6826 6925: gap of unknown length
* 6926 112025: contig of 105100 bp in length
* 112026 112125: gap of unknown length
* 112126 200613: contig of 88487 bp in length
* 200613 200713: gap of unknown length
* 200713 213425: contig of 12713 bp in length
* 213426 213525: gap of unknown length
* 213526 216973: contig of 3448 bp in length
* 216974 217073: gap of unknown length
* 217074 221686: contig of 4613 bp in length
* 221687 223129: contig of 1343 bp in length
* 223130 223228: gap of unknown length
* 223229 224422: contig of 1193 bp in length
* 224423 224522: gap of unknown length
* 224523 225689: contig of 1167 bp in length
* 225690 225789: gap of unknown length
* 225790 226872: contig of 1083 bp in length
* 226873 226972: gap of unknown length
* 226973 229239: contig of 2267 bp in length
* 229240 229339: gap of unknown length
* 229340 245318: contig of 15979 bp in length.
  
```

FEATURES

source

```

1. .245318
  /organism="Rattus norvegicus"
  /mol_type="genomic DNA"
  /db_xref="taxon:10116"
  /clone="CH230-13311"
  112126..113262
    /note="wgs contig"
  203834..205488
    /note="wgs contig"
  217074..218922
    /note="wgs contig"
  
```

ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 245318;  
Best Local Similarity 85.7%; Pred. No. 99;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNN 18

DB 163709 TCCTGAGAGNNNNN 163722

RESULT 107

CR812481/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Danio rerio

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

```

CR812481 247436 bp DNA linear HTG 03-OCT-2004
Danio rerio clone DKEY-225D17, *** SEQUENCING IN PROGRESS ***
unnumbered pieces.
CR812481.3 GI:53755942
HTG; HTGS PHASE1.
Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 247436)
McLay, K.
Submitted (02-OCT-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
fish-help@sanger.ac.uk Clone request: clonerequest@sanger.ac.uk
On Oct 3, 2004 this sequence version replaced gi:52851212.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: fish-help@sanger.ac.uk
----- Project Information
Center project name: ZK225D17
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 245295 bases at least Q40
Consensus quality: 245732 bases at least Q30
Consensus quality: 246014 bases at least Q20
Insert size: 246836; sum-of-contigs
Insert coverage: 6.92x in Q20 bases; sum-of-contigs Quality
coverage: 7.58x in Q20 bases; agarose-fp
  
```

```

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 55502: contig of 55502 bp in length
* 55503 55602: gap of 100 bp
* 55603 72285: contig of 16683 bp in length
* 72286 72385: gap of 100 bp
* 72386 80502: contig of 8117 bp in length
* 80503 80602: gap of 100 bp
* 80603 129020: contig of 48418 bp in length
* 129021 129120: gap of 100 bp
* 129121 195746: contig of 66626 bp in length
* 195747 195846: gap of 100 bp
* 195847 205719: contig of 9873 bp in length
* 205720 205819: gap of 100 bp
* 205820 247436: contig of 41617 bp in length.
  
```

FEATURES

source

```

1. .247436
  /organism="Danio rerio"
  /mol_type="genomic DNA"
  /db_xref="taxon:7953"
  /clone="DKEY-225D17"
  /clone_idb="DanioKey"
  1..55502
    /note="assembly fragment: 01325
    fragment chain:1"
  55603..72285
    /note="assembly fragment: 00168
    fragment chain:1"
  72386..80502
  
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misc\_feature

misc\_feature

misc\_feature

[illegible]

RELLY, B., RELLY, M., REN, Y., REUTER, M., RICHARDS, S., RIGGS, F.,  
 RIVAS, C., RODKEY, T., ROJAS, A., ROSE, M., ROSE, R., RUIZ, S.J.,  
 SANDERS, W., SAAVEDRA, G., SCHERER, S., SCOTT, G., SHATTAM, S., SHEN, H.,  
 SHELLEY, J., SILVATREBAY, A., SLOSSON, I., SILLER, C.D., SNAPE, D.,  
 SNEED, A., SODERGREN, E., SONG, X.-Z., SORRELLER, R., SOSSA, J.,  
 STEIMLE, M., STRONG, R., SUTTON, A., SWATEK, A., TABOR, P., TAYLOR, C.,  
 TAYLOR, T., THOMAS, N., THOMAS, S., TINGEY, A., TREJOS, Z., UMANIA, K.,  
 VALAS, R., VERA, V., VILLASANA, D., WALDRON, L., WALKER, B., WANG, J.,  
 WANG, Q., WANG, S., WARREN, J., WARREN, R., WEI, X., WHITE, F.,  
 WILLIAMS, G., WILSON, R., WLECZYK, R., WOODEN, H., WORLEY, K.,  
 WRIGHT, D., WRIGHT, R., WU, J., YAKUB, S., YEN, J., YOON, L., YOON, V.,  
 YU, F., ZHANG, J., ZHOU, J., ZHOU, X., ZHAO, S., ZHANG, D., VON  
 NIEDERHAUSEN, A., WEISS, R., SMITH, D.R., HOLT, R.A., SMITH, H.O.,  
 WEINSTECK, G. and Gibbs, R.A.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 248358)  
 Worley, K.C.  
 Direct Submission  
 Submitted (26-MAY-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 248358)  
 Rat Genome Sequencing Consortium.  
 Direct Submission  
 Submitted (09-MAY-2003) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On May 9, 2003 this sequence version replaced gi:23265699.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separated  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
 table.

---

--- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu  
 --- Project Information  
 Center project name: GAP3  
 Center clone name: CH230-4F17  
 --- Summary Statistics  
 Assembly program: Atlas;  
 Consensus quality: 225281 bases at least Q40  
 Consensus quality: 229208 bases at least Q30  
 Consensus quality: 231758 bases at least Q20  
 Estimated insert size: 236600; sum-of-contigs estimation  
 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

---

\* NOTE: Estimated insert size may differ from sequence length  
 \* (see <http://www.hgsc.bcm.tmc.edu/docs/genbankdraftdata.html>)  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 2 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 246878: contig of 246878 bp in length  
 \* 246879 246978: gap of unknown length  
 \* 246979 248358: contig of 1380 bp in length.  
 Location/Qualifiers  
 1..248358  
 /Organism="Rattus norvegicus"



```

/misc_feature      /mol_type="genomic DNA"
                   /db_xref="taxon:10116"
                   /clone="CH230-4F17"
                   1..2474
                   /note="wgs_end_extension
                   clone_end:T7"
                   complement(3585..4463)
                   /note="clone_boundary
                   clone_end:T7
                   site:ECORI
                   end_sequence:BH305410"
                   complement(243979..244808)
                   /note="clone_boundary
                   clone_end:Sp6
                   site:ECORI
                   end_sequence:BH305412"

ORIGIN
Query Match      77.8%; Score 14; Length 24358;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      5 UCCUGGAGANNNNNN 18
        :|||:|||||
        246871 TCCTGGAGANNNNNN 246884

RESULT 109
AC127927      250161 bp      DNA      linear      HTG 21-SEP-2002
LOCUS      AC127927
DEFINITION      Rattus norvegicus clone CH230-129119, *** SEQUENCING IN PROGRESS
ACCESSION      AC127927
VERSION      AC127927.2 GI:23265377
KEYWORDS      HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE      Rattus norvegicus
ORGANISM      Rattus norvegicus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
              Rattus.
REFERENCE      1 (bases 1 to 250161)
              Muzny,D.,Matte,M.,Lee,A.,Abramson,S.,Adams,C.,Alder,J.,
              Allen,C.,Allen,H.,Alsbrooks,S.,Amin,A.,Angulano,D.,
              Anyalebechi,V.,Aoyagi,A.,Ayodeji,M.,Baca,E.,Baden,H.,
              Baldwin,D.,Bandaraike,D.,Barber,M.,Barnstead,M.,Benahmed,F.,
              Biswal,K.,Blair,J.,Blankenburg,K.,Blych,P.,Brown,M.,
              Bryant,N.,Buhay,C.,Burch,P.,Burrell,K.,Calderon,E.,
              Cardenas,V.,Carter,K.,Cavazos,I.,Ceasar,H.,Center,A.,
              Chacko,J.,Chavez,D.,Chen,G.,Chen,R.,Chen,Y.,Chen,Z.,Chu,J.,
              Cleveland,C.,Cockrell,R.,Cox,C.,Coyle,M.,Cree,A.,D'Souza,L.,
              Davila,M.L.,Davis,C.,Davy-Carroll,L.,De Anda,C.,Dederich,D.,
              Delgado,O.,Denson,S.,Deramo,C.,Ding,Y.,Dinh,H.,Diyaa,K.,
              Draper,H.,Dugan-Rocha,S.,Dunn,A.,Durbin,K.,Duvall,B.,Eaves,K.,
              Egan,A.,Escotto,M.,Eugene,C.,Evans,C.A.,Falls,T.,Fan,G.,
              Fernandez,S.,Finley,M.,Flanagan,N.,Forbes,L.,Foster,M.,Foster,P.,
              Fraser,C.M.,Gabisi,A.,Ganta,R.,Garcia,A.,Garnier,T.,Garza,M.,
              Gebregeorgis,E.,Geer,K.,Gill,R.,Grady,M.,Guerra,W.,Guevara,W.,
              Gunaratne,P.,Haaland,W.,Hamil,C.,Hamilton,C.,Hamilton,K.,
              Harvey,Y.,Havlak,P.,Hawes,A.,Henderson,N.,Hernandez,J.,
              Hernandez,R.,Hines,S.,Hladun,S.L.,Hodgeson,A.,Hogues,M.,
              Hollins,B.,Howells,S.,Hui,Y.,Hume,J.,Idlebird,D.,Jackson,A.,
              Jackson,L.,Jacob,L.,Jiang,H.,Johnson,B.,Johnson,R.,Jolivet,A.,
              Karpathy,S.,Kelly,S.,Kelly,S.,Khan,Z.,King,L.,Kovar,C.,
              Kowis,C.,Kraft,C.L.,Lebow,H.,Leyan,J.,Lewis,L.,Li,Z.,Liu,J.,
              Liu,J.,Liu,W.,Liu,Y.,London,P.,Longacre,S.,Lopez,J.,
              Lorensueta,L.,Louisege,H.,Lozado,R.J.,Lu,X.,Ma,J.,
              Maheshwari,M.,Mahindartine,M.,Mahmoud,M.,Mailloy,K.,Mangum,A.,
              Mangum,B.,Mapua,P.,Martin,K.,Martin,R.,Martinez,E.,
              Mawhinney,S.,McLeod,M.P.,McNeill,T.Z.,Meenan,E.,
              Molsaevljeric,A.,Miner,G.,Minja,E.,Montemayor,J.,Moore,S.,
              Morgan,M.,Morris,K.,Morris,S.,Munida,M.,Murphy,M.,Nair,L.,
              Nankervis,C.,Neal,D.,Newton,N.,Nguyen,N.,Norris,S.,
              Nwaokelemeh,O.,Okwuonu,G.,Olarunpugoon,A.,Pal,S.,Parks,K.,

```

```

Pastermak,S.,Paul,H.,Perez,A.,Perez,L.,Pflankoch,C.,
Plopper,F.,Poindexter,A.,Popovic,D.,Primus,E.,Pu,L.-L.,
Puzo,M.,Quiroz,J.,Rachlin,E.,Reeves,K.,Regier,M.A.,Reign,R.,
Reilly,B.,Reilly,M.,Ren,Y.,Reuter,M.,Richards,S.,Riggs,F.,
Rives,C.,Rodkey,T.,Rojas,A.,Rose,M.,Rose,R.,Ritz,S.J.,
Sanders,M.,Savery,G.,Scherer,S.,Scott,G.,Shatman,S.,Shen,H.,
Shetty,J.,Shvartsbeyn,A.,Sisson,I.,Sitter,C.D.,Smajd,D.,
Sneed,A.,Sodergren,E.,Song,X.-Z.,Sorelle,R.,Soza,J.,
Stemle,M.,Strong,R.,Sutton,A.,Svatek,A.,Tabori,P.,Taylor,C.,
Taylor,T.,Thomas,N.,Thomas,S.,Tingey,A.,Treyos,Z.,Umanan,K.,
Valas,R.,Vera,V.,Villasana,D.,Waldron,L.,Walker,B.,Wang,J.,
Wang,Q.,Wang,S.,Warren,J.,Warren,R.,Wei,X.,White,F.,
Williams,G.,Willson,R.,Wleczek,R.,Wooden,H.,Worley,K.,
Wright,D.,Wright,R.,Wu,J.,Yakub,S.,Yen,J.,Yoon,L.,Yoon,V.,
Yu,F.,Zhang,U.,Zhou,J.,Zhou,X.,Zhao,S.,Dunn,D.,von
Niederhausen,A.,Weiss,R.,Smith,D.R.,Holt,R.A.,Smith,H.O.,
Weinstock,G. and Gibbs,R.A.

Direct Submission
Unpublished
2 (bases 1 to 250161)
Mortley,K.C.
Direct Submission
Submitted (19-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 250161)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (21-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 21, 2002 this sequence version replaced gi:21908454.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Actis
(http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the
sequence may extend beyond the ends of the clone and there may be
contigs that consist entirely of whole genome shotgun sequence
reads. Both end sequences and whole genome shotgun sequence only
contigs will be indicated in the feature table.

-----Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
-----Project Information
Center project name: GKRV
Center clone name: CH230-129119
-----Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 221556 bases at least Q40
Consensus quality: 223903 bases at least Q30
Consensus quality: 225468 bases at least Q20
Estimated insert size: 240281; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 250161: contig of 250161 bp in length.
Location/Qualifiers
1.250161
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-129119"

```

## FEATURES

source



```

misc_feature      1403..1950
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                  clone_end:Sp8
                  site:ECORI
                  end_sequence:BH307614"
                  complement(246893..247494)
                  /note="clone_boundary
                  clone_end:T7
                  site:ECORI
                  end_sequence:BH307613"

ORIGIN
Query Match      77.8% Score 14; DB 2; Length 250161;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      5 UCCUGAGACNNNNNN 18
       :||:|||||||
Db      138792 TCCTGAGAGNNNNN 138805

RESULT 110
AC11204/C
LOCUS
DEFINITION
AC11204      256409 bp    DNA    linear    HTG 10-MAY-2003
Rattus norvegicus clone CH230-31G2, *** SEQUENCING IN PROGRESS ***,
3 unordered pieces.
AC11204
VERSION
AC11204.5 GI:30522768
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 256409)
Muzny,D,Marie., Metzker,M,lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Albrooks,S., Amin,A., Anguiano,D.,
Avalaibechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswalto,K., Blair,U., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Devila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denison,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Gantier,R., Garcia,A., Garner,T., Garza,M.,
Gedregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunnarsson,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howell,S., Huliy,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovac,K.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Loper,J.,
Lorenzhuwa,L., Louissege,H., Lozada,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartine,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapus,P., Martin,K., Martin,R., Martinez,B.,
Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenan,E.,
Mlloasavilevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nmaokleheneh,O., Okwoumu,G., Olarnpusagoon,A., Pal,S., Patis,K.,
Plopper,F., Poindecker,A., Popovic,D., Primus,E., Pu,L.L.,
Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojase,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savary,G., Scherer,S., Scott,G., Shateman,S., Shen,H.,

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
Worley,K.C.
Direct Submission
Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 256409)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:24818075.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GERC
Center clone name: CH230-31G2
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 224869 bases at least Q40
Consensus quality: 228396 bases at least Q30
Consensus quality: 230824 bases at least Q20
Estimated insert size: 239124; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 253304: contig of 253304 bp in length
* 253305 253404: gap of unknown length
* 253405 254643: contig of 1239 bp in length
* 254644 254743: gap of unknown length
* 254744 256409: contig of 1666 bp in length.
Location/Qualifiers
1. 256409
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
FEATURES
source

```

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/db xref="taxon:10116"
/clone="CH230-31c2"
misc_feature
1..2255
/note="wgs_contig"
misc_feature
25190..253304
/note="wgs_contig"
ORIGIN
Query Match 77.8% Score 14; DB 2; Length 256409;
Best Local Similarity 85.7% Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Cy 5 UCCUGAGANNNNNN 18
Db 254751 TCCTGAGANNNNNN 254738

RESULT 111
AC106994/c
LOCUS
DEFINITION
AC106994 259219 bp DNA linear HTG 08-OCT-2002
Rattus norvegicus clone CH230-121024, *** SEQUENCING IN PROGRESS
*** 8 unordered pieces.
AC106994
AC106994.4 GI:23270269
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 259219)
Muzny, D., Marie, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooke, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, K., Cavazos, I., Ceasar, H., Center, A.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M., Davis, C., Davy, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escoto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Frazer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebreyes, E., Geer, K., Galli, R., Grady, M., Guerra, W., Guevara, W.,
Gumatare, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogue, M.,
Hollins, B., Howells, S., Hulik, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpeth, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kows, C., Kraft, C.L., Ledow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorenz, L., Louie, H., Lozano, R., Lu, X., Ma, J.,
Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E.,
Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Mikolajczyk, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munday, M., Murphy, M., Nait, L.,
Nwankwelu, O., Okunolu, G., Olarnunsgoon, A., Pal, S., Parks, K.,
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Plopper, F., Polinder, A., Popovic, D., Primus, E., Pu, L., L.,
Puzo, M., Quirroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,
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Shetty, J., Shvartbeyn, A., Sison, I., Sitter, C.D., Smajic, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorrelle, R., Sosa, J.,
Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uemant, K.,

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TITLE
JOURNAL
AUTHORS
REFERENCE
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Submitted (08-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 259219)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (08-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 23, 2002 this sequence version replaced gi:21737508.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: CH230-121024
Center clone name: CH230-121024
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 222280 bases at least Q40
Consensus quality: 226331 bases at least Q30
Consensus quality: 228820 bases at least Q20
Estimated insert size: 250992; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
87120..contig of 87120 bp in length
87121
87221..contig of unknown length
87222
230567..contig of 143347 bp in length
87223
230667..gap of unknown length
87224
230668..contig of 22694 bp in length
87225
253362..gap of unknown length
87226
253462..contig of 1033 bp in length
87227
254494..gap of unknown length
87228
254594..gap of unknown length
87229
254595..contig of 1002 bp in length
87230
255596..gap of unknown length
87231
255697..contig of 1038 bp in length
87232
256734..gap of unknown length
87233
256834..gap of unknown length

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FEATURES
    source
        * 256835 258095: contig of 1261 bp in length
        * 258096 258195: gap of unknown length
        * 258196 259219: contig of 1024 bp in length.
            Location/Qualifiers
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                    /mol_type="genomic DNA"
                    /db_xref="taxon:10116"
                    /clone="CH230-121024"
                        1..1440
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                                misc_feature
                                    7279..8766
                                        /note="wgs_contig"
                                            misc_feature
                                                87221..88474
                                                    /note="wgs_contig"
                                                        ORIGIN
Query Match      77.8% Score 14; DB 2; Length 259219;
Best Local Similarity 85.7% Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy              5 UCCUGAGACNNNNNNN 18
               :||:|||
Db              30898 TCCTGAGACNNNNNNN 30885

RESULT 112
AC128915          272053 bp   DNA       linear   HTG 19-NOV-2002
AC128915 LOCUS
AC128915 DEFINITION
Rattus norvegicus clone CH230-332D13, *** SEQUENCING IN PROGRESS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 272053)
Munry,D.Maria., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Albrooks,S., Amin,A., Angiano,D.,
Ayalabechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barneslead,M., Benahmed,F.,
Blawalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Byran,N., Buhey,C., Burck,P., Burrell,K., Calderon,E.,
Cardenas,J., Carter,K., Cavazos,I., Caesar,H., Center,A.,
Chacko,V., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dedrich,D.,
Degado,O., Denison,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Diaper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
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Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Frazer,C.M., Gabisi,A., Ganca,R., Garcia,A., Garner,T., Garza,W.,
Georgescu,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamli,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladin,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howells,S., Hulky,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovac,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levay,J., Lewis,L., Li.Z., Liu,J.,
Liu,J., Liu.W., Liu.Y., London,P., Longacre,S., Lopez,J.,
Lotunshwa,L., Louisedge,H., Loyado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindratne,M., Mahmood,M., Malloy,K., Mangum,A.,
Manungu,B., Magna,P., Martin,K., Martin,R., Martinez,E.,
Mathewey,J., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minj,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Mundasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Parks,K.,
Patekneh,O., Okwonon,G., Olarinmasegon,A., Pal,S., Parks,K.,
Patelnaek,S., Paul,H., Perez,A., Perez,L., Plannkoch,C.,

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Plöpper, F., Poldexer, A., Popovic, D., Primus, E., Pu, L.-L.,  
Puzzo, M., Quirico, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R.,  
Reilly, B., Reilly, M., Ren, Y., Reuter, R. M., Richards, S., Riggs, F.,  
Rivas, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J.,  
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H.,  
Shetty, J., Shvartsbeyn, A., Slason, I., Sliker, C. D., Smaj, D.,  
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,  
Steinle, M., Strong, R., Sutton, A., Svatok, A., Tabot, P., Taylor, C.,  
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uemari, K.,  
Valas, R., Vera, V., Villaseña, D., Waldron, L., Walker, B., Wang, J.,  
Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, P.,  
Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K.,  
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,  
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von  
Nedehausen, A., Weiser, R., Smith, D. R., Holt, R. A., Smith, H. O.,  
Weinstock, G. and Gibbs, R. A.

Direct Submission  
Unpublished  
2 (bases 1 to 272053)

Worley, K. C.  
Direct Submission  
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 272053)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23196153.  
The sequence in this assembly is a combination of BAC based reads  
and whole genome shotgun sequencing reads assembled using Atlas  
(<http://www.hgsc.bcm.tmc.edu/Projects/rat/>). Each contig described  
in the feature table below represents a scaffold in the Atlas  
assembly (a 'contig-scaffold'). Within each contig-scaffold,  
individual sequence contigs are ordered and oriented, and separated  
by sized gaps filled with Ns to the estimated size. The sequence  
may extend beyond the ends of the clone and there may be sequence  
contigs within a contig-scaffold that consist entirely of whole  
genome shotgun sequence reads. Both end sequences and whole genome  
shotgun sequence only contigs will be indicated in the feature  
table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: KBDJ  
Center clone name: CH230-332D13  
----- Summary Statistics  
Assembly program: Phrap, version 0.990329  
Consensus quality: 245349 bases at least Q40  
Consensus quality: 250712 bases at least Q30  
Consensus quality: 254043 bases at least Q20  
Estimated insert size: 256776; sum-of-contigs estimation  
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html))  
\* NOTE: This sequence may represent more than one clone.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 3 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 27109: contig of 27109 bp in length  
\* 27110 27209: gap of unknown length  
\* 270524: contig of 24315 bp in length

```

FEATURES
  * 270525 270624: gap of unknown length
  * 270625 272053: contig of 1429 bp in length.
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        /mol_type="genomic DNA"
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        /clone="CH230-332D13"
        complement(633..1531)
        /note="clone boundary"
        clone_end:17
        site:
          end_sequence: BZ232511"
          68676..70602
          /note="wgs_contig"
          258419..259483
          /note="wgs_contig"
          263476..264931
          /note="wgs_contig"
          268470..270524
          /note="wgs_contig"

ORIGIN
Query Match 77.8%; Score 14; DB 2; Length 272053;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGGAGNNNNN 18
Db 237761 TCCTGAGANNNNN 237774

RESULT 113
AC097979/c 276376 bp DNA linear HTG 21-SEP-2002
LOCUS Rattus norvegicus clone CH230-44022, *** SEQUENCING IN PROGRESS
DEFINITION
  **, 6 unordered pieces.
ACCESSION
  AC097979
  GI:23264455
VERSION
  HTG; HTG_PHASE1; HTG_DRAFT; HTG_ENRICHED.
KEYWORDS
  Rattus norvegicus (Norway rat)
SOURCE
  Rattus norvegicus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
  Rattus.
  1 (bases 1 to 276376)
REFERENCE
  AUTHORS
    Muzny, D., Marie, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J.,
    Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
    Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
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    Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Cencer, A.,
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    Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
    Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
    Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diya, K.,
    Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
    Egan, A., Escoto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
    Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
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    Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolyet, A.,
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    Kowals, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
    Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
    Lorenshelew, L., Louieged, H., Lozano, R.J., Lu, X., Ma, T.,
    Maheshwari, M., Mahindaratne, M., Mahmoud, R., Mallory, K., Mangum, A.,
    Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,

```

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TITLE
  JOURNAL
REFERENCE
  AUTHORS
    Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
    Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
    Morgan, M., Morris, K., Morris, S., Muniasa, M., Murphy, M., Nair, L.,
    Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
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    Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
    Weinstock, G. and Gibbs, R.A.
  Direct Submission
  Unpublished
  2 (bases 1 to 276376)
  Worley, K.C.
  Direct Submission
  Submitted (23-SEP-2001) Human Genome Sequencing Center, Department
  of Molecular and Human Genetics, Baylor College of Medicine, One
  Baylor Plaza, Houston, TX 77030, USA
  3 (bases 1 to 276376)
  Rat Genome Sequencing Consortium.
  Direct Submission
  Submitted (21-SEP-2002) Human Genome Sequencing Center, Department
  of Molecular and Human Genetics, Baylor College of Medicine, One
  Baylor Plaza, Houston, TX 77030, USA
  On Sep 21, 2002 this sequence version replaced gi:212733901.
  The sequence in this assembly is a combination of BAC based reads
  and whole genome shotgun sequencing reads assembled using Atlas
  (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the
  sequence may extend beyond the ends of the clone and there may be
  contigs that consist entirely of whole genome shotgun sequence
  reads. Both end sequences and whole genome shotgun sequence only
  contigs will be indicated in the feature table.
  ----- Genome Center
  Center: Baylor College of Medicine
  Center code: BCM
  Web site: http://www.hgsc.bcm.tmc.edu/
  Contact: hgsc-help@bcm.tmc.edu
  ----- Project Information
  Center project name: GRTH
  Center clone name: CH230-44022
  ----- Summary Statistics
  Assembly program: Phrap; version 0.9903229
  Consensus quality: 203480 bases at least Q40
  Consensus quality: 205742 bases at least Q30
  Consensus quality: 207204 bases at least Q20
  Estimated insert size: 231400; sum-of-contigs estimation
  Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
  -----
  ** NOTE: Estimated insert size may differ from sequence length
  (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
  ** NOTE: This is a "working draft" sequence. It currently
  consists of 6 contigs. The true order of the pieces
  is not known and their order in this sequence record is
  arbitrary. Gaps between the contigs are represented as
  runs of N, but the exact sizes of the gaps are unknown.
  * This record will be updated with the finished sequence
  as soon as it is available and the accession number will
  be preserved.
  * 1 231096: contig of 231096 bp in length
  * 231097 231196: gap of unknown length
  * 231197 233408: contig of 2212 bp in length

```

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* 233409 233508: contig of unknown length
* 233509 234638: contig of 1130 bp in length
* 234639 234738: gap of unknown length
* 234739 238474: contig of 3736 bp in length
* 238475 238574: gap of unknown length
* 238575 257956: contig of 19382 bp in length
* 257957 258056: gap of unknown length
* 258057 276376: contig of 18320 bp in length.
FEATURES
    Source
        1..276376
        /organism="Rattus norvegicus"
        /mol_type="genomic DNA"
        /db_xref="taxon:10116"
        /clone="CH230-44022"
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        /note="wgs_end_extension
        clone_end:5p6"
        2214..3072
        /note="clone boundary
        clone_end:3p6
        site:ECORI
        end_sequence:BH295921"
    misc_feature
        229632..230700
        /note="clone boundary
        clone_end:T7
        site:ECORI
        end_sequence:BH295918"
ORIGIN
Query Match 77.8%; Score 14; DB 2; Length 276376;
Best Local Similarity 85.7%; Pred. No. 99;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 5 UCCGCGAGNNNNN 18
Db 171866 TCCTGAGNNNNN 171853
RESULT 114
AC095110/c
LOCUS
DEFINITION
AC095110 278311 bp DNA linear HTG 09-MAY-2003
Rattus norvegicus clone CH230-7M3, *** SEQUENCING IN PROGRESS ***
AC095110
6 uncloned pieces.
AC095110.6 GI:30467662
HTG; HTG_PHASE1; HTG_DRAFT; HTG_ENRICHED.
SOURCE
Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 278311)
Mazny,D,Marie, Metzker,M,lee, Abramzon,S, Adams,C, Alder,J,
Allen,C, Allen,H, Albrooks,S, Amin,A, Anguiano,D,
Avalaibeche,V, Aoyagi,A, Ayodeji,M, Baca,E, Baden,H,
Baldwin,D, Bandaranaike,D, Barber,M, Barnstead,M, Benahmed,F,
Blawalo,K, Blair,D, Blankenburg,K, Blyth,P, Brown,M,
Bryant,N, Buhay,C, Burch,P, Burrell,K, Calderon,E,
Cardenas,V, Carter,K, Cavazos,I, Cessari,H, Center,A,
Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J,
Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L,
David,M,L, Davis,C, Davy-Carroll,L, De Anda,C, Dederich,D,
Delgado,O, Denison,S, Deramo,C, Ding,Y, Dinh,H, Diya,K,
Diaper,H, Dugan-Rocha,S, Dunn,A, Durbin,K, Duval,B, Eaves,K,
Egan,A, Escotto,M, Eugene,C, Evans,C,A, Falls,T, Fan,G,
Fernandez,S, Finley,M, Flagg,N, Forbes,L, Foster,M, Foster,P,
Fraser,C,M, Gabisi,A, Ganta,R, Garcia,A, Garner,T, Garza,M,
Gebregregis,E, Geer,K, Gill,R, Grady,M, Guerra,M, Guevara,W,
Gunaratne,P, Haaland,W, Hamill,C, Hamilton,C, Hamilton,K,
Harvey,Y, Havlak,P, Hawes,A, Henderson,N, Hernandez,J,
Hernandez,R, Hines,S, Hladun,S,L, Hodgson,A, Hogues,M,
Hollins,B, Howells,S, Hulik,S, Hume,J, Idlebird,D, Jackson,A,
Jackson,L, Jacob,L, Jiang,H, Johnson,B, Johnson,R, Joliver,A,

```

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Karpachy,S, Kelly,S, Kelly,S, Khan,Z, King,L, Kovar,C,
Kovis,C, Kraft,C,L, Lebow,H, Leven,J, Lewis,L, Li,Z, Liu,J,
Liu,J, Liu,W, Liu,Y, London,P, Longacre,S, Lopez,J,
Lorenshweta,L, Louisedge,H, Lozano,R,J, Lu,X, Ma,J,
Maheshwari,M, Mahindartine,M, Mahmud,M, Malloy,K, Mangum,A,
Mangum,B, Mapua,P, Martin,K, Martin,R, Martinez,E,
Mawhney,S, McLeod,M,P, McNeill,T,Z, Meenen,E,
Milosavljevic,A, Miner,G, Minia,E, Montemayor,J, Moore,S,
Morgan,M, Morris,K, Morris,S, Mundasa,M, Murphy,M, Nair,T,
Nankervis,C, Neal,D, Newton,N, Nguyen,N, Norris,S,
Nockelemech,O, Okunolu,G, Olarunsaogun,A, Pal,S, Parks,K,
Paternak,S, Paul,H, Perez,A, Perez,L, Pfannkuch,C,
Pioppert,F, Polidexter,A, Popovic,D, Primus,E, Pu,L,
Puzo,M, Quiroz,J, Rachin,E, Reeves,K, Regier,M,A, Reigh,R,
Kelly,B, Reilly,M, Ren,Y, Reuter,M, Richards,S, Riggs,F,
Rivers,C, Rodkey,T, Rojase,A, Rose,M, Rose,R, Ruiz,S,
Sanders,W, Savary,G, Scherer,S, Scott,G, Shatsman,S, Shen,H,
Shetty,J, Shvartsbeyn,A, Sisson,I, Sitter,C,D, Smajic,D,
Sneed,A, Sodergren,E, Song,X-Z, Sorelle,R, Sosa,J,
Steinle,M, Strong,R, Sutton,A, Swatek,A, Taber,P, Taylor,C,
Taylor,T, Thomas,N, Thomas,S, Tingey,A, Trejos,Z, Umanit,K,
Valas,R, Vera,V, Villaseana,D, Waldron,L, Walker,B, Wang,J,
Wang,Q, Wang,S, Warren,J, Warren,R, Wei,X, White,F,
Williams,G, Willson,R, Wleczky,R, Wooden,H, Worley,K,
Wright,D, Wright,R, Wu,J, Yakub,S, Yen,J, Yoon,L, Yoon,V,
Yu,F, Zhang,J, Zhou,J, Zhou,X, Zhao,S, Dunn,D, von
Niederhausern,A, Weis,R, Smith,D,R, Holt,R,A, Smith,H,O,
Weinstock,G, and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 278311)
Direct Submission
Mortley,K,C.
Direct Submission
Submitted (16-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 278311)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 9, 2003 this sequence version replaced gi:24818166.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GCCR
Center clone name: CH230-7M3
----- Summary Statistics
Assembly program: Atlas;
Consensus quality: 241903 bases at least Q40
Consensus quality: 247369 bases at least Q30
Estimated insert size: 268229; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)

```

\* NOTE: This sequence may represent more than one clone.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 6 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 6190: contig of 6190 bp in length  
 6291 6290: gap of unknown length  
 10709 10708: contig of 4418 bp in length  
 10809 10808: gap of unknown length  
 256932 256931: contig of 246123 bp in length  
 257032 257031: gap of unknown length  
 272937 272936: contig of 15906 bp in length  
 273038 273037: gap of unknown length  
 276082 276081: contig of 3044 bp in length  
 276182 276181: gap of unknown length  
 278311 278310: contig of 2130 bp in length.

## FEATURES

## SOURCE

1. 278311  
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 /clone="CH230-7M3"  
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 6291. 8143  
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## ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 278311;  
 Best Local Similarity 85.7%; Pred. No. 99;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 UCCUGAGANNNNNN 18

Db 212784 TCCTGAGANNNNNN 212771

## RESULT 115

## AC132498/c

## LOCUS

## DEFINITION

## AC132498

## AC132498

## AC132498.3

## GI:25139047

## HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_ENRICHED.

## KEYWORDS

## Rattus norvegicus

## Rattus norvegicus

## Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

## Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

## REFERENCE

## AUTHORS

1 (bases 1 to 292735)  
 Muzny, D., Maric, M., Metzger, M., Lee, A., Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,  
 Anyalebuchi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,  
 Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benhmed, F.,  
 Blawie, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,  
 Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,  
 Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A.,  
 Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,  
 Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cre, A., D'Souza, L.,  
 Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,  
 Delgado, O., Denison, S., Deramo, C., Ding, Y., Dim, H., Divya, K.,  
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 Hollins, B., Howells, S., Hui, S., Hume, J., Idlebird, D., Jackson, A.,  
 Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolyet, A.,  
 Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,  
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 Lohenshewa, L., Louisedge, H., Lozano, R. J., Lu, X., Ma, J.,  
 Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A.,  
 Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E.,  
 Mawhinney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,  
 Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,  
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 Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,  
 Plopper, F., Polindexter, A., Popovic, D., Primus, E., Pu, L.,  
 Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R.,  
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 Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,  
 Weinstock, G., and Gibbs, R. A.

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

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## JOURNAL

may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: KBYK  
Center clone name: CH230-12L9

----- Summary Statistics  
Assembly program: Phrap; version 0.990129  
Consensus quality: 247040 bases at least Q40  
Consensus quality: 249556 bases at least Q30  
Consensus quality: 251629 bases at least Q20  
Estimated insert size: 254147; sum-of-contigs estimation  
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html))  
\* NOTE: This sequence may represent more than one clone.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 2 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 289860: contig of 289860 bp in length  
\* 289861 289860: gap of unknown length  
\* 289861 292735: contig of 2775 bp in length.  
Location/Qualifiers

1. 292735  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-12L9"  
1. 1218  
/notes="wgs contig"  
2438. 3924  
/note="wgs\_contig"  
288298. 289860  
/note="wgs\_contig"

## ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 292735;  
Best Local Similarity 85.7%; Pred. NO. 98;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 UCCUGAGANNNNNN 18  
Db 2445 TCCTGGAGANNNNN 2432

RESULT 116  
AC097975/c  
LOCUS  
DEFINITION Rattus norvegicus clone CH230-29D22, \*\*\* SEQUENCING IN PROGRESS  
AC097975 303281 bp DNA linear HTG 10-MAY-2003  
AC097975  
AC097975.6 GI:30520737  
VERSION HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_ENRICHED.  
KEYWORDS Rattus norvegicus (Norway rat)  
SOURCE Rattus norvegicus  
ORGANISM Rattus norvegicus; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE 1 (bases 1 to 303281)  
AUTHORS Muzny, D., Marle, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alebrooks, S., Amin, A., Angulano, D., Ayala-Becchi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Banstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dedrich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, P., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Dublin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, P., Fraser, C., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S., Hodgson, A., Hogues, M., Hollins, B., Howell, S., Hulik, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshewa, L., Louisedge, H., Lozada, R., Lu, X., Ma, J., Maheewari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E., McWhiney, S., McLeod, M., McNeill, T., Meenen, E., Mlosovljevic, A., Miner, G., Ming, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nsokeleleh, O., Okwono, G., Olarunpasegun, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Plankoch, C., Plopper, F., Potindexter, A., Popovic, D., Primus, E., Pu, L., L., Pizzo, M., Quiroz, J., Rachin, E., Reeves, K., Regier, M., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richard, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C., D., Smales, D., Sneed, A., Sodergren, E., Song, X., Z., Sotelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseca, D., Waldron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlezyk, R., Woodin, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhou, S., Dunn, D., von Niederhausern, A., Weis, R., Smith, D., Holt, R., A., Smith, H., O., Weinstock, G., and Gibbs, R. A.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Unpublished  
2 (bases 1 to 303281)  
Worley, K.C.  
Direct Submission  
Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 303281)  
Rat Genome Sequencing Consortium.  
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On May 10, 2003 this sequence version replaced gi:23096370.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome



shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: GFTY  
Center clone name: CH230-29D22  
----- Summary Statistics  
Assembly program: Atlas 3.0;  
Consensus quality: 270760 bases at least Q40  
Consensus quality: 276779 bases at least Q30  
Consensus quality: 281358 bases at least Q20  
Estimated insert size: 306451; sum-of-contigs estimation  
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html))  
\* NOTE: This sequence may represent more than one clone.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 5 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 15667: contig of 15667 bp in length  
\* 15668 15767: gap of unknown length  
\* 15768 28208: contig of 12441 bp in length  
\* 28209 28308: gap of unknown length  
\* 28309 59043: contig of 30735 bp in length  
\* 59044 59143: gap of unknown length  
\* 59144 302110: contig of 242967 bp in length  
\* 302111 302210: gap of unknown length  
\* 302211 303281: contig of 1071 bp in length.  
Location/Qualifiers

## FEATURES

source  
1. 303281  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-29D22"  
1. 1232  
/note="wgs end extension  
clone\_end:Sp6"  
922. 1673  
/note="clone boundary  
clone\_end:Sp6  
site:ECORI  
end sequence: BH259351"  
misc\_feature  
1902. 7387  
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misc\_feature  
13702. 15667  
/note="wgs\_contig"  
misc\_feature  
15768. 21867  
/note="wgs\_contig"  
misc\_feature  
21918 24246  
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24375. 28208  
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28309. 33287  
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42566 47456  
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misc\_feature  
47532. 52697  
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misc\_feature  
53520. 56324  
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misc\_feature  
56626. 59043  
/note="wgs\_contig"  
misc\_feature  
139627. 139698

## misc\_feature

/note="clone boundary  
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end sequence: BH259350"  
299505. 302110  
/note="wgs end extension  
clone\_end:T7"

## ORIGIN

Query Match 77.8%; Score 14; DB 2; Length 303281;  
Best Local Similarity 85.7%; Pred. No. 98;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

## QY

5 UCCUGAGNNNNNN 18  
:|||||

## Db

264712 TCTTGAGNNNNNN 264699

## RESULT 117

## AC105854

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

AC105854 303894 bp DNA linear HTG 11-OCT-2002  
Rattus norvegicus clone CH230-336G16, \*\*\* SHUNNING IN PROGRESS  
\*, 16 unordered pieces.  
AC105854  
AC105854.3 GI:23603227  
HTG, HTGS\_PHASE1, HTGS\_DRAFT, HTGS\_ENRICHED.  
Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

## REFERENCE

## AUTHORS

1 (bases 1 to 303894)  
Muzny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J.,  
Allen, C., Allen, H., Alsebrook, S., Amin, A., Angilano, D.,  
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,  
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,  
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,  
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,  
Cardenas, V., Carter, K., Cavazos, I., Ceaar, H., Center, A.,  
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,  
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,  
David, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,  
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,  
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,  
Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,  
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,  
Frazer, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,  
Gebregiorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,  
Gunnarane, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,  
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,  
Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hughes, M.,  
Hollins, E., Howells, S., Hulik, S., Hume, J., Idelbirt, D., Jackson, A.,  
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,  
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,  
Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,  
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,  
Lorenshewa, L., Louissege, H., Lovado, R. J., Lu, X., Ma, J.,  
Maheshwari, M., Mahindaratne, M., Mahmood, M., Malloy, K., Mangum, A.,  
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,  
Mawliny, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,  
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J.,  
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,  
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,  
Nwaekemele, O., Okunnu, G., Olariu, A., Pal, S., Parks, K.,  
Pasternak, S., Paul, H., Perez, A., Perez, L., Pflanzkoch, C.,  
Plopper, F., Polidexter, A., Popovic, D., Primus, E., Pu, L. L.,  
Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R.,  
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,  
Rivers, C., Rodkey, T., Rojase, A., Rose, M., Rose, R., Ruiz, S. J.,  
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H.,  
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajs, D.,  
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,  
Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,



Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Wilson, R., Wleczyk, R., Woodson, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhauser, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

Direct Submission  
Unpublished  
2 (bases 1 to 303894)  
Worley, K. C.

Direct Submission  
Submitted (10-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 303894)  
Rat Genome Sequencing Consortium.

Direct Submission  
Submitted (11-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Oct 9, 2002 this sequence version replaced gi:21736956.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: GNM1  
Center clone name: CH230-336G16  
----- Summary Statistics  
Assembly program: Phrap, version 0.990329  
Consensus quality: 228462 bases at least Q40  
Consensus quality: 239424 bases at least Q30  
Estimated insert size: 232995; sum-of-contigs estimation  
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

----- NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_difft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_difft_data.html)).  
NOTE: This is a 'working draft' sequence. It currently  
consists of 16 contigs. The true order of the pieces  
is not known and their order in this sequence record is  
arbitrary. Gaps between the contigs are represented as  
runs of N, but the exact sizes of the gaps are unknown.  
This record will be updated with the finished sequence  
as soon as it is available and the accession number will  
be preserved.

1 13303: contig of 13303 bp in length  
\* 13304 13403: gap of unknown length  
\* 13404 28005: contig of 14602 bp in length  
\* 28006 28105: gap of unknown length  
\* 28106 54260: contig of 26155 bp in length  
\* 54261 54360: gap of unknown length  
\* 54361 66354: contig of 11994 bp in length  
\* 66355 66454: gap of unknown length  
\* 66455 74904: contig of 8450 bp in length  
\* 74905 75004: gap of unknown length  
\* 75005 90386: contig of 15382 bp in length  
\* 90387 90486: gap of unknown length

90487 291741: contig of 201255 bp in length  
\* 291742 291841: gap of unknown length  
\* 291842 292873: contig of 1032 bp in length  
\* 292874 292973: gap of unknown length  
\* 292974 294062: contig of 1089 bp in length  
\* 294063 294162: gap of unknown length  
\* 294163 295422: contig of 1260 bp in length  
\* 295423 295522: gap of unknown length  
\* 295523 296705: contig of 1183 bp in length  
\* 296706 296805: gap of unknown length  
\* 296806 297824: contig of 1019 bp in length  
\* 297825 297924: gap of unknown length  
\* 297925 299158: contig of 1234 bp in length  
\* 299159 299258: gap of unknown length  
\* 299259 300609: contig of 1351 bp in length  
\* 300610 300709: gap of unknown length  
\* 300710 302210: contig of 1501 bp in length  
\* 302211 302310: gap of unknown length  
\* 302311 303894: contig of 1584 bp in length.

FEATURES  
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1. .303894  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-336G16"  
1. .1129  
/note="wgs\_end\_extension  
clone\_end:T7"  
8025. .8867  
/note="clone\_boundary  
clone\_end:T7  
site:Mbol  
end\_sequence:RXAPV44TV"  
13404. .16741  
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42706. .45474  
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48415. .50766  
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54361. .56464  
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66455. .68048  
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75005. .76092  
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76641. .78149  
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90487. .91649  
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91700. .93465  
/note="wgs\_contig"  
complement(199710. .200620)  
/note="clone\_boundary  
clone\_end:Sp6  
site:Mbol  
end\_sequence:RXAPV44TV"

ORIGIN  
Query Match 77.8%; Score 14; DB 2; Length 303894;  
Best Local Similarity 85.7%; Pred. No. 98;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGGAGNNNNN 18  
Db 229336 TCCTGGAGNNNNN 229349

RESULT 118  
AX555067/c AX555067 20 bp DNA linear PAT 27-NOV-2002  
LOCUS Sequence 30 from Patent WO0233128.  
DEFINITION AX555067  
ACCESSION AX555067.1 GI:25898622  
VERSION

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
Pharmasset, Ltd. (BB)  
Location/Qualifiers  
1. .20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="labeled oligonucleotide (probe) used to detect HCV viral load"  
misc\_feature  
1  
/note="n=FAM modified cytosine"  
misc\_feature  
20  
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ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 20;  
Best Local Similarity 84.6%; Pred. No. 6e+02;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAGN 13  
Db 13 GGGGTCCTGGAGN 1  
RESULT 119  
AX037216/c  
LOCUS AX037216 21 bp DNA PAT 16-NOV-2000  
DEFINITION Sequence 128 from Patent WO0056923.  
ACCESSION AX037216  
VERSION AX037216.1 GI:11226641  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB); CLATTERBRIDGE CANCER RES TRUST (GB)  
Location/Qualifiers  
1. .21  
/organism="synthetic construct"  
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ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 21;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CCUGAGNNNNNN 18  
Db 21 CCTGGAGNNNNNN 9  
RESULT 120  
AX037233/c  
LOCUS AX037233 21 bp DNA PAT 16-NOV-2000  
DEFINITION Sequence 145 from Patent WO0056923.  
ACCESSION AX037233  
VERSION AX037233.1 GI:11226658  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB); CLATTERBRIDGE CANCER RES TRUST (GB)  
Location/Qualifiers  
1. .27  
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/note="replacement plasmid sequence"

REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB); CLATTERBRIDGE CANCER RES TRUST (GB)  
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Query Match 72.2%; Score 13; DB 6; Length 21;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CCUGAGNNNNNN 18  
Db 20 CCTGGAGNNNNNN 8  
RESULT 121  
AX037217  
LOCUS AX037217 27 bp DNA PAT 16-NOV-2000  
DEFINITION Sequence 129 from Patent WO0056923.  
ACCESSION AX037217  
VERSION AX037217.1 GI:11226642  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB); CLATTERBRIDGE CANCER RES TRUST (GB)  
Location/Qualifiers  
1. .27  
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/note="replacement plasmid sequence"  
ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CCUGAGNNNNNN 18  
Db 6 CCTGGAGNNNNNN 18  
RESULT 122  
AX037218  
LOCUS AX037218 27 bp DNA PAT 16-NOV-2000  
DEFINITION Sequence 130 from Patent WO0056923.  
ACCESSION AX037218  
VERSION AX037218.1 GI:11226643  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB); CLATTERBRIDGE CANCER RES TRUST (GB)  
Location/Qualifiers  
1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/note="replacement plasmid sequence"

ORIGIN /db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
||:|||||  
6 CCTGAGAGNNNNNN 18

## RESULT 123

LOCUS AX037219 27 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 131 from Patent WO0056923.  
ACCESSION AX037219  
VERSION AX037219.1 GI:11226644  
KEYWORDS

SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 131 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source 1. .27  
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## ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
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6 CCTGAGAGNNNNNN 18

## RESULT 124

LOCUS AX037220 27 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 132 from Patent WO0056923.  
ACCESSION AX037220  
VERSION AX037220.1 GI:11226645  
KEYWORDS

SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 132 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
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## ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18

Db ||:|||||  
6 CCTGAGAGNNNNNN 18

RESULT 125  
LOCUS AX037221 27 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 133 from Patent WO0056923.  
ACCESSION AX037221  
VERSION AX037221.1 GI:11226646  
KEYWORDS

SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 133 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
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## ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
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6 CCTGAGAGNNNNNN 18

## RESULT 126

LOCUS AX037222 27 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 134 from Patent WO0056923.  
ACCESSION AX037222  
VERSION AX037222.1 GI:11226647  
KEYWORDS

SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 134 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
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/note="replacement plasmid sequence"

## ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
||:|||||  
6 CCTGAGAGNNNNNN 18

## RESULT 127

LOCUS AX037223 27 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 135 from Patent WO0056923.  
ACCESSION AX037223

VERSION AX037223.1 GI:11226648  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 135 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source 1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNNN 18  
||:|||||  
6 CCTGAGANNNNNN 18

Db 6 CCUGAGANNNNNN 18  
||:|||||  
6 CCTGAGANNNNNN 18

RESULT 128  
AX037224 27 bp DNA linear PAT 16-NOV-2000  
LOCUS Sequence 136 from Patent WO0056923.  
DEFINITION AX037224  
ACCESSION AX037224.1 GI:11226649  
VERSION  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 136 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source 1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNNN 18  
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6 CCTGAGANNNNNN 18

Db 6 CCUGAGANNNNNN 18  
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6 CCTGAGANNNNNN 18

RESULT 129  
AX037225 27 bp DNA linear PAT 16-NOV-2000  
LOCUS Sequence 137 from Patent WO0056923.  
DEFINITION AX037225  
ACCESSION AX037225  
VERSION AX037225.1 GI:11226650  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 137 28-SEP-2000;

FEATURES  
source 1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNNN 18  
||:|||||  
6 CCTGAGANNNNNN 18

Db 6 CCUGAGANNNNNN 18  
||:|||||  
6 CCTGAGANNNNNN 18

RESULT 130  
AX037226 27 bp DNA linear PAT 16-NOV-2000  
LOCUS Sequence 138 from Patent WO0056923.  
DEFINITION AX037226  
ACCESSION AX037226  
VERSION AX037226.1 GI:11226651  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 138 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source 1. .27  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNNN 18  
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6 CCTGAGANNNNNN 18

Db 6 CCUGAGANNNNNN 18  
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6 CCTGAGANNNNNN 18

RESULT 131  
AX037227 27 bp DNA linear PAT 16-NOV-2000  
LOCUS Sequence 139 from Patent WO0056923.  
DEFINITION AX037227  
ACCESSION AX037227  
VERSION AX037227.1 GI:11226652  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Sibson,R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 139 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
FEATURES  
source 1. .27  
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/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN  
Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNNN 18  
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6 CCTGAGANNNNNN 18

Db 6 CCUGAGANNNNNN 18  
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6 CCTGAGANNNNNN 18

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
||:|||||  
6 CCTGAGAGNNNNNN 18

Db

RESULT 132  
AX037228 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 140 from Patent WO0056923.  
AX037228  
ACCESSION  
VERSION AX037228.1 GI:11226653  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
1. .27  
/organism="synthetic construct"  
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/note="replacement plasmid sequence"

ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
||:|||||  
6 CCTGAGAGNNNNNN 18

Db

RESULT 133  
AX037229 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 141 from Patent WO0056923.  
AX037229  
ACCESSION  
VERSION AX037229.1 GI:11226654  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
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/organism="synthetic construct"  
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/note="replacement plasmid sequence"

ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
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6 CCTGAGAGNNNNNN 18

Db

RESULT 134  
AX037230 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 142 from Patent WO0056923.  
AX037230  
ACCESSION  
VERSION AX037230.1 GI:11226655  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
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/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
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QY 6 CCUGAGAGNNNNNN 18  
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6 CCTGAGAGNNNNNN 18

Db

RESULT 135  
AX037231 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 143 from Patent WO0056923.  
AX037231  
ACCESSION  
VERSION AX037231.1 GI:11226656  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
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/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN

Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
||:|||||  
6 CCTGAGAGNNNNNN 18

Db

RESULT 136  
AX037232 27 bp DNA linear PAT 16-NOV-2000  
LOCUS  
DEFINITION Sequence 144 from Patent WO0056923.  
AX037232  
ACCESSION  
VERSION AX037232.1 GI:11226657  
KEYWORDS  
SOURCE  
ORGANISM  
FEATURES  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
LOCATION/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="replacement plasmid sequence"

ORIGIN

REFERENCE 1 other sequences; artificial sequences.  
AUTHORS Sibson, R.  
TITLE Genetic analysis  
JOURNAL Patent: WO 0056923-A 144 28-SEP-2000;  
SIBSON ROSS (GB) ; CLATTERBRIDGE CANCER RES TRUST (GB)  
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SOURCE Location/Qualifiers  
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/note="replacement plasmid sequence"  
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Query Match 72.2%; Score 13; DB 6; Length 27;  
Best Local Similarity 92.3%; Pred. No. 6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CCUGAGAGNNNNNN 18  
6 CCTGAGAGNNNNNN 18  
Db  
RESULT 137  
G06767 761 bp DNA linear STS 19-OCT-1995  
LOCUS human STS WI-7926, sequence tagged site.  
DEFINITION G06767  
ACCESSION G06767  
VERSION G06767.1 GI:860012  
KEYWORDS STS; STS sequence; primer; sequence tagged site.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 761)  
AUTHORS Hudson, T.  
TITLE Whitehead Institute/MIT Center for Genome Research; Physically  
JOURNAL Mapped ESTs  
COMMENT Unpublished (1995)  
Contact: Thomas Hudson  
Whitehead Institute/MIT Center for Genome Research  
Whitehead Institute for Biomedical Research  
9 Cambridge Center, Cambridge MA 02142 USA  
Tel: 617 252 1900  
Fax: 617 252 1902  
Email: thudson@genome.wi.mit.edu  
Primer A: CATTCGCATCTGTCACG  
Primer B: CCTTCCTCAATAATGAAACG  
STS size: 347  
PCR Profile:  
Presoak:  
Denaturation:  
Annealing: 56 degrees C  
Polymerization:  
PCR Cycles: 35  
Thermal Cycler:  
Protocol:  
Template: 10 ng  
Primer: each 5 pm  
dNTPs: each 4 mM  
Tag Polymerase: 0.025 units/ul  
Total Vol: 20 ul  
Buffer:  
MgCl2: 1.5 mM  
KCl: 50 mM  
Tris-HCl: 10 mM  
pH: 9.3  
Prepared with primer pairs derived from U09368 -- Unigene.  
Location/Qualifiers

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primer\_bind  
complement(690..710)  
ORIGIN  
Query Match 72.2%; Score 13; DB 11; Length 761;  
Best Local Similarity 92.3%; Pred. No. 5.3e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CCUGAGAGNNNNNN 18  
142 CCTGAGAGNNNNNN 154  
Db  
RESULT 138  
BD021433 784 bp DNA linear PAT 27-AUG-2002  
LOCUS BD021433  
DEFINITION Novel gene and novel gene fragment cloned in human neuroblastoma.  
ACCESSION BD021433  
VERSION BD021433.1 GI:22562656  
KEYWORDS JP 2001245671-A/3671.  
SOURCE JP 2001245671-A/3671.  
Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 784)  
AUTHORS Nakagawara, A.  
TITLE Novel gene and novel gene fragment cloned in human neuroblastoma  
JOURNAL Patent: JP 2001245671-A 3671 11-SEP-2001;  
CHIBA PREP. HISAMITSU PHARMACEUTICAL CO INC  
COMMENT OS Homo sapiens (human)  
PN JP 2001245671-A/3671  
PD 11-SEP-2001  
PF 07-MAR-2000 JP 2000159195  
PI AKIRA NAKAGAWARA  
PC C12N15/09, C12Q1/68, G01N33/53, G01N33/566//C12Q1/68, C12R1:91),  
PC C12N15/00  
CC Novel gene and novel gene fragment cloned in human CC  
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Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUGAGAGN 13  
570 GGGGTCCTCGAGN 558  
Db  
RESULT 139  
BD101371 784 bp DNA linear PAT 27-AUG-2002  
LOCUS BD101371  
DEFINITION Novel genes cloned in humanneuroblastoma and fragments thereof.  
ACCESSION BD101371  
VERSION BD101371.1 GI:22646945  
KEYWORDS WO 0166719-A/3671.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
AUTHORS 1 (bases 1 to 784)  
TITLE Nakagawara, A.  
JOURNAL Novel genes cloned in humanneuroblastoma and fragments thereof  
COMMENT Patent: WO 0166719-A 3671 13-SEP-2001;  
CHIBA PREF, HISAMITSU PHARMACEUTICAL CO INC, AKIRA NAKAGAWARA  
OS Homo sapiens (human)  
PN WO 0166719-A/3671  
PD 13-SEP-2001  
PF 02-MAR-2001 WO 2001JP001629  
PR 07-MAR-2000 JP 00P 159195  
PI AKIRA NAKAGAWARA  
PC A12N15/11, C1201/68, G01N33/53, G01N33/566  
CC Novel genes cloned in humanneuroblastoma and fragments thereof  
FH Key Location/Qualifiers  
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QY 1 GGGGUCGAGN 13  
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Db 570 GGGGTCCTCGAGN 558  
RESULT 140  
LOCUS AC015491 30040 bp DNA linear HTG 13-JUL-2000  
DEFINITION Homo sapiens clone Rpl1-20L18, LOW-PASS SEQUENCE SAMPLING.  
AC015491  
AC015491.2 GI:9123963  
VERSION  
KEYWORDS HTG; HTGS\_PHASE0.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 30040)  
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,  
Baldwin, J., Barina, N., Becker, R., Boguslavsky, L., Bouckgeater, B.,  
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,  
Cooke, P., DeArrellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,  
Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,  
Gallagan, J., Gardyna, S., Grant, G., Hages, B., Heath, A., Horton, L.,  
Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,  
Lencock, J., Liu, C., Locke, K., Macdonald, P., Marquis, N.,  
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,  
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,  
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,  
Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Teafye, S., Tirelli, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,  
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome  
COMMENT Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced gi:6437626.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WtBR

Web site: <http://www-geq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
Project Information  
Center Project name: L3925  
Center Clone name: 20\_L\_18  
-----  
\* NOTE: This record contains 33 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
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824 823: contig of 823 bp in length  
924 923: gap of 100 bp  
924 1773: contig of 850 bp in length  
1774 1873: gap of 100 bp  
1874 2677: contig of 804 bp in length  
2678 2777: gap of 100 bp  
2778 3578: contig of 801 bp in length  
3579 3678: gap of 100 bp  
3679 4455: contig of 778 bp in length  
4456 4557: gap of 100 bp  
4558 5338: contig of 782 bp in length  
5339 5438: gap of 100 bp  
5439 6230: contig of 792 bp in length  
6231 6331: gap of 100 bp  
6331 7128: contig of 793 bp in length  
7129 7229: gap of 100 bp  
7230 8035: contig of 806 bp in length  
8036 8135: gap of 100 bp  
8136 8973: contig of 838 bp in length  
8974 9073: gap of 100 bp  
9074 9888: contig of 816 bp in length  
9889 9989: gap of 100 bp  
9990 10826: contig of 837 bp in length  
10827 10926: gap of 100 bp  
10927 11716: contig of 790 bp in length  
11717 11816: gap of 100 bp  
11817 12671: contig of 855 bp in length  
12672 12771: gap of 100 bp  
12772 13593: contig of 822 bp in length  
13594 13693: gap of 100 bp  
13694 14493: contig of 800 bp in length  
14494 14593: gap of 100 bp  
14594 15387: contig of 794 bp in length  
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16317 16416: gap of 100 bp  
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17236 17335: gap of 100 bp  
17336 18142: contig of 807 bp in length  
18143 18242: gap of 100 bp  
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19043 19142: gap of 100 bp  
19143 19934: contig of 792 bp in length  
19935 20034: gap of 100 bp  
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20881 20980: gap of 100 bp  
20981 21835: contig of 855 bp in length  
21836 21935: gap of 100 bp  
21937 22747: contig of 812 bp in length  
22748 22847: gap of 100 bp  
22848 23670: contig of 823 bp in length  
23671 23770: gap of 100 bp  
23771 24552: contig of 782 bp in length  
24553 24652: gap of 100 bp  
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\* 26412 26511: gap of 100 bp  
\* 26512 27324: contig of 813 bp in length  
\* 27325 27424: gap of 100 bp  
\* 27425 28242: contig of 818 bp in length  
\* 28243 28343: gap of 100 bp  
\* 28343 29183: contig of 841 bp in length  
\* 29184 29283: gap of 100 bp  
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/clone\_1lb="RP11-11 Human Male BAC"

## ORIGIN

Query Match 72.2% Score 13; DB 2; Length 30040;  
Best Local Similarity 92.3%; Pred. No. 4.7e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNN 18  
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Db 24546 CCTGAGAGNNNNN 24558

RESULT 141  
AC025943/c  
LOCUS  
DEFINITION  
Homo sapiens chromosome 19 clone RP11-747B8 map 19, LOW-PASS  
SEQUENCE SAMPLING.  
AC025943 41107 bp DNA linear HTG 17-MAR-2000

AC025943  
AC025943.1 GI:7259784  
HTG; HTGS\_PHASE0.  
Homo sapiens (human)  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
Unpublished  
2 (bases 1 to 41107)  
1 (bases 1 to 41107)  
Birren, B., Linton, L., Nussbaum, C. and Lander, E.  
Homo sapiens chromosome 19, clone RP11-747B8

Anderson, S., Baldwin, J., Barina, N., Bastien, V., Bedalov, F.,  
Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,  
Campbell, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S.,  
Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,  
Dodgson, S., Domingo, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,  
Galagan, J., Gardiner, S., Ginde, S., Goette, M., Graham, L.,  
Grand-Pierre, N., Grant, G., Hago, B., Heaford, A., Horton, L.,  
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,  
Klein, J., Larocque, K., Lamazares, R., Landers, T., Lehotzky, J.,  
Levine, R., Liu, G., Locke, K., Macdonald, P., Margulis, N.,  
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,  
Meldrum, J., Meneses, L., Mihova, T., Miranda, C., Mianga, V., Morrow, J.,  
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,  
O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pletzer, N.,  
Pisanu, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,  
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,  
Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Tessier, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,  
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wymann, D., Ye, W.J.,  
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE  
JOURNAL  
COMMENT  
Submitted (17-MAR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: W1B8  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: 18601  
Center clone name: 747\_B\_8

\* NOTE: This record contains 46 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 793: contig of 793 bp in length  
794 893: gap of 100 bp  
894 1694: contig of 801 bp in length  
1695 1794: gap of 100 bp  
1795 2585: contig of 791 bp in length  
2586 2686: gap of 100 bp  
2686 3498: contig of 813 bp in length  
3499 3598: gap of 100 bp  
3598 4391: contig of 793 bp in length  
4392 4491: gap of 100 bp  
4491 5285: contig of 794 bp in length  
5286 5385: gap of 100 bp  
5386 6184: contig of 799 bp in length  
6185 6284: gap of 100 bp  
6285 7082: contig of 798 bp in length  
7083 7182: gap of 100 bp  
7183 7974: contig of 792 bp in length  
7975 8074: gap of 100 bp  
8075 8875: contig of 801 bp in length  
8876 8975: gap of 100 bp  
8976 9771: contig of 796 bp in length  
9772 9871: gap of 100 bp  
9872 10651: contig of 780 bp in length  
10652 10751: gap of 100 bp  
10752 11525: contig of 774 bp in length  
11526 11625: gap of 100 bp  
11626 12423: contig of 798 bp in length  
12424 12523: gap of 100 bp  
12524 13340: contig of 817 bp in length  
13341 13440: gap of 100 bp  
13441 14247: contig of 807 bp in length  
14248 14347: gap of 100 bp  
14348 15153: contig of 806 bp in length  
15154 15253: gap of 100 bp  
15254 16060: contig of 807 bp in length  
16061 16160: gap of 100 bp  
16161 16960: contig of 800 bp in length  
16962 17060: gap of 100 bp  
17061 17860: contig of 800 bp in length  
17861 17960: gap of 100 bp  
17961 18723: contig of 763 bp in length  
18724 18823: gap of 100 bp  
18824 19616: contig of 793 bp in length  
19617 19716: gap of 100 bp  
19717 20503: contig of 787 bp in length  
20504 20603: gap of 100 bp  
20604 21404: contig of 801 bp in length  
21405 21504: gap of 100 bp  
21505 22395: contig of 791 bp in length  
22396 22995: gap of 100 bp  
22996 23187: contig of 792 bp in length  
23188 23287: gap of 100 bp  
23288 24072: contig of 785 bp in length  
24073 24172: gap of 100 bp  
24173 24975: contig of 803 bp in length



```

* 24976 25075: gap of 100 bp
* 25076 25854: contig of 779 bp in length
* 25855 25954: gap of 100 bp
* 25955 26764: contig of 810 bp in length
* 26765 26864: gap of 100 bp
* 26865 27557: contig of 793 bp in length
* 27558 27757: gap of 100 bp
* 27758 28546: contig of 789 bp in length
* 28547 28647: gap of 100 bp
* 28647 29440: contig of 794 bp in length
* 29441 30329: contig of 789 bp in length
* 30330 30429: gap of 100 bp
* 30430 31218: contig of 789 bp in length
* 31219 31319: gap of 100 bp
* 31319 32121: contig of 803 bp in length
* 32122 32222: gap of 100 bp
* 32222 33010: contig of 789 bp in length
* 33011 33111: gap of 100 bp
* 33111 33906: contig of 796 bp in length
* 33907 34006: gap of 100 bp
* 34007 34810: contig of 804 bp in length
* 34811 34910: gap of 100 bp
* 34911 35696: contig of 786 bp in length
* 35697 35796: gap of 100 bp
* 35797 36594: contig of 798 bp in length
* 36595 36694: gap of 100 bp
* 36695 37498: contig of 804 bp in length
* 37499 37598: gap of 100 bp
* 37599 38405: contig of 807 bp in length
* 38406 38505: gap of 100 bp
* 38506 39302: contig of 797 bp in length
* 39303 39402: gap of 100 bp
* 39403 40197: contig of 795 bp in length
* 40198 40297: gap of 100 bp
* 40298 41107: contig of 810 bp in length.

```

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FEATURES
  source          1..41107
                  /organism="Homo sapiens"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:9606"
                  /chromosome="19"
                  /map="19"
                  /clone="RP11-74788"
                  /clone_id="RP11-74788"

```

```

ORIGIN
Query Match      72.2%; Score 13; DB 2; Length 41107;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      6 CCUGAGAGNNNNNN 18
Db      17967 CCTGAGAGNNNNNN 17955

```

```

RESULT 142
AC087168
LOCUS      AC087168             45685 bp    DNA             linear      HTG 11-DEC-2000
DEFINITION Homo sapiens chromosome 8 clone RP11-235A15 map 8, LOW-PASS
SEQUENCE SAMPLING.
ACCESSION AC087168
VERSION   AC087168.1 GI:11612589
KEYWORDS  HTG; HTGS_PHASED.
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 45685)
AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE     Homo sapiens chromosome 8, clone RP11-235A15
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 45685)

```

## AUTHORS

TITLE  
JOURNAL  
COMMENT

```

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barna,N., Baskien,V., Boguslavsky,L., Bouhagalter,B., Brown,A.,
Camata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J.,
Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-pierre,N.,
Hagos,B., Haefford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Karatas,A., Labocque,K., Lamazares,R., Landers,T.,
Lenczky,J., Levine,R., Liu,G., Maclean,C., Macdonald,P.,
Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,
McPheters,R., Meldrim,J., Meneses,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunhkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,
Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
Roy,A., Santos,R., Schauer,S., Schupack,R., Seaman,S., Severy,P.,
Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (11-DEC-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Salt, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L11603
Center clone name: 235_A_15
-----
* NOTE: This record contains 59 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*
* 1 646: contig of 646 bp in length
* 647 746: gap of 100 bp
* 747 1427: contig of 681 bp in length
* 1428 1527: gap of 100 bp
* 1528 2207: contig of 680 bp in length
* 2208 2307: gap of 100 bp
* 2308 2967: contig of 660 bp in length
* 2968 3067: gap of 100 bp
* 3068 3733: contig of 666 bp in length
* 3734 3833: gap of 100 bp
* 3834 4516: contig of 683 bp in length
* 4517 4616: gap of 100 bp
* 4617 5302: contig of 686 bp in length
* 5303 5402: gap of 100 bp
* 5403 6078: contig of 676 bp in length
* 6079 6178: gap of 100 bp
* 6179 6833: contig of 655 bp in length
* 6834 6933: gap of 100 bp
* 6934 7611: contig of 678 bp in length
* 7612 7711: gap of 100 bp
* 7712 8394: contig of 683 bp in length
* 8395 8494: gap of 100 bp
* 8495 9173: contig of 679 bp in length
* 9174 9273: gap of 100 bp
* 9274 9953: contig of 680 bp in length
* 9954 10053: gap of 100 bp

```

```

* 10054 10696: contig of 643 bp in length
* 10697 10796: gap of 100 bp
* 10797 11481: contig of 685 bp in length
* 11482 11581: gap of 100 bp
* 11582 12248: contig of 667 bp in length
* 12249 12348: gap of 100 bp
* 12349 13016: contig of 668 bp in length
* 13017 13116: gap of 100 bp
* 13117 13797: contig of 681 bp in length
* 13798 13897: gap of 100 bp
* 13898 14562: contig of 665 bp in length
* 14563 15346: contig of 684 bp in length
* 15347 15446: gap of 100 bp
* 15447 16107: contig of 661 bp in length
* 16108 16207: gap of 100 bp
* 16208 16903: contig of 696 bp in length
* 16904 17003: gap of 100 bp
* 17004 17692: contig of 689 bp in length
* 17693 17793: gap of 100 bp
* 17793 18457: contig of 665 bp in length
* 18458 18557: gap of 100 bp
* 18558 19228: contig of 671 bp in length
* 19229 19328: gap of 100 bp
* 19329 19996: contig of 668 bp in length
* 19997 20096: gap of 100 bp
* 20097 20764: contig of 668 bp in length
* 20765 20864: gap of 100 bp
* 20865 21545: contig of 681 bp in length
* 21546 21645: gap of 100 bp
* 21646 22342: contig of 697 bp in length
* 22343 22442: gap of 100 bp
* 22443 23098: contig of 656 bp in length
* 23099 23198: gap of 100 bp
* 23199 23903: contig of 705 bp in length
* 23904 24003: gap of 100 bp
* 24004 24661: contig of 658 bp in length
* 24662 24761: gap of 100 bp
* 24762 25441: contig of 680 bp in length
* 25442 25541: gap of 100 bp
* 25542 26208: contig of 667 bp in length
* 26209 26308: gap of 100 bp
* 26309 26979: contig of 671 bp in length
* 26980 27079: gap of 100 bp
* 27080 27759: contig of 680 bp in length
* 27760 27859: gap of 100 bp
* 27860 28558: contig of 699 bp in length
* 28559 28658: gap of 100 bp
* 28659 29326: contig of 668 bp in length
* 29327 29426: gap of 100 bp
* 29427 30122: contig of 696 bp in length
* 30123 30223: gap of 100 bp
* 30223 30886: contig of 664 bp in length
* 30887 30986: gap of 100 bp
* 30987 31662: contig of 676 bp in length
* 31663 31762: gap of 100 bp
* 31763 32453: contig of 691 bp in length
* 32454 32553: gap of 100 bp
* 32554 33238: contig of 685 bp in length
* 33239 33338: gap of 100 bp
* 33339 34006: contig of 668 bp in length
* 34007 34106: gap of 100 bp
* 34107 34807: contig of 701 bp in length
* 34808 34907: gap of 100 bp
* 34908 35556: contig of 649 bp in length
* 35557 35656: gap of 100 bp
* 35657 36343: contig of 687 bp in length
* 36344 36443: gap of 100 bp
* 36444 37080: contig of 637 bp in length
* 37081 37180: gap of 100 bp
* 37181 37854: contig of 674 bp in length
* 37855 37954: gap of 100 bp
* 37955 38646: contig of 692 bp in length

```

## ORIGIN

```

Query Match          72.2%; Score 13; DB 2; Length 45685;
Best Local Similarity 92.3%; Pred. No. 4.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

## QY

```

6 CCUGAGANNNNN 18
||:|||||
Db      1421 CCTGAGANNNNN 1433

```

## RESULT 143

```

CER08A5
LOCUS      CER08A5          51920 bp    DNA       linear   HTG 14-OCT-1998
DEFINITION Caenorhabditis elegans chromosome V clone ROB45, *** SEQUENCING IN
PROGRESS ***, 15 unordered pieces.
ACCESSION  Z82281
VERSION    Z82281.1 GI:3377979
KEYWORDS   HTG; HTGS PHASE1.
SOURCE     Caenorhabditis elegans
ORGANISM   Caenorhabditis elegans

```

## REFERENCE

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1 (bases 1 to 51920)
Rhabditidae; Rhabditidae; Pseudocercariae; Caenorhabditis.
Sulston, J.

```

## JOURNAL

```

Submitted (14-OCT-1998) Nematode Sequencing Project, Sanger Centre,
Hinxton, Cambridge CB10 1RO, UK and Department of Genetics,
Washington University, St. Louis, MO 63110, USA. E-mail:
jesse.sanger@wustl.edu

```

## COMMENT

```

On Aug 3, 1998 this sequence version replaced gi:166615.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
segments.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

1 2711: contig of 2711 bp in length  
\* 2712 3511: gap of 800 bp in length  
\* 3512 6616: contig of 3105 bp in length  
\* 6617 7416: gap of 800 bp in length  
\* 7417 11750: contig of 4334 bp in length  
\* 11751 12550: gap of 800 bp in length  
\* 12551 13852: contig of 1302 bp in length  
\* 13853 14652: gap of 800 bp in length  
\* 14653 16018: contig of 1366 bp in length  
\* 16019 16818: gap of 800 bp in length  
\* 16819 21109: contig of 4291 bp in length  
\* 21110 21909: gap of 800 bp in length  
\* 21910 23528: contig of 1619 bp in length  
\* 23529 24328: gap of 800 bp in length  
\* 24329 27047: contig of 2719 bp in length  
\* 27048 27847: gap of 800 bp in length  
\* 27848 31484: contig of 3637 bp in length  
\* 31485 32285: gap of 800 bp in length  
\* 32285 34192: contig of 1908 bp in length  
\* 34193 34992: gap of 800 bp in length  
\* 34993 36387: contig of 1395 bp in length  
\* 36388 37187: gap of 800 bp in length  
\* 37188 42955: contig of 5768 bp in length  
\* 42956 43756: gap of 800 bp in length  
\* 43756 46806: contig of 3051 bp in length  
\* 46807 47607: gap of 800 bp in length  
\* 47607 49371: contig of 1764 bp in length  
\* 49371 50170: gap of 800 bp in length  
\* 50171 51920: contig of 1750 bp in length.  
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1. 51920  
/organism="Caenorhabditis elegans"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:6239"  
/chromosome="V"  
/clone="R08A5"

ORIGIN  
Query Match 72.2%; Score 13; DB 2; Length 51920;  
Best Local Similarity 92.3%; Pred. No. 4.6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CCGAGAGNNNNNN 18  
DB 11744 CCGAGAGNNNNNN 11756

RESULT 144  
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LOCUS AC021293  
DEFINITION Homo sapiens clone RP11-22P22, LOW-PASS SEQUENCE SAMPLING.  
AC021293  
VERSION AC021293.2 GI:9124425  
KEYWORDS HTG: HTGS PHASED.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 52867)  
Birtren,B., Linton,L., Nusbaum,C. and Lander,E.  
Homo sapiens, clone RP11-22P22  
Unpublished  
2 (bases 1 to 52867)  
Birtren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,  
Boguslavsky,L., Bouckgalter,B., Brown,A., Burkett,G., Castle,A.,  
Chenopel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,  
DeArtilano,K., Dewar,K., Domino,M., Doyle,M., Fenesstor,J.,  
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,  
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,  
Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K.,  
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,

TITLE  
JOURNAL  
COMMENT  
McPheters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,  
Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,  
Pierre,N., Pisanl,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,  
Roy,A., Santos,R., Severy,P., Spencer,B., Strange-Thomann,N.,  
Stojanovic,N., Subramanian,A., Talamas,J., Teeffaye,S., Theodore,J.,  
Tirrell,A., Vasilev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,  
Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced gi:6705813.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submission@genome.wi.mit.edu  
----- Project Information  
Center project name: U4158  
Center clone name: 22\_P\_22  
-----  
\* NOTE: This record contains 52 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
1 889: contig of 889 bp in length  
\* 890 989: gap of 100 bp in length  
\* 990 1904: contig of 915 bp in length  
\* 1905 2004: gap of 100 bp in length  
\* 2005 2937: contig of 933 bp in length  
\* 2938 3037: gap of 100 bp in length  
\* 3038 3968: contig of 931 bp in length  
\* 3969 4068: gap of 100 bp in length  
\* 4069 4973: contig of 905 bp in length  
\* 4974 5073: gap of 100 bp in length  
\* 5074 5952: contig of 879 bp in length  
\* 5953 6052: gap of 100 bp in length  
\* 6053 6964: contig of 912 bp in length  
\* 6965 7064: gap of 100 bp in length  
\* 7065 7950: contig of 886 bp in length  
\* 7951 8050: gap of 100 bp in length  
\* 8051 8972: contig of 922 bp in length  
\* 8973 9072: gap of 100 bp in length  
\* 9073 9990: contig of 918 bp in length  
\* 9991 10090: gap of 100 bp in length  
\* 10091 11026: contig of 936 bp in length  
\* 11027 11126: gap of 100 bp in length  
\* 11127 12048: contig of 922 bp in length  
\* 12049 12148: gap of 100 bp in length  
\* 12149 13075: contig of 927 bp in length  
\* 13076 13175: gap of 100 bp in length  
\* 13176 14102: contig of 927 bp in length  
\* 14103 14202: gap of 100 bp in length  
\* 14203 15114: contig of 912 bp in length  
\* 15115 15214: gap of 100 bp in length  
\* 15215 16129: contig of 915 bp in length  
\* 16130 16229: gap of 100 bp in length  
\* 16230 17164: contig of 935 bp in length  
\* 17165 17264: gap of 100 bp in length  
\* 17265 18204: contig of 940 bp in length  
\* 18205 18304: gap of 100 bp in length  
\* 18305 19263: contig of 959 bp in length  
\* 19264 19363: gap of 100 bp in length  
\* 19364 20281: contig of 918 bp in length

```

* 20282 20381: gap of 100 bp
* 20382 21319: contig of 938 bp in length
* 21320 21419: gap of 100 bp
* 21420 22349: contig of 930 bp in length
* 22350 22449: gap of 100 bp
* 22450 23345: contig of 896 bp in length
* 23346 23445: gap of 100 bp
* 23446 24328: contig of 883 bp in length
* 24329 25347: contig of 919 bp in length
* 25348 25447: gap of 100 bp
* 25448 26374: contig of 927 bp in length
* 26375 26474: gap of 100 bp
* 26475 27388: contig of 914 bp in length
* 27389 27488: gap of 100 bp
* 27489 28387: contig of 899 bp in length
* 28388 28487: gap of 100 bp
* 28488 29423: contig of 936 bp in length
* 29424 29523: gap of 100 bp
* 29524 30436: contig of 913 bp in length
* 30437 30536: gap of 100 bp
* 30537 31494: contig of 958 bp in length
* 31495 31594: gap of 100 bp
* 31595 32508: contig of 914 bp in length
* 32509 32608: gap of 100 bp
* 32609 33513: contig of 905 bp in length
* 33514 33613: gap of 100 bp
* 33614 34564: contig of 951 bp in length
* 34565 34664: gap of 100 bp
* 34665 35573: contig of 909 bp in length
* 35574 35673: gap of 100 bp
* 35674 36594: contig of 921 bp in length
* 36595 36694: gap of 100 bp
* 36695 37703: contig of 1009 bp in length
* 37704 37803: gap of 100 bp
* 37804 38708: contig of 905 bp in length
* 38709 38808: gap of 100 bp
* 38809 39716: contig of 908 bp in length
* 39717 39816: gap of 100 bp
* 39817 40706: contig of 890 bp in length
* 40707 40806: gap of 100 bp
* 40807 41719: contig of 913 bp in length
* 41720 41819: gap of 100 bp
* 41820 42728: contig of 909 bp in length
* 42729 42828: gap of 100 bp
* 42830 43736: contig of 908 bp in length
* 43737 43836: gap of 100 bp
* 43837 44736: contig of 900 bp in length
* 44737 44836: gap of 100 bp
* 44837 45735: contig of 899 bp in length
* 45736 46756: gap of 100 bp
* 46757 46856: contig of 921 bp in length
* 46857 47772: gap of 100 bp
* 47773 47872: contig of 916 bp in length
* 47873 48791: contig of 919 bp in length
* 48792 48891: gap of 100 bp
* 48892 49773: contig of 882 bp in length
* 49774 49873: gap of 100 bp
* 49874 50784: contig of 911 bp in length
* 50785 50884: gap of 100 bp
* 50885 51843: contig of 959 bp in length
* 51844 51943: gap of 100 bp
* 51944 52867: contig of 924 bp in length.

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## FEATURES

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  /mol_type="genomic DNA"
  /db_xref="taxon:9606"
  /clone="RP11-22P22"
  /clone_1b="RP11-11 Human Male BAC"

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## ORIGIN

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Query Match      72.2%; Score 13; DB 2; Length 52867;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy      6 CCGGAGNNNNNN 18
Db      1898 CCGGAGNNNNNN 1910

RESULT 145
AC111183
LOCUS      AC111183
DEFINITION Homo sapiens chromosome 17 clone RP11-958E8 map 17, LOW-PASS
SEQUENCE SAMPLING.
AC111183
VERSION    AC111183.1 GI:18699948
KEYWORDS   HTG; HTGS PHASE0.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
            1 (bases 1 to 56611)
            Birren, B., Linton, L., Nussbaum, C. and Lander, E.
            Homo sapiens chromosome 17, clone RP11-958E8
            Unpublished
            2 (bases 1 to 56611)
            Birren, B., Linton, L., Nussbaum, C., Lander, E., Ali, A., Allen, N.,
            Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhvalter, B.,
            Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
            Chopel, Y., Colangelo, M., Collins, S., Collinmore, A., Cook, A.,
            Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fato, S.,
            Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gaidyna, S.,
            Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
            Hagos, B., Horton, L., Huime, M., Iliev, I., Johnson, R., Jones, C.,
            Kamat, A., Karatas, A., Kelle, C., LaRoque, K., Lamazares, R.,
            Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C.,
            MacDonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M.,
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            Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
            Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
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            Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
            Strauss, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J.,
            Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,
            Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
            Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
            Direct Submission
            Submitted (18-FEB-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            All repeats were identified using RepeatMasker:
            http://ftp.genome.washington.edu/RM/RepeatMasker.html

-- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L25445
Center clone name: 958_E_8

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* NOTE: This record contains 71 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will

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\* be preserved.  
1 699: contig of 699 bp in length  
700 799: gap of 100 bp  
800 1487: contig of 688 bp in length  
1488 1587: gap of 100 bp  
1588 2276: contig of 689 bp in length  
2277 2376: gap of 100 bp  
2377 3084: contig of 708 bp in length  
3085 3184: gap of 100 bp  
3185 3890: contig of 706 bp in length  
3891 3990: gap of 100 bp  
3991 4696: contig of 706 bp in length  
4697 4797: gap of 100 bp  
4797 5508: contig of 712 bp in length  
5509 5608: gap of 100 bp  
5609 6307: contig of 699 bp in length  
6308 6407: gap of 100 bp  
6408 7111: contig of 704 bp in length  
7112 7211: gap of 100 bp  
7212 7923: contig of 712 bp in length  
7924 8023: gap of 100 bp  
8024 8725: contig of 702 bp in length  
8726 8825: gap of 100 bp  
8826 9534: contig of 709 bp in length  
9535 9634: gap of 100 bp  
9635 10350: contig of 716 bp in length  
10351 10450: gap of 100 bp  
10451 11147: contig of 697 bp in length  
11148 11247: gap of 100 bp  
11248 11947: contig of 700 bp in length  
11948 12047: gap of 100 bp  
12048 12725: contig of 678 bp in length  
12726 12825: gap of 100 bp  
12826 13545: contig of 720 bp in length  
13546 13645: gap of 100 bp  
13646 14346: contig of 701 bp in length  
14347 14446: gap of 100 bp  
14447 15146: contig of 700 bp in length  
15147 15246: gap of 100 bp  
15247 15945: contig of 699 bp in length  
15946 16045: gap of 100 bp  
16046 16731: contig of 686 bp in length  
16732 16831: gap of 100 bp  
16832 17536: contig of 705 bp in length  
17537 17636: gap of 100 bp  
17637 18336: contig of 700 bp in length  
18337 18437: gap of 100 bp  
18438 19114: contig of 678 bp in length  
19115 19214: gap of 100 bp  
19215 19913: contig of 699 bp in length  
19914 20013: gap of 100 bp  
20014 20686: contig of 673 bp in length  
20687 20786: gap of 100 bp  
20787 21497: contig of 711 bp in length  
21498 21597: gap of 100 bp  
21598 22267: contig of 670 bp in length  
22268 22367: gap of 100 bp  
22368 23059: contig of 692 bp in length  
23060 23159: gap of 100 bp  
23160 23864: contig of 705 bp in length  
23865 23964: gap of 100 bp  
23965 24667: contig of 703 bp in length  
24668 24767: gap of 100 bp  
24768 25484: contig of 717 bp in length  
25485 25584: gap of 100 bp  
25585 26272: contig of 688 bp in length  
26273 26372: gap of 100 bp  
26373 27068: contig of 696 bp in length  
27069 27168: gap of 100 bp  
27169 27870: contig of 702 bp in length  
27871 27970: gap of 100 bp  
27971 28677: contig of 707 bp in length  
28678 28777: gap of 100 bp

\* 28778 29479: contig of 702 bp in length  
29480 29579: gap of 100 bp  
29580 30274: contig of 695 bp in length  
30275 30374: gap of 100 bp  
30375 31083: contig of 709 bp in length  
31084 31183: gap of 100 bp  
31184 31884: contig of 701 bp in length  
31885 31984: gap of 100 bp  
31985 32686: contig of 702 bp in length  
32687 32786: gap of 100 bp  
32787 33500: contig of 714 bp in length  
33501 33600: gap of 100 bp  
33601 34307: contig of 707 bp in length  
34308 34407: gap of 100 bp  
34408 35097: contig of 690 bp in length  
35098 35197: gap of 100 bp  
35198 35899: contig of 702 bp in length  
35900 35999: gap of 100 bp  
36000 36692: contig of 693 bp in length  
36693 36792: gap of 100 bp  
36793 37491: contig of 699 bp in length  
37492 37591: gap of 100 bp  
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46251 46350: gap of 100 bp  
46351 47056: contig of 706 bp in length  
47057 47156: gap of 100 bp  
47157 47860: contig of 704 bp in length  
47861 47960: gap of 100 bp  
47961 48657: contig of 697 bp in length  
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48758 49457: contig of 700 bp in length  
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49558 50267: contig of 710 bp in length  
50268 50367: gap of 100 bp  
50368 51067: contig of 700 bp in length  
51068 51167: gap of 100 bp  
51168 51861: contig of 694 bp in length  
51862 51961: gap of 100 bp  
51962 52644: contig of 683 bp in length  
52645 52744: gap of 100 bp  
52745 53426: contig of 682 bp in length  
53427 53526: gap of 100 bp  
53527 54224: contig of 698 bp in length  
54225 54324: gap of 100 bp  
54325 55019: contig of 695 bp in length

Query Match 6 CCUGAGAGNNNNNN 18  
Best Local Similarity 92.3%; Score 13; DB 2; Length 56611;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Db 45433 CCUGAGAGNNNNNN 45445

RESULT 146  
AC101344  
LOCUS  
DEFINITION Mus musculus clone RP23-110N1, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC101344  
VERSION AC101344.1 GI:17060119  
KEYWORDS HTG, HTGS PHASEO.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 57736)  
Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
Mus musculus, clone RP23-110N1  
JOURNAL  
TITLE Unpublished  
AUTHORS 2 (bases 1 to 57736)  
Anderson, S., Barna, N., Nusbaum, C., Lander, E., Ali, A., Allen, N.,  
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,  
Choepel, T., Colangelo, M., Collins, S., Collymore, A., Cook, A.,  
Cooke, P., Deatellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S.,  
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,  
Gande, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,  
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,  
Jones, C., Kamat, A., Karatas, A., Kells, C., Lacroque, K.,  
Lamazares, R., Landers, T., Lehotzky, J., Levine, R., Liu, G.,  
Maclean, C., MacDonald, P., Major, J., Marguis, N., Matthews, C.,  
McCarthy, M., Macdonald, P., McKernan, K., McPheters, R., Meldrum, J.,  
Meneus, L., Mihova, T., Mlenka, V., Murphy, T., Naylor, J., Nguyen, C.,  
Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D.,  
Oliver, J., Peterson, K., Phunhthang, P., Pierre, N., Pollara, V.,  
Raymond, C., Retter, M., Rieback, M., Riley, R., Rise, C., Rogov, P.,  
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Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,  
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L16494  
Center clone name: 110\_N\_1  
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\* NOTE: This record contains 74 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlaid relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
\* 1 765: contig of 765 bp in length  
\* 766 865: gap of 100 bp  
\* 866 1545: contig of 680 bp in length  
\* 1546 1645: gap of 100 bp  
\* 1646 2332: contig of 687 bp in length  
\* 2333 2432: gap of 100 bp  
\* 2433 3120: contig of 688 bp in length

\* 3121 3220: gap of 100 bp  
\* 3221 3891: contig of 671 bp in length  
\* 3891 3991: gap of 100 bp  
\* 3992 4682: contig of 691 bp in length  
\* 4683 4783: gap of 100 bp  
\* 4783 5426: contig of 644 bp in length  
\* 5427 5526: gap of 100 bp  
\* 5527 6206: contig of 680 bp in length  
\* 6207 6306: gap of 100 bp  
\* 6307 6967: contig of 661 bp in length  
\* 6968 7067: gap of 100 bp  
\* 7068 7752: contig of 695 bp in length  
\* 7763 7862: gap of 100 bp  
\* 7863 8542: contig of 680 bp in length  
\* 8543 8643: gap of 100 bp  
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\* 10908 11097: gap of 100 bp  
\* 11098 11697: contig of 690 bp in length  
\* 11698 11797: gap of 100 bp  
\* 11798 12480: contig of 683 bp in length  
\* 12481 12580: gap of 100 bp  
\* 12581 13251: contig of 671 bp in length  
\* 13252 13351: gap of 100 bp  
\* 13352 14007: contig of 656 bp in length  
\* 14008 14107: gap of 100 bp  
\* 14108 14768: contig of 661 bp in length  
\* 14769 15567: gap of 100 bp  
\* 15568 15657: contig of 689 bp in length  
\* 15658 16340: gap of 100 bp  
\* 16341 16440: contig of 683 bp in length  
\* 16441 17082: contig of 642 bp in length  
\* 17083 17182: gap of 100 bp  
\* 17183 17665: contig of 683 bp in length  
\* 17666 17965: gap of 100 bp  
\* 17966 18629: contig of 664 bp in length  
\* 18630 18729: gap of 100 bp  
\* 18730 19419: contig of 690 bp in length  
\* 19420 19519: gap of 100 bp  
\* 19520 20213: contig of 694 bp in length  
\* 20214 20313: gap of 100 bp  
\* 20314 20997: contig of 684 bp in length  
\* 20998 21097: gap of 100 bp  
\* 21098 21775: contig of 678 bp in length  
\* 21776 21875: gap of 100 bp  
\* 21876 22582: contig of 707 bp in length  
\* 22583 22682: gap of 100 bp  
\* 22683 23364: contig of 682 bp in length  
\* 23365 23464: gap of 100 bp  
\* 23465 24134: contig of 670 bp in length  
\* 24135 24234: gap of 100 bp  
\* 24235 24889: contig of 655 bp in length  
\* 24890 24989: gap of 100 bp  
\* 24990 25678: contig of 669 bp in length  
\* 25679 25778: gap of 100 bp  
\* 25779 26461: contig of 663 bp in length  
\* 26462 26561: gap of 100 bp  
\* 26562 27235: contig of 674 bp in length  
\* 27236 27335: gap of 100 bp  
\* 27336 28014: contig of 679 bp in length  
\* 28015 28114: gap of 100 bp  
\* 28115 28803: contig of 689 bp in length  
\* 28804 28903: gap of 100 bp  
\* 28904 29573: contig of 670 bp in length  
\* 29574 29674: gap of 100 bp  
\* 29674 30358: contig of 685 bp in length  
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\* 31144 31243: gap of 100 bp

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* 31244 31942: contig of 639 bp in length
* 31943 32042: gap of 100 bp
* 32043 32740: contig of 638 bp in length
* 32741 32840: gap of 100 bp
* 32841 33507: contig of 667 bp in length
* 33508 33607: gap of 100 bp
* 33608 34313: contig of 706 bp in length
* 34314 34413: gap of 100 bp
* 34414 35057: contig of 644 bp in length
* 35058 35157: gap of 100 bp
* 35158 35843: contig of 686 bp in length
* 35844 35943: gap of 100 bp
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* 36720 37414: contig of 635 bp in length
* 37415 37514: gap of 100 bp
* 37515 38206: contig of 632 bp in length
* 38207 38306: gap of 100 bp
* 38307 38990: contig of 684 bp in length
* 38991 39090: gap of 100 bp
* 39091 39774: contig of 684 bp in length
* 39775 39874: gap of 100 bp
* 39875 40579: contig of 705 bp in length
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* 42098 42197: gap of 100 bp
* 42198 42867: contig of 670 bp in length
* 42868 42967: gap of 100 bp
* 42968 43740: contig of 673 bp in length
* 43641 43740: gap of 100 bp
* 43741 44412: contig of 672 bp in length
* 44413 44512: gap of 100 bp
* 44513 45213: contig of 701 bp in length
* 45214 45313: gap of 100 bp
* 45314 45998: contig of 685 bp in length
* 45999 46098: gap of 100 bp
* 46099 46804: contig of 706 bp in length
* 46805 46904: gap of 100 bp
* 46905 47593: contig of 689 bp in length
* 47594 47693: gap of 100 bp
* 47694 48371: contig of 678 bp in length
* 48372 48471: gap of 100 bp
* 48472 49160: contig of 689 bp in length
* 49161 49260: gap of 100 bp
* 49261 49926: contig of 666 bp in length
* 49927 50026: gap of 100 bp
* 50027 50718: contig of 692 bp in length
* 50719 50818: gap of 100 bp
* 50819 51493: contig of 675 bp in length
* 51494 51593: gap of 100 bp
* 51594 52247: contig of 654 bp in length
* 52248 52347: gap of 100 bp
* 52348 53066: contig of 719 bp in length
* 53067 53167: gap of 100 bp
* 53167 53849: contig of 683 bp in length
* 53850 53949: gap of 100 bp

Query Match      72.2%: Score 13; DB 2; Length 57736;
Best Local Similarity 92.3%: Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 6 CCUSGAGNNNNNN 18
Db 33501 CCTGAGNNNNNN 33513

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RESULT 147
AC127514 58456 bp DNA linear HTG 17-JUL-2002
LOCUS AC127514 Homo sapiens chromosome 17 clone RP11-246P6 map 17, LOW-PASS
DEFINITION SEQUENCE SAMPLING.

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ACCESSION AC127514
VERSION AC127514.1 GI:21886933
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 58456)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 17, clone RP11-246P6
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 58456)
AUTHORS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguski,V., Boukhalter,B.,
Camata,J., Chang,J., Chazaro,B., Choquet,Y., Collins,A.,
Cook,A., Cooke,P., Dearlano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferrer,P., Fitzgerald,M., Gage,D., Galagan,J.,
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Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrum,V., Meneus,L., Minova,T., Mieng,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupack,R., Seaman,S., Severy,P.,
Sulth,C., Spencer,B., Strange-Thomann,N., Stojanovic,N., Talamas,U.,
Tefaye,S., Theodore,J., Topnam,K., Travers,W., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (17-JUL-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L27495
Center clone name: 246_P_6
-----
* NOTE: This record contains 71 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
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* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
737 736: contig of 736 bp in length
837 836: gap of 100 bp
1577 837: contig of 741 bp in length
1678 1577: gap of 100 bp
1678 1677: gap of 100 bp
2388 1678: contig of 710 bp in length
2487 2388: gap of 100 bp
2488 2487: gap of 100 bp
3212 2488: contig of 724 bp in length
3211 3212: gap of 100 bp
3312 3211: contig of 729 bp in length
4041 3312: gap of 100 bp
4141 4041: gap of 100 bp
4141 4848: contig of 708 bp in length
4849 4141: gap of 100 bp
4949 4849: gap of 100 bp
5659 4949: contig of 711 bp in length
5759 5659: gap of 100 bp
5760 5759: contig of 738 bp in length
6597 5760: gap of 100 bp
6598 6597: contig of 728 bp in length
7325 6598: contig of 728 bp in length

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* 7326 7425: gap of 100 bp
* 7426 8156: contig of 731 bp in length
* 8157 8256: gap of 100 bp
* 8257 8920: contig of 664 bp in length
* 8921 9020: gap of 100 bp
* 9021 9742: contig of 722 bp in length
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* 9843 10567: contig of 725 bp in length
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* 11503 12235: contig of 733 bp in length
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* 12336 13066: contig of 731 bp in length
* 13067 13166: gap of 100 bp
* 13167 13902: contig of 736 bp in length
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* 14733 14832: gap of 100 bp
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* 22281 23013: contig of 733 bp in length
* 23014 23113: gap of 100 bp
* 23114 23830: contig of 717 bp in length
* 23831 23930: gap of 100 bp
* 23931 24646: contig of 716 bp in length
* 24647 24746: gap of 100 bp
* 24747 25482: contig of 736 bp in length
* 25483 25582: gap of 100 bp
* 25583 26308: contig of 726 bp in length
* 26309 26408: gap of 100 bp
* 26409 27125: contig of 717 bp in length
* 27126 27225: gap of 100 bp
* 27226 27954: contig of 729 bp in length
* 27955 28054: gap of 100 bp
* 28055 28780: contig of 726 bp in length
* 28781 28880: gap of 100 bp
* 28881 29603: contig of 723 bp in length
* 29604 29703: gap of 100 bp
* 29704 30427: contig of 724 bp in length
* 30428 30527: gap of 100 bp
* 30529 31250: contig of 723 bp in length
* 31251 31350: gap of 100 bp
* 31351 32061: contig of 711 bp in length
* 32062 32161: gap of 100 bp
* 32162 32889: contig of 728 bp in length
* 32890 32989: gap of 100 bp
* 32990 33695: contig of 706 bp in length
* 33696 33795: gap of 100 bp
* 33796 34510: contig of 715 bp in length
* 34511 34610: gap of 100 bp
* 34611 35333: contig of 723 bp in length
* 35334 35433: gap of 100 bp
* 35434 36165: contig of 732 bp in length
* 36166 36265: gap of 100 bp
* 36266 36997: contig of 732 bp in length
* 36998 37097: gap of 100 bp

```

```

* 37098 37823: contig of 726 bp in length
* 37824 37923: gap of 100 bp
* 37924 38657: contig of 734 bp in length
* 38658 38757: gap of 100 bp
* 38758 39488: contig of 730 bp in length
* 39489 39587: gap of 100 bp
* 39588 40312: contig of 725 bp in length
* 40313 40412: gap of 100 bp
* 40413 41140: contig of 728 bp in length
* 41141 41240: gap of 100 bp
* 41241 41965: contig of 725 bp in length
* 41966 42065: gap of 100 bp
* 42066 42800: contig of 735 bp in length
* 42801 42900: gap of 100 bp
* 42901 43637: contig of 737 bp in length
* 43638 43737: gap of 100 bp
* 43738 44479: contig of 742 bp in length
* 44480 44579: gap of 100 bp
* 44580 45314: contig of 735 bp in length
* 45315 45414: gap of 100 bp
* 45415 46091: contig of 677 bp in length
* 46092 46191: gap of 100 bp
* 46192 46895: contig of 704 bp in length
* 46896 46995: gap of 100 bp
* 46996 47724: contig of 728 bp in length
* 47725 47824: gap of 100 bp
* 47825 48543: contig of 719 bp in length
* 48544 48643: gap of 100 bp
* 48644 49371: contig of 728 bp in length
* 49372 49471: gap of 100 bp
* 49472 50206: contig of 735 bp in length
* 50207 50306: gap of 100 bp
* 50307 51019: contig of 713 bp in length
* 51020 51119: gap of 100 bp
* 51120 51846: contig of 727 bp in length
* 51847 51946: gap of 100 bp
* 51947 52689: contig of 743 bp in length
* 52690 52789: gap of 100 bp
* 52790 53515: contig of 726 bp in length
* 53516 53615: gap of 100 bp
* 53616 54327: contig of 712 bp in length
* 54328 54427: gap of 100 bp
* 54428 55158: contig of 731 bp in length
* 55159 55258: gap of 100 bp
* 55259 55988: contig of 730 bp in length
* 55989 56088: gap of 100 bp
* 56089 56815: contig of 727 bp in length
* 56816 56915: gap of 100 bp
* 56916 57633: contig of 718 bp in length
* 57634 57733: gap of 100 bp
* 57734 58456: contig of 723 bp in length.

Query Match      72.2%  Score 13;  DB 2;  Length 58456;
Best Local Similarity 92.3%  Pred. No. 4.6e+02;
Matches 12;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

QY      6 CCUGAGNNNNNN 18
Db      15546 CCTGGAGNNNNNN 15558

RESULT 148
AC100999
LOCUS      AC100999      59550 bp      DNA      linear      HTG 23-NOV-2001
DEFINITION Mus musculus clone RP23-77A24, LOW-PASS SEQUENCE SAMPLING.
ACCESSION  AC100999
VERSION    AC100999.1 GI:17059773
KEYWORDS  HTG; HTGS PHASED.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 59550)

```



AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
TITLE Mus musculus, clone RP23-77A24  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 59550)  
AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,  
Anderson, S., Barina, N., Baerlein, V., Boguslavsky, L., Boukhalter, B.,  
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,  
Chapel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,  
Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fato, S.,  
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,  
Gardes, B., Heath, A., Horvath, L., Hulme, W., Iliev, I., Johnson, R.,  
Jones, C., Kamat, A., Karatsas, A., Kelle, C., Labocque, K.,  
Lamaze, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,  
Maclean, C., Macdonald, P., Major, J., Margulis, N., Matthews, C.,  
McCarthy, M., McEwan, P., McKernan, K., McKeeters, R., Meldrum, J.,  
Menues, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,  
Nobu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D.,  
Oliver, J., Peterson, K., Phukhang, P., Pierre, N., Pollara, V.,  
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,  
Roman, J., Rosetti, M., Roy, A., Santoe, R., Schauer, S., Schupbach, R.,  
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
Strauss, A., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J.,  
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,  
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE Direct Submission  
JOURNAL Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome  
COMMENT Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)  
Project Information  
Center project name: 77\_A\_24  
Center clone name: 77\_A\_24

NOTE: This record contains 73 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 687: contig of 687 bp in length  
\* 688 787: gap of 100 bp  
\* 788 1515: contig of 728 bp in length  
\* 1516 2333: contig of 738 bp in length  
\* 2334 3171: contig of 718 bp in length  
\* 3172 3271: gap of 100 bp  
\* 3272 3969: contig of 698 bp in length  
\* 3970 4069: gap of 100 bp  
\* 4070 4774: contig of 705 bp in length  
\* 4775 4874: gap of 100 bp  
\* 4875 5593: contig of 719 bp in length  
\* 5594 5693: gap of 100 bp  
\* 5694 6411: contig of 718 bp in length  
\* 6412 6511: gap of 100 bp  
\* 6512 7228: contig of 717 bp in length  
\* 7229 7329: gap of 100 bp  
\* 7330 8053: contig of 725 bp in length  
\* 8054 8154: gap of 100 bp  
\* 8155 8875: contig of 722 bp in length

8876 8975: gap of 100 bp  
\* 8976 9681: contig of 706 bp in length  
\* 9682 9781: gap of 100 bp  
\* 9782 10484: contig of 703 bp in length  
\* 10485 10584: gap of 100 bp  
\* 10585 11283: contig of 698 bp in length  
\* 11283 11383: gap of 100 bp  
\* 11383 12089: contig of 706 bp in length  
\* 12089 12188: gap of 100 bp  
\* 12188 12890: contig of 702 bp in length  
\* 12890 12990: gap of 100 bp  
\* 12991 13716: contig of 726 bp in length  
\* 13716 13815: gap of 100 bp  
\* 13815 13917: contig of 731 bp in length  
\* 13917 14547: contig of 721 bp in length  
\* 14547 14647: gap of 100 bp  
\* 14648 15367: contig of 720 bp in length  
\* 15368 15467: gap of 100 bp  
\* 15468 16206: contig of 739 bp in length  
\* 16207 16306: gap of 100 bp  
\* 16307 17046: contig of 740 bp in length  
\* 17047 17146: gap of 100 bp  
\* 17147 17838: contig of 692 bp in length  
\* 17839 17938: gap of 100 bp  
\* 17939 18639: contig of 701 bp in length  
\* 18640 18739: gap of 100 bp  
\* 18740 19444: contig of 705 bp in length  
\* 19445 19544: gap of 100 bp  
\* 19545 20261: contig of 717 bp in length  
\* 20262 20361: gap of 100 bp  
\* 20362 21087: contig of 725 bp in length  
\* 21087 21187: gap of 100 bp  
\* 21187 21918: contig of 731 bp in length  
\* 21918 22017: gap of 100 bp  
\* 22018 22754: contig of 736 bp in length  
\* 22755 22853: gap of 100 bp  
\* 22854 23561: contig of 707 bp in length  
\* 23561 24405: gap of 100 bp  
\* 24406 24505: contig of 745 bp in length  
\* 24506 25235: gap of 100 bp  
\* 25236 25335: contig of 730 bp in length  
\* 25336 26069: contig of 734 bp in length  
\* 26070 26169: gap of 100 bp  
\* 26170 26872: contig of 703 bp in length  
\* 26873 26972: gap of 100 bp  
\* 26973 27680: contig of 708 bp in length  
\* 27681 27781: gap of 100 bp  
\* 27781 28497: contig of 716 bp in length  
\* 28497 28597: gap of 100 bp  
\* 28597 29328: contig of 732 bp in length  
\* 29329 29428: gap of 100 bp  
\* 29429 30157: contig of 729 bp in length  
\* 30158 30257: gap of 100 bp  
\* 30258 30994: contig of 737 bp in length  
\* 30995 31094: gap of 100 bp  
\* 31095 31834: contig of 740 bp in length  
\* 31835 31934: gap of 100 bp  
\* 31935 32578: contig of 644 bp in length  
\* 32579 32678: gap of 100 bp  
\* 32679 33406: contig of 728 bp in length  
\* 33407 33506: gap of 100 bp  
\* 33507 34225: contig of 719 bp in length  
\* 34226 34325: gap of 100 bp  
\* 34326 35030: contig of 705 bp in length  
\* 35031 35130: gap of 100 bp  
\* 35131 35831: contig of 701 bp in length  
\* 35832 35931: gap of 100 bp  
\* 35932 36637: contig of 706 bp in length  
\* 36638 36737: gap of 100 bp  
\* 36738 37451: contig of 714 bp in length  
\* 37452 37551: gap of 100 bp  
\* 37552 38271: contig of 720 bp in length  
\* 38272 38371: gap of 100 bp

```

* 38372 39116: contig of 745 bp in length
* 39117 39216: gap of 100 bp
* 39217 39910: contig of 694 bp in length
* 39911 40010: gap of 100 bp
* 40011 40725: contig of 715 bp in length
* 40726 40825: gap of 100 bp
* 40826 41534: contig of 709 bp in length
* 41535 41634: gap of 100 bp
* 41635 42321: contig of 687 bp in length
* 42322 42421: gap of 100 bp
* 42422 43147: contig of 726 bp in length
* 43148 43247: gap of 100 bp
* 43248 43975: contig of 728 bp in length
* 43976 44075: gap of 100 bp
* 44076 44821: contig of 746 bp in length
* 44822 44921: gap of 100 bp
* 44922 45648: contig of 727 bp in length
* 45649 45749: gap of 100 bp
* 45749 46490: contig of 742 bp in length
* 46491 46590: gap of 100 bp
* 46591 47328: contig of 738 bp in length
* 47329 47428: gap of 100 bp
* 47429 48142: contig of 714 bp in length
* 48143 48242: gap of 100 bp
* 48243 48936: contig of 694 bp in length
* 48937 49035: gap of 100 bp
* 49037 49748: contig of 712 bp in length
* 49749 49848: gap of 100 bp
* 49849 50559: contig of 711 bp in length
* 50560 51384: contig of 725 bp in length
* 51385 51484: gap of 100 bp
* 51485 52217: contig of 733 bp in length
* 52218 52317: gap of 100 bp
* 52318 53048: contig of 731 bp in length
* 53049 53149: gap of 100 bp
* 53149 53833: contig of 684 bp in length
* 53833 53933: gap of 100 bp
* 53933 54641: contig of 709 bp in length
* 54642 54741: gap of 100 bp
* 54742 55432: contig of 691 bp in length
* 55433 55533: gap of 100 bp
* 55533 56242: contig of 710 bp in length
* 56243 56342: gap of 100 bp

```

```

Query Match      72.2%  Score 13; DB 2; Length 59550;
Best Local Similarity 92.3%  Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      6 CCUGAGNNNNNN 18
Db      27674 CCTGAGNNNNNN 27686

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RESULT 149
AC087334
LOCUS    Homo sapiens chromosome 17 clone RP11-73H6 map 17, LOW-PASS
DEFINITION
SEQUENCE SAMPLING.
AC087334      60323 bp      DNA      linear      HTG 30-DEC-2001
AC087334      AC087334.3      GI:17998705
VERSION      AC087334.3      GI:17998705
KEYWORDS     HTG: HTGS PHASE0.
SOURCE      Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 60323)
AUTHORS     Birren,B., Linton,L., Nuebaum,C. and Lander,E.
TITLE       Homo sapiens chromosome 17, clone RP11-73H6
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 60323)
AUTHORS     Birren,B., Linton,L., Nuebaum,C., Lander,E., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A.,

```

# TITLE JOURNAL COMMENT

Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Glnde,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Karatas,A., Lakoque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., Maclean,C., Macdonald,P., Margulis,N., Matthews,C., McCarthy,J., McEwan,P., McKernan,K., McPheters,R., Meldrim,T., Menes,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R., Seaman,S., Severy,P., Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission  
Submitted (28-DEC-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Dec 30, 2001 this sequence version replaced gi:12658045.  
All repeats were identified using RepeatMasker:  
Smit,A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research  
Genome Center  
Center code: MIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
Center project name: L10327  
Center clone name: 73\_H\_5

\* NOTE: This record contains 72 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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* 1
* 723 722: contig of 722 bp in length
* 823 822: gap of 100 bp
* 1576 1575: contig of 753 bp in length
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* 2435 2434: contig of 759 bp in length
* 2535 2534: gap of 100 bp
* 3263 3262: contig of 728 bp in length
* 3363 3362: gap of 100 bp
* 4098 4097: contig of 735 bp in length
* 4198 4197: gap of 100 bp
* 4952 4951: contig of 754 bp in length
* 5052 5051: gap of 100 bp
* 5810 5810: contig of 759 bp in length
* 5910 5910: gap of 100 bp
* 5911 6680: contig of 770 bp in length
* 6681 6780: gap of 100 bp
* 6781 7511: contig of 731 bp in length
* 7512 7611: gap of 100 bp
* 7612 8341: contig of 730 bp in length
* 8342 8441: gap of 100 bp
* 8442 9174: contig of 733 bp in length
* 9175 9274: gap of 100 bp
* 9275 10016: contig of 742 bp in length
* 10017 10116: gap of 100 bp
* 10117 10860: contig of 744 bp in length
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* 10961 11709: contig of 749 bp in length

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* 11710 11809: gap of 100 bp
* 11810 12383: contig of 574 bp in length
* 12384 12483: gap of 100 bp
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* 13345 14041: contig of 697 bp in length
* 14042 14141: gap of 100 bp
* 14142 14894: contig of 753 bp in length
* 14895 14994: gap of 100 bp
* 14995 15751: contig of 757 bp in length
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* 15852 16575: contig of 724 bp in length
* 16576 16766: gap of 100 bp
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* 17402 17501: gap of 100 bp
* 17502 18237: contig of 736 bp in length
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* 19074 19173: gap of 100 bp
* 19174 19907: contig of 734 bp in length
* 19908 20007: gap of 100 bp
* 20008 20762: contig of 755 bp in length
* 20763 20862: gap of 100 bp
* 20863 21569: contig of 707 bp in length
* 21570 21669: gap of 100 bp
* 21670 22380: contig of 711 bp in length
* 22381 22480: gap of 100 bp
* 22481 23231: contig of 751 bp in length
* 23232 23331: gap of 100 bp
* 23332 24101: contig of 770 bp in length
* 24102 24201: gap of 100 bp
* 24202 24959: contig of 758 bp in length
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* 25060 25780: contig of 721 bp in length
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* 25881 26614: contig of 734 bp in length
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* 26715 27436: contig of 722 bp in length
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* 27537 28277: contig of 741 bp in length
* 28278 28377: gap of 100 bp
* 28378 29108: contig of 731 bp in length
* 29109 29208: gap of 100 bp
* 29209 29963: contig of 755 bp in length
* 29964 30063: gap of 100 bp
* 30064 30831: contig of 768 bp in length
* 30832 30931: gap of 100 bp
* 30932 31641: contig of 710 bp in length
* 31642 31741: gap of 100 bp
* 31742 32490: contig of 749 bp in length
* 32491 32590: gap of 100 bp
* 32591 33338: contig of 748 bp in length
* 33339 33438: gap of 100 bp
* 33439 34170: contig of 732 bp in length
* 34171 34270: gap of 100 bp
* 34271 35010: contig of 740 bp in length
* 35011 35110: gap of 100 bp
* 35111 35936: contig of 826 bp in length
* 35937 36036: gap of 100 bp
* 36037 36800: contig of 764 bp in length
* 36801 36900: gap of 100 bp
* 36901 37632: contig of 732 bp in length
* 37633 37732: gap of 100 bp
* 37733 38436: contig of 704 bp in length
* 38437 38536: gap of 100 bp
* 38537 39309: contig of 773 bp in length
* 39310 39409: gap of 100 bp
* 39410 40153: contig of 744 bp in length
* 40154 40253: gap of 100 bp
* 40254 40981: contig of 728 bp in length
* 40982 41081: gap of 100 bp
* 41082 41819: contig of 738 bp in length
* 41819: gap of 100 bp

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* 41920 42646: contig of 727 bp in length
* 42647 42746: gap of 100 bp
* 42747 43477: contig of 731 bp in length
* 43478 43577: gap of 100 bp
* 43578 44310: contig of 733 bp in length
* 44311 44410: gap of 100 bp
* 44411 45176: contig of 766 bp in length
* 45177 45276: gap of 100 bp
* 45277 46043: contig of 767 bp in length
* 46044 46143: gap of 100 bp
* 46144 46849: contig of 706 bp in length
* 46850 46949: gap of 100 bp
* 46950 47701: contig of 752 bp in length
* 47702 47801: gap of 100 bp
* 47802 48543: contig of 742 bp in length
* 48544 48643: gap of 100 bp
* 48644 49411: contig of 768 bp in length
* 49412 49511: gap of 100 bp
* 49512 50236: contig of 725 bp in length
* 50237 50336: gap of 100 bp
* 50337 51067: contig of 731 bp in length
* 51068 51167: gap of 100 bp
* 51168 51895: contig of 728 bp in length
* 51896 51995: gap of 100 bp
* 51996 52703: contig of 708 bp in length
* 52704 52803: gap of 100 bp
* 52804 53550: contig of 747 bp in length
* 53551 53650: gap of 100 bp
* 53651 54364: contig of 714 bp in length
* 54365 54464: gap of 100 bp
* 54465 55227: contig of 763 bp in length
* 55228 55327: gap of 100 bp
* 55328 56118: contig of 791 bp in length
* 56119 56218: gap of 100 bp
* 56219 56961: contig of 743 bp in length
* 56962 57061: gap of 100 bp
* 57062 57773: contig of 712 bp in length

Query Match      72.2%  Score 13; DB 2; Length 60323;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCUGAGNNNNNN 18
Db      46037 CCTGGAGNNNNNN 46049

RESULT 150
LOCUS      RN499P20/c
DEFINITION Rattus norvegicus clone RPCI-31-499P20 strain Brown Norway, WORKING
ACCESSION  AL603720.2 GI:17154523
VERSION     HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS    Rattus norvegicus (Norway rat)
SOURCE      Rattus norvegicus
ORGANISM    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
REFERENCE   1
AUTHORS     Sudbrak, R., Borzys, K., Mueller, I., Klages, S., Kosiura, A.,
            Walter, L., Guenther, E., Hurt, P., Lehrach, H., Himmelbauer, H. and
            Reinhardt, R.
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 61582)
AUTHORS     MolGENR.
JOURNAL     Direct Subsequen
            Submitted (10-AUG-2001) MPMG, Abt. Lehrach, Max Planck Institut
            fuer Molekulare Genetik, Ihnestrasse 73, Berlin, 14195 Germany
            On Nov 29, 2001 this sequence version replaced gi:15149582.
COMMENT     contig 01      1. .171
            contig 02      272. .495

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contig 03 596. .853  
 contig 04 954. .1040  
 contig 05 1141. .1441  
 contig 06 1542. .1682  
 contig 07 1783. .2107  
 contig 08 2208. .2576  
 contig 09 2677. .2776  
 contig 10 2877. .12941  
 contig 11 13042. .14190  
 contig 12 14291. .14828  
 contig 13 14929. .15502  
 contig 14 15603. .21365  
 contig 15 21466. .26703  
 contig 16 26804. .32901  
 contig 17 33002. .40856  
 contig 18 40957. .49047  
 contig 19 49148. .50018  
 contig 20 50119. .50909  
 contig 21 51010. .51922  
 contig 22 52023. .53560  
 contig 23 53661. .54827  
 contig 24 54928. .58361  
 contig 25 58462. .61582.

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 25 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of 'N', but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 171: contig of 171 bp in length  
 172 271: gap of 100 bp  
 272 495: contig of 224 bp in length  
 496 595: gap of 100 bp  
 596 853: contig of 258 bp in length  
 854 954: gap of 100 bp  
 954 1040: contig of 87 bp in length  
 1041 1141: gap of 100 bp  
 1141 1441: contig of 301 bp in length  
 1442 1541: gap of 100 bp  
 1542 1682: contig of 141 bp in length  
 1683 1782: gap of 100 bp  
 1783 2107: contig of 325 bp in length  
 2108 2207: gap of 100 bp  
 2208 2576: contig of 365 bp in length  
 2577 2676: gap of 100 bp  
 2677 2776: contig of 100 bp in length  
 2777 2876: gap of 100 bp  
 2877 12941: contig of 10065 bp in length  
 12942 13041: gap of 100 bp  
 13042 14190: contig of 1149 bp in length  
 14191 14290: gap of 100 bp  
 14291 14828: contig of 538 bp in length  
 14829 14928: gap of 100 bp  
 14929 15502: contig of 574 bp in length  
 15503 15603: gap of 100 bp  
 15604 21365: contig of 5763 bp in length  
 21366 21465: gap of 100 bp  
 21466 26703: contig of 5238 bp in length  
 26704 26803: gap of 100 bp  
 26804 32901: contig of 6098 bp in length  
 32902 33001: gap of 100 bp  
 33002 40856: contig of 7855 bp in length  
 40857 40956: gap of 100 bp  
 40957 49047: contig of 8091 bp in length  
 49048 49147: gap of 100 bp  
 49148 50018: contig of 871 bp in length  
 50019 50118: gap of 100 bp  
 50119 50909: contig of 791 bp in length  
 51010 51922: gap of 100 bp  
 51923 52022: contig of 913 bp in length

## FEATURES

Source  
 1. 61582  
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 /mol\_type="genomic DNA"  
 /strain="Brown Norway"  
 /db\_xref="taxon:10116"  
 /clone="RPCT-31-49920"  
 /note="R1 region on chromosome 20"

## ORIGIN

Query Match 72.2% Score 13; DB 2; Length 61582;  
 Best Local Similarity 92.3% Pred. No. 4,6e+02;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

6 CCUGAGNNNNN 18  
 602 CCTGAGNNNNN 590

## RESULT 151

## AC100819

## LOCUS

AC100819 61837 bp DNA linear HTG 22-NOV-2001  
 Homo sapiens chromosome 8 clone RP11-94F15 map 8, LOW-PASS SEQUENCE

## DEFINITION

## SAMPLING

AC100819  
 AC100819.1 GI:17048189

## VERSION

HTG, HTGS PHASE0.

## KEYWORDS

HTG, HTGS PHASE0.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 61837)  
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.

## REFERENCE

Homo sapiens chromosome 8, clone RP11-94F15  
 Unpublished

## JOURNAL

Unpublished

## AUTHORS

Unpublished

## REFERENCES

Unpublished

## REFERENCES

Unpublished

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## REFERENCES

Unpublished

## REFERENCES

Unpublished

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: MIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L21504  
Center clone name: 94\_F\_15

\* NOTE: This record contains 76 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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677 676: contig of 676 bp in length  
777 776: gap of 100 bp  
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1490 1589: gap of 100 bp  
1590 2284: contig of 695 bp in length  
2285 2384: gap of 100 bp  
2385 3067: contig of 683 bp in length  
3068 3167: gap of 100 bp  
3168 3913: contig of 746 bp in length  
3914 4013: gap of 100 bp  
4014 4722: contig of 709 bp in length  
4723 4822: gap of 100 bp  
4823 5557: contig of 735 bp in length  
5558 5657: gap of 100 bp  
5659 6394: contig of 737 bp in length  
6395 6494: gap of 100 bp  
6495 7191: contig of 697 bp in length  
7192 7291: gap of 100 bp  
7292 8000: contig of 709 bp in length  
8001 8100: gap of 100 bp  
8101 8820: contig of 720 bp in length  
8821 8920: gap of 100 bp  
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9607 9706: gap of 100 bp  
9707 10420: contig of 714 bp in length  
10421 10520: gap of 100 bp  
10521 11257: contig of 736 bp in length  
11258 11356: gap of 100 bp  
11357 12072: contig of 716 bp in length  
12073 12172: gap of 100 bp  
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12896 12995: gap of 100 bp  
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13724 13823: gap of 100 bp  
13824 14540: contig of 717 bp in length  
14541 14640: gap of 100 bp  
14641 15354: contig of 714 bp in length  
15355 15455: gap of 100 bp  
15456 16162: contig of 708 bp in length  
16163 16262: gap of 100 bp  
16263 17043: contig of 781 bp in length  
17044 17143: gap of 100 bp  
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17852 17951: gap of 100 bp  
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18661 18760: gap of 100 bp  
18761 19454: contig of 694 bp in length  
19455 19554: gap of 100 bp  
19555 20289: contig of 735 bp in length  
20290 20389: gap of 100 bp  
20390 21125: contig of 736 bp in length  
21126 21225: gap of 100 bp  
21226 21962: contig of 737 bp in length  
21963 22062: gap of 100 bp

22063 22786: contig of 724 bp in length  
22787 22886: gap of 100 bp  
22887 23601: contig of 715 bp in length  
23602 23701: gap of 100 bp  
23702 24411: contig of 710 bp in length  
24412 24511: gap of 100 bp  
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26849 26948: gap of 100 bp  
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27679 27778: gap of 100 bp  
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28502 29322: contig of 721 bp in length  
29323 29422: gap of 100 bp  
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32629 33329: contig of 702 bp in length  
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39035 39134: gap of 100 bp  
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40635 40734: gap of 100 bp  
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42261 42360: gap of 100 bp  
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43049 43148: gap of 100 bp  
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43870 44697: gap of 100 bp  
44698 44797: contig of 728 bp in length  
44798 45523: gap of 100 bp  
45524 45623: contig of 726 bp in length  
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* 26092 26828: contig of 737 bp in length
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* 38713 39450: contig of 738 bp in length
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* 42832 42931: gap of 100 bp
* 42932 43665: contig of 735 bp in length
* 43666 43765: gap of 100 bp
* 43767 44518: contig of 752 bp in length
* 44519 44618: gap of 100 bp
* 44619 45365: contig of 747 bp in length
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* 45466 46213: contig of 748 bp in length
* 46214 46313: gap of 100 bp
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Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 27682 CCTGAGAGNNNNNN 27694

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VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

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Mus musculus clone RP23-17C18, LOW-PASS SEQUENCE SAMPLING.
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AC099931.1 GI:17047297
HTG; HTGS PHASE0.
Mus musculus (house mouse)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Birren, B., Linton, L., Nuebaum, C. and Lander, E.
Mus musculus, clone RP23-17C18
Unpublished
2 (bases 1 to 63831)
Anderson, S., Barina, N., Bastien, V., Boguslavsky, L., Bouhgalter, B.,
Brown, A., Camarata, J., Campiano, A., Chang, J., Chararo, B.,
Choedel, Y., Colangelo, M., Collins, S., Collamore, A., Cook, A.,
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Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L15577
Center clone name: 17_C_18

```

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* NOTE: This record contains 79 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.

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\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
1  
672 771: contig of 671 bp in length  
772 1489: contig of 718 bp in length  
1490 1589: gap of 100 bp  
1590 2277: contig of 688 bp in length  
2278 2377: gap of 100 bp  
2378 3081: contig of 704 bp in length  
3082 3181: gap of 100 bp  
3182 3897: contig of 716 bp in length  
3898 3997: gap of 100 bp  
3998 4714: contig of 717 bp in length  
4715 4814: gap of 100 bp  
4815 5525: contig of 711 bp in length  
5526 5625: gap of 100 bp  
5626 6335: contig of 710 bp in length  
6336 6435: gap of 100 bp  
6436 7151: contig of 716 bp in length  
7152 7251: gap of 100 bp  
7252 7958: contig of 707 bp in length  
7959 8058: gap of 100 bp  
8059 8771: contig of 713 bp in length  
8772 8871: gap of 100 bp  
8872 9555: contig of 684 bp in length  
9556 9655: gap of 100 bp  
9656 10360: contig of 705 bp in length  
10361 10460: gap of 100 bp  
10461 11163: contig of 703 bp in length  
11164 11263: gap of 100 bp  
11264 11962: contig of 699 bp in length  
11963 12062: gap of 100 bp  
12063 12774: contig of 712 bp in length  
12775 12874: gap of 100 bp  
12875 13575: contig of 701 bp in length  
13576 13675: gap of 100 bp  
13676 14383: contig of 708 bp in length  
14384 14483: gap of 100 bp  
14484 15197: contig of 714 bp in length  
15198 15297: gap of 100 bp  
15299 16007: contig of 710 bp in length  
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16919 17634: contig of 716 bp in length  
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18456 18555: gap of 100 bp  
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22505 22604: gap of 100 bp  
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23319 23418: gap of 100 bp  
23419 24139: contig of 721 bp in length  
24140 24239: gap of 100 bp  
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24954 25053: gap of 100 bp  
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25760 25859: gap of 100 bp  
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27371 27470: gap of 100 bp  
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\* 28185 28284: gap of 100 bp  
\* 28285 28990: contig of 706 bp in length  
\* 28991 29090: gap of 100 bp  
\* 29091 29789: contig of 699 bp in length  
\* 29790 29890: gap of 100 bp  
\* 29890 30605: contig of 716 bp in length  
\* 30606 30705: gap of 100 bp  
\* 30706 31423: contig of 718 bp in length  
\* 31424 32236: contig of 713 bp in length  
\* 32237 32336: gap of 100 bp  
\* 32337 33041: contig of 705 bp in length  
\* 33042 33141: gap of 100 bp  
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\* 33834 33933: gap of 100 bp  
\* 33934 34654: contig of 721 bp in length  
\* 34655 34754: gap of 100 bp  
\* 34755 35467: contig of 713 bp in length  
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\* 35568 36263: contig of 696 bp in length  
\* 36264 36363: gap of 100 bp  
\* 36364 37073: contig of 710 bp in length  
\* 37074 37173: gap of 100 bp  
\* 37174 37894: contig of 721 bp in length  
\* 37895 37994: gap of 100 bp  
\* 37995 38709: contig of 715 bp in length  
\* 38710 38809: gap of 100 bp  
\* 38810 39532: contig of 723 bp in length  
\* 39533 39632: gap of 100 bp  
\* 39633 40342: contig of 710 bp in length  
\* 40343 40442: gap of 100 bp  
\* 40443 41115: contig of 673 bp in length  
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\* 41216 41938: contig of 723 bp in length  
\* 41939 42038: gap of 100 bp  
\* 42039 42747: contig of 709 bp in length  
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\* 43552 43651: gap of 100 bp  
\* 43652 44361: contig of 710 bp in length  
\* 44362 44461: gap of 100 bp  
\* 44462 45138: contig of 677 bp in length  
\* 45139 45238: gap of 100 bp  
\* 45239 45943: contig of 705 bp in length  
\* 45944 46043: gap of 100 bp  
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\* 46859 47594: contig of 736 bp in length  
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\* 48511 49202: contig of 692 bp in length  
\* 49203 49302: gap of 100 bp  
\* 49303 50100: contig of 708 bp in length  
\* 50110 50110: gap of 100 bp  
\* 50111 50801: contig of 691 bp in length  
\* 50802 50901: gap of 100 bp  
\* 50902 51622: contig of 721 bp in length  
\* 51623 51722: gap of 100 bp  
\* 51723 52429: contig of 707 bp in length  
\* 52430 52529: gap of 100 bp  
\* 52530 53248: contig of 719 bp in length  
\* 53249 53348: gap of 100 bp  
\* 53349 54065: contig of 717 bp in length  
\* 54066 54165: gap of 100 bp  
\* 54166 54891: contig of 726 bp in length  
\* 54892 54991: gap of 100 bp  
\* 54992 55704: contig of 713 bp in length  
\* 55705 55804: gap of 100 bp

Query Match 72.2%; Score 13; DB 2; Length 63831;  
Best Local Similarity 92.3%; Pred. No. 4.6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



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 Db 58969 CCTGGAGNNNNNN 58961  
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 DEFINITION Mus musculus clone RP23-70E20, LOW-PASS SEQUENCE SAMPLING.  
 AC100902  
 VERSION AC100902.1 GI:17059676  
 KEYWORDS HTG; HTGS PHASEO.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;  
 1 (bases 1 to 64919)  
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
 Mus musculus, clone RP23-70E20  
 Unpublished  
 2 (bases 1 to 64919)  
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,  
 Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,  
 Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,  
 Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,  
 Cooke, P., DeArrellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fato, S.,  
 Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,  
 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,  
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 Lamasares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,  
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 Meneses, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,  
 Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D.,  
 Oliver, J., Peterson, K., Phunhthang, P., Plerre, N., Pollara, V.,  
 Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,  
 Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R.,  
 Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
 Straus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, D.,  
 Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliou, H.,  
 Vell, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,  
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIRB  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: U14539  
 Center clone name: 70\_E\_20  
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 \* NOTE: This record contains 80 individual  
 \* sequencing reads that have not been assembled into  
 \* contigs. Runs of N are used to separate the reads  
 \* and the order in which they appear is completely  
 \* arbitrary. Low-pass sequence sampling is useful for  
 \* identifying clones that may be gene-rich and allows  
 \* overlap relationships among clones to be deduced.  
 \* However, it should not be assumed that this clone  
 \* will be sequenced to completion. In the event that  
 \* the record is updated, the accession number will  
 \* be preserved.  
 \* 1 696: contig of 696 bp in length  
 \* 697 796: gap of 100 bp  
 \* 797 1528: contig of 732 bp in length

1529 1628: gap of 100 bp  
 1529 2363: contig of 735 bp in length  
 2364 2463: gap of 100 bp  
 2464 3207: contig of 744 bp in length  
 3208 3307: gap of 100 bp  
 3308 4002: contig of 695 bp in length  
 4003 4103: gap of 100 bp  
 4103 4787: contig of 685 bp in length  
 4788 4887: gap of 100 bp  
 4888 5588: contig of 701 bp in length  
 5589 5688: gap of 100 bp  
 5689 6357: contig of 668 bp in length  
 6357 6457: gap of 100 bp  
 6457 7154: contig of 698 bp in length  
 7155 7254: gap of 100 bp  
 7255 7971: contig of 716 bp in length  
 7971 8071: gap of 100 bp  
 8071 8783: contig of 712 bp in length  
 8783 8883: gap of 100 bp  
 8883 9585: contig of 704 bp in length  
 9585 9685: gap of 100 bp  
 9687 10437: contig of 750 bp in length  
 10437 10537: gap of 100 bp  
 10537 11282: contig of 745 bp in length  
 11282 11382: gap of 100 bp  
 11382 12070: contig of 689 bp in length  
 12071 12170: gap of 100 bp  
 12171 12802: contig of 632 bp in length  
 12803 12902: gap of 100 bp  
 12903 13588: contig of 686 bp in length  
 13588 13688: gap of 100 bp  
 13689 14008: contig of 720 bp in length  
 14008 14508: gap of 100 bp  
 14509 15246: contig of 738 bp in length  
 15247 15346: gap of 100 bp  
 15347 16084: contig of 738 bp in length  
 16085 16184: gap of 100 bp  
 16185 16921: contig of 737 bp in length  
 16922 17021: gap of 100 bp  
 17022 17755: contig of 733 bp in length  
 17755 17854: gap of 100 bp  
 17855 18570: contig of 716 bp in length  
 18571 18670: gap of 100 bp  
 18671 19392: contig of 722 bp in length  
 19393 19492: gap of 100 bp  
 19493 20233: contig of 741 bp in length  
 20234 20333: gap of 100 bp  
 20334 21026: contig of 693 bp in length  
 21027 21126: gap of 100 bp  
 21127 21818: contig of 692 bp in length  
 21819 21918: gap of 100 bp  
 21919 22614: contig of 696 bp in length  
 22615 22714: gap of 100 bp  
 22715 23429: contig of 715 bp in length  
 23430 23529: gap of 100 bp  
 23530 24231: contig of 702 bp in length  
 24232 24331: gap of 100 bp  
 24332 25052: contig of 721 bp in length  
 25053 25152: gap of 100 bp  
 25153 25880: contig of 728 bp in length  
 25881 25980: gap of 100 bp  
 25981 26680: contig of 700 bp in length  
 26681 26780: gap of 100 bp  
 26781 27530: contig of 750 bp in length  
 27531 27630: gap of 100 bp  
 27631 28332: contig of 702 bp in length  
 28333 28432: gap of 100 bp  
 28433 29118: contig of 686 bp in length  
 29119 29218: gap of 100 bp  
 29219 29913: contig of 695 bp in length  
 29914 30013: gap of 100 bp  
 30014 30715: contig of 702 bp in length  
 30716 30815: gap of 100 bp

*	30816	31519:	contig of 704 bp in length
*	31520	31619:	gap of 100 bp
*	31620	32352:	contig of 733 bp in length
*	32353	32452:	gap of 100 bp
*	32453	33169:	contig of 717 bp in length
*	33170	33269:	gap of 100 bp
*	33270	33960:	contig of 691 bp in length
*	33961	34060:	gap of 100 bp
*	34061	34731:	contig of 671 bp in length
*	34732	34831:	gap of 100 bp
*	34832	35572:	contig of 741 bp in length
*	35573	35672:	gap of 100 bp
*	35673	36416:	contig of 744 bp in length
*	36417	36516:	gap of 100 bp
*	36517	37214:	contig of 698 bp in length
*	37215	37314:	gap of 100 bp
*	37315	37993:	contig of 679 bp in length
*	37994	38093:	gap of 100 bp
*	38094	38790:	contig of 697 bp in length
*	38791	38890:	gap of 100 bp
*	38891	39590:	contig of 700 bp in length
*	39591	39690:	gap of 100 bp
*	39691	40416:	contig of 726 bp in length
*	40417	40516:	gap of 100 bp
*	40517	41256:	contig of 740 bp in length
*	41257	41356:	gap of 100 bp
*	41357	42053:	contig of 697 bp in length
*	42054	42153:	gap of 100 bp
*	42154	42886:	contig of 733 bp in length
*	42887	43734:	contig of 748 bp in length
*	42987	43735:	gap of 100 bp
*	43735	44579:	contig of 745 bp in length
*	44580	44679:	gap of 100 bp
*	44680	45385:	contig of 706 bp in length
*	45386	45485:	gap of 100 bp
*	45486	46179:	contig of 694 bp in length
*	46180	46279:	gap of 100 bp
*	46280	46974:	contig of 695 bp in length
*	46975	47074:	gap of 100 bp
*	47075	47796:	contig of 722 bp in length
*	47797	47896:	gap of 100 bp
*	47897	48604:	contig of 708 bp in length
*	48605	48704:	gap of 100 bp
*	48705	49434:	contig of 730 bp in length
*	49435	49534:	gap of 100 bp
*	49535	50252:	contig of 718 bp in length
*	50253	50352:	gap of 100 bp
*	50353	51027:	contig of 675 bp in length
*	51028	51127:	gap of 100 bp
*	51128	51847:	contig of 720 bp in length
*	51848	51947:	gap of 100 bp
*	51948	52682:	contig of 735 bp in length
*	52683	52782:	gap of 100 bp
*	52783	53476:	contig of 694 bp in length
*	53477	53576:	gap of 100 bp
*	53577	54238:	contig of 662 bp in length
*	54239	54338:	gap of 100 bp
*	54339	55057:	contig of 715 bp in length
*	55058	55157:	gap of 100 bp
*	55158	55874:	contig of 717 bp in length
*	55875	55974:	gap of 100 bp

Query Match 72.2% Score 13; DB 2; Length 64919;  
 Best Local Similarity 92.3% Pred. NO. 4.6e+02;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNNN 18  
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 Db 45379 CCTGAGANNNNNN 45391

RESULT 155

AC124644  
 LOCUS 64962 bp DNA linear HTG 27-NOV-2002  
 AC124644  
 DEFINITION Mus musculus clone RP23-135G22, LOW-PASS SEQUENCE SAMPLING.  
 AC124644  
 ACCESSION AC124644  
 VERSION 1  
 KEYWORDS HTG, HTGS PHASE0.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 64962)  
 Birren, B., Nusbaum, C., and Lander, E.  
 Mus musculus, clone RP23-135G22  
 Unpublished  
 2 (bases 1 to 64962)  
 Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N.,  
 Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,  
 Boukhgalter, B., Brown, A., Camarata, J., Campiano, A., Chang, J.,  
 Chazaro, B., Choquel, Y., Colangelo, M., Collins, S., Collumore, A.,  
 Cook, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J. S., Dodge, S.,  
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 Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,  
 Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Larcagne, K.,  
 Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K.,  
 Liu, G., Maclean, C., MacDonald, P., Major, J., Marquis, N.,  
 Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meltrim, J.,  
 Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,  
 Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P.,  
 O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,  
 Pollara, V., Raymond, C., Retta, R., Riaback, M., Riley, R., Rise, C.,  
 Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,  
 Schupack, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,  
 Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S.,  
 Theodore, J., Tophan, K., Travets, M., Travets, N., Trigillo, J.,  
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,  
 Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (15-JUN-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 64962)  
 Birren, B., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S.,  
 Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B.,  
 Camarata, J., Chang, J., Chazaro, B., Choquel, Y., Collumore, A.,  
 Cook, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J. S., Dodge, S.,  
 Gaidyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,  
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 Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,  
 Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,  
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 Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupack, R.,  
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 Travets, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,  
 Wyman, D., Young, G., Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (27-NOV-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Nov 27, 2002 this sequence version replaced gi:21427876.  
 ALL repeats were identified using RepeatMasker:  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIRB  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 Project Information  
 Center project name: L26856

Center clone name: 135\_G\_22

NOTE: This record contains 79 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.

1 709: contig of 709 bp in length  
710 809: gap of 100 bp  
810 1531: contig of 722 bp in length  
1532 1631: gap of 100 bp  
1632 2343: contig of 712 bp in length  
2344 2443: gap of 100 bp  
2444 3150: contig of 707 bp in length  
3151 3250: gap of 100 bp  
3251 3972: contig of 722 bp in length  
3973 4072: gap of 100 bp  
4073 4807: contig of 735 bp in length  
4808 4907: gap of 100 bp  
4908 5629: contig of 722 bp in length  
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5730 6451: contig of 722 bp in length  
6452 6551: gap of 100 bp  
6552 7281: contig of 730 bp in length  
7282 7381: gap of 100 bp  
7382 8104: contig of 723 bp in length  
8105 8204: gap of 100 bp  
8205 8922: contig of 718 bp in length  
8923 9022: gap of 100 bp  
9023 9736: contig of 714 bp in length  
9737 9836: gap of 100 bp  
9837 10569: contig of 733 bp in length  
10570 10669: gap of 100 bp  
10670 11388: contig of 719 bp in length  
11389 11488: gap of 100 bp  
11489 12217: contig of 729 bp in length  
12218 12317: gap of 100 bp  
12318 13054: contig of 737 bp in length  
13055 13154: gap of 100 bp  
13155 13884: contig of 730 bp in length  
13885 13984: gap of 100 bp  
13985 14714: contig of 730 bp in length  
14715 14814: gap of 100 bp  
14815 15534: contig of 720 bp in length  
15535 15634: gap of 100 bp  
15636 16352: contig of 718 bp in length  
16353 16452: gap of 100 bp  
16453 17175: contig of 723 bp in length  
17176 17275: gap of 100 bp  
17276 17998: contig of 723 bp in length  
17999 18098: gap of 100 bp  
18099 18835: contig of 737 bp in length  
18836 18935: gap of 100 bp  
18936 19656: contig of 721 bp in length  
19657 19756: gap of 100 bp  
19757 20481: contig of 725 bp in length  
20482 20581: gap of 100 bp  
20582 21299: contig of 718 bp in length  
21300 21399: gap of 100 bp  
21399 22130: contig of 731 bp in length  
22131 22230: gap of 100 bp  
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22969 23069: gap of 100 bp  
23069 23786: contig of 717 bp in length  
23787 23886: gap of 100 bp  
23887 24605: contig of 719 bp in length  
24606 24705: gap of 100 bp

24706 25426: contig of 721 bp in length  
25427 25526: gap of 100 bp  
25527 26254: contig of 728 bp in length  
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27090 27189: gap of 100 bp  
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27912 28011: gap of 100 bp  
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30392 30491: gap of 100 bp  
30492 31211: contig of 720 bp in length  
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31312 32031: contig of 720 bp in length  
32032 32131: gap of 100 bp  
32132 32860: contig of 729 bp in length  
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37780 37879: gap of 100 bp  
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38595 38695: gap of 100 bp  
38695 39417: contig of 723 bp in length  
39418 39517: gap of 100 bp  
39518 40245: contig of 728 bp in length  
40246 40345: gap of 100 bp  
40346 41072: contig of 727 bp in length  
41073 41172: gap of 100 bp  
41173 41891: contig of 719 bp in length  
41892 41991: gap of 100 bp  
41992 42714: contig of 723 bp in length  
42715 42814: gap of 100 bp  
42815 43539: contig of 725 bp in length  
43540 43639: gap of 100 bp  
43640 44373: contig of 734 bp in length  
44374 44473: gap of 100 bp  
44474 45192: contig of 719 bp in length  
45193 45292: gap of 100 bp  
45293 46003: contig of 711 bp in length  
46004 46103: gap of 100 bp  
46104 46833: contig of 730 bp in length  
46834 46933: gap of 100 bp  
46934 47658: contig of 725 bp in length

Query Match 72.2% Score 13; DB 2; Length 64962;  
Best Local Similarity 92.3%; Pred. No. 4.6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCGGAGNNNNNN 18  
Db 22962 CCGGAGNNNNNN 22974

RESULT 156  
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DEFINITION Mus musculus clone RP23-136W7, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC100429  
VERSION AC100429.1 GI:17047795  
KEYWORDS HTG; HTGS PHASED.  
SOURCE Mus musculus (house mouse)

ORGANISM  
Mus musculus

REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS  
1 (bases 1 to 65158)

TITLE  
Mus musculus, clone RP23-136M7

JOURNAL  
Unpublished

REFERENCE  
2 (bases 1 to 65158)

AUTHORS  
Birren, B., Linton, L., Nusbaum, C. and Lander, E.

2 (bases 1 to 65158)

AUTHORS  
Anderson, S., Barina, N., Baetli, V., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, W., Gram, L., Grand-Pierre, N., Hagos, B., Harford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Labocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C., MacDonald, P., Major, J., Marguis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrum, J., Menes, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunhthang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuppback, R., Seaman, S., Severy, P., Spencer, B., Stange-Rhmann, N., Stojanovic, N., Topham, K., Travers, M., Travis, N., Triggillo, J., Tsafaye, S., Theodore, J., Vael, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
Project Information  
Center project name: L15320  
Center clone name: 136\_M\_7

NOTE: This record contains 81 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
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\* the record is updated, the accession number will  
\* be preserved.

1  
710: contig of 710 bp in length  
711 810: gap of 100 bp  
811 1502: contig of 692 bp in length  
1503 1602: gap of 100 bp  
1603 2321: contig of 719 bp in length  
2322 2421: gap of 100 bp  
2422 3121: contig of 700 bp in length  
3122 3221: gap of 100 bp  
3222 3914: contig of 693 bp in length  
3915 4014: gap of 100 bp  
4015 4707: contig of 693 bp in length  
4708 4807: gap of 100 bp  
4808 5489: contig of 682 bp in length  
5489 5590: gap of 100 bp  
5590 6302: contig of 712 bp in length  
6302 6401: gap of 100 bp  
6401 7109: contig of 708 bp in length  
7109: gap of 100 bp

7110 7209: gap of 100 bp  
7210 7928: contig of 719 bp in length  
7929 8028: gap of 100 bp  
8029 8731: contig of 703 bp in length  
8732 8831: gap of 100 bp  
8832 9557: contig of 726 bp in length  
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9658 10389: contig of 732 bp in length  
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10490 11185: contig of 696 bp in length  
11186 11285: gap of 100 bp  
11286 11989: contig of 704 bp in length  
11990 12089: gap of 100 bp  
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14482 15199: contig of 718 bp in length  
15200 15299: gap of 100 bp  
15299 16104: contig of 705 bp in length  
16105 16104: gap of 100 bp  
16105 16811: contig of 707 bp in length  
16812 16911: gap of 100 bp  
16912 17602: contig of 691 bp in length  
17603 17702: gap of 100 bp  
17703 18417: contig of 715 bp in length  
18418 18517: gap of 100 bp  
18518 19287: contig of 770 bp in length  
19288 19387: gap of 100 bp  
19388 20105: contig of 718 bp in length  
20106 20205: gap of 100 bp  
20206 20899: contig of 694 bp in length  
20900 20999: gap of 100 bp  
21000 21694: contig of 695 bp in length  
21695 21794: gap of 100 bp  
21795 22477: contig of 683 bp in length  
22478 22577: gap of 100 bp  
22578 23275: contig of 698 bp in length  
23276 23375: gap of 100 bp  
23376 24080: contig of 705 bp in length  
24081 24180: gap of 100 bp  
24181 24894: contig of 714 bp in length  
24895 24994: gap of 100 bp  
24995 25701: contig of 707 bp in length  
25702 25801: gap of 100 bp  
25802 26502: contig of 701 bp in length  
26503 26602: gap of 100 bp  
26603 27293: contig of 691 bp in length  
27294 27393: gap of 100 bp  
27394 28098: contig of 705 bp in length  
28099 28198: gap of 100 bp  
28199 28914: contig of 716 bp in length  
28915 29014: gap of 100 bp  
29015 29705: contig of 691 bp in length  
29706 29805: gap of 100 bp  
29806 30494: contig of 689 bp in length  
30495 30594: gap of 100 bp  
30595 31291: contig of 697 bp in length  
31292 31391: gap of 100 bp  
31392 32092: contig of 701 bp in length  
32093 32192: gap of 100 bp  
32193 32801: contig of 709 bp in length  
32802 33001: gap of 100 bp  
33003 33699: contig of 698 bp in length  
33700 33799: gap of 100 bp  
33800 34501: contig of 702 bp in length  
34502 34601: gap of 100 bp  
34602 35325: contig of 724 bp in length  
35326 35425: gap of 100 bp  
35426 36137: contig of 712 bp in length  
36138 36237: gap of 100 bp

```

* 36238 36942: contig of 705 bp in length
* 36943 37042: gap of 100 bp
* 37043 37748: contig of 706 bp in length
* 37749 37848: gap of 100 bp
* 37849 38571: contig of 723 bp in length
* 38572 38671: gap of 100 bp
* 38672 39368: contig of 696 bp in length
* 39368 39468: gap of 100 bp
* 39468 40185: contig of 718 bp in length
* 40185 40286: gap of 100 bp
* 40286 41009: contig of 724 bp in length
* 41010 41817: gap of 100 bp
* 41817 41917: contig of 708 bp in length
* 41918 42620: gap of 100 bp
* 41918 42620: contig of 703 bp in length
* 42621 42721: gap of 100 bp
* 42721 43424: contig of 704 bp in length
* 43425 43525: gap of 100 bp
* 43525 44243: contig of 719 bp in length
* 44244 44344: gap of 100 bp
* 44344 45039: contig of 696 bp in length
* 45040 45140: gap of 100 bp
* 45140 45827: contig of 688 bp in length
* 45828 45927: gap of 100 bp
* 45928 46617: contig of 689 bp in length
* 46617 46716: gap of 100 bp
* 46717 47424: contig of 708 bp in length
* 47425 47524: gap of 100 bp
* 47525 48232: contig of 708 bp in length
* 48233 48332: gap of 100 bp
* 48333 48053: contig of 721 bp in length
* 48054 49154: gap of 100 bp
* 49154 49843: contig of 689 bp in length
* 49843 49943: gap of 100 bp
* 49943 50632: contig of 690 bp in length
* 50633 50732: gap of 100 bp
* 50733 51435: contig of 703 bp in length
* 51436 51536: gap of 100 bp
* 51536 52247: contig of 712 bp in length
* 52248 52347: gap of 100 bp
* 52348 53048: contig of 700 bp in length
* 53048 53147: gap of 100 bp
* 53148 53838: contig of 690 bp in length
* 53838 53937: gap of 100 bp
* 53938 54640: contig of 703 bp in length
* 54641 54741: gap of 100 bp
* 54741 55439: contig of 699 bp in length
* 55440 55539: gap of 100 bp

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```

Query Match 72.2% Score 13; DB 2; Length 65158;
Best Local Similarity 92.3%; Pred. NO. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 6 CCUGAGNNNNNN 18
Db 15193 CCTGAGNNNNNN 15205

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RESULT 157
AC100675 65199 bp DNA linear HTG 22-NOV-2001
DEFINITION Mus musculus clone RP23-167M2; LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC100675.1 GI:17048041
VERSION HTG; HTGS PHASED.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 65199)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Mus musculus, clone RP23-167M2
JOURNAL Unpublished

```

## REFERENCE

2 (bases 1 to 65199)  
 AUTHORS  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
 Anderson,S., Barna,J., Baxendale,V., Boguski,M., Bouckgeert,B.,  
 Brown,A., Camarata,J., Campilioni,A., Chang,D., Chazaro,B.,  
 Choquet,Y., Collinge,M., Collins,S., Collymore,A., Cook,A.,  
 Cooke,P., DeArillano,K., Dewar,J.S., Dodge,S., Faro,S.,  
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 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,  
 Hagos,B., Heaton,A., Horton,M., Hulme,M., Iliev,I., Johnson,R.,  
 Jones,C., Kamal,A., Karatas,A., Kellis,C., Labèque,K.,  
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 Maclean,C., MacDonald,P., Major,J., Margulis,N., Matthews,C.,  
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 Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,  
 Oliver,J., Peterson,K., Phukhang,P., Pierre,N., Pollara,V.,  
 Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,  
 Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupbach,R.,  
 Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
 Strauss,N., Subramanian,A., Talmas,J., Tesfaye,S., Theodore,J.,  
 Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,  
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
 Zaitoun,J., Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 All repeats were identified using RepeatMasker:  
 Smit,A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WtBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
 ----- Project Information  
 Center project name: L15933  
 Center clone name: 167\_M2

```

* NOTE: This record contains 77 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1
* 702 701: contig of 701 bp in length
* 802 801: gap of 100 bp
* 1545 1544: contig of 743 bp in length
* 1645 1644: gap of 100 bp
* 2399 2398: contig of 754 bp in length
* 2499 2498: gap of 100 bp
* 3239 3238: contig of 740 bp in length
* 3339 3338: gap of 100 bp
* 4088 4087: contig of 749 bp in length
* 4188 4187: gap of 100 bp
* 4933 4932: contig of 745 bp in length
* 5033 5032: gap of 100 bp
* 5749 5748: contig of 716 bp in length
* 5849 5848: gap of 100 bp
* 6599 6598: gap of 100 bp
* 6699 6698: gap of 100 bp
* 7412 7411: contig of 713 bp in length
* 7512 7511: gap of 100 bp
* 8275 8274: contig of 763 bp in length
* 8375 8374: gap of 100 bp
* 9129 9128: contig of 755 bp in length
* 9230 9229: gap of 100 bp
* 9947 9946: contig of 717 bp in length
* 10046: gap of 100 bp

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* 10047 10772: contig of 726 bp in length
* 10873 10872: gap of 100 bp
* 11634 11633: contig of 761 bp in length
* 11734 11733: gap of 100 bp
* 12485 12485: contig of 752 bp in length
* 12486 12485: gap of 100 bp
* 12586 13348: contig of 763 bp in length
* 13349 13448: gap of 100 bp
* 13449 14183: contig of 735 bp in length
* 14184 14283: gap of 100 bp
* 14284 15071: contig of 788 bp in length
* 15072 15171: gap of 100 bp
* 15172 15944: contig of 773 bp in length
* 15945 16044: gap of 100 bp
* 16045 16809: contig of 765 bp in length
* 16810 16909: gap of 100 bp
* 16910 17661: contig of 752 bp in length
* 17662 18494: contig of 733 bp in length
* 18495 18595: gap of 100 bp
* 18595 19353: contig of 759 bp in length
* 19354 19453: gap of 100 bp
* 19454 20168: contig of 715 bp in length
* 20169 20268: gap of 100 bp
* 20269 21014: contig of 746 bp in length
* 21015 21114: gap of 100 bp
* 21115 21850: contig of 736 bp in length
* 21851 21950: gap of 100 bp
* 21951 22714: contig of 764 bp in length
* 22715 22814: gap of 100 bp
* 22815 23562: contig of 748 bp in length
* 23563 23662: gap of 100 bp
* 23663 24428: contig of 766 bp in length
* 24429 24528: gap of 100 bp
* 24529 25275: contig of 747 bp in length
* 25276 25375: gap of 100 bp
* 25376 26115: contig of 740 bp in length
* 26116 26973: contig of 758 bp in length
* 26974 27073: gap of 100 bp
* 27074 27825: contig of 752 bp in length
* 27826 27925: gap of 100 bp
* 27926 28666: contig of 741 bp in length
* 28667 28766: gap of 100 bp
* 28767 29500: contig of 734 bp in length
* 29501 29600: gap of 100 bp
* 29601 30342: contig of 742 bp in length
* 30343 30442: gap of 100 bp
* 30443 31237: contig of 795 bp in length
* 31238 31337: gap of 100 bp
* 31338 32076: contig of 739 bp in length
* 32077 32176: gap of 100 bp
* 32177 32933: contig of 757 bp in length
* 32934 33033: gap of 100 bp
* 33034 33801: contig of 768 bp in length
* 33802 33901: gap of 100 bp
* 33902 34647: contig of 746 bp in length
* 34648 34747: gap of 100 bp
* 34748 35477: contig of 730 bp in length
* 35478 35577: gap of 100 bp
* 35578 36322: contig of 745 bp in length
* 36323 36422: gap of 100 bp
* 36423 37155: contig of 733 bp in length
* 37156 37255: gap of 100 bp
* 37256 37987: contig of 732 bp in length
* 37988 38087: gap of 100 bp
* 38088 38835: contig of 748 bp in length
* 38836 38935: gap of 100 bp
* 38936 39690: contig of 755 bp in length
* 39691 39790: gap of 100 bp
* 39791 40533: contig of 743 bp in length
* 40534 40633: gap of 100 bp
* 41404: contig of 771 bp in length
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* 41405 41504: gap of 100 bp
* 41505 42215: contig of 711 bp in length
* 42216 42315: gap of 100 bp
* 42316 43074: contig of 758 bp in length
* 43074 43173: gap of 100 bp
* 43174 43925: contig of 751 bp in length
* 43925 44024: gap of 100 bp
* 44025 44771: contig of 747 bp in length
* 44772 44871: gap of 100 bp
* 44872 45599: contig of 728 bp in length
* 45600 45699: gap of 100 bp
* 45700 46459: contig of 760 bp in length
* 46460 46559: gap of 100 bp
* 46560 47275: contig of 716 bp in length
* 47276 47375: gap of 100 bp
* 47376 48099: contig of 724 bp in length
* 48100 48199: gap of 100 bp
* 48200 48964: contig of 765 bp in length
* 48965 49064: gap of 100 bp
* 49065 49824: contig of 760 bp in length
* 49825 49924: gap of 100 bp
* 49925 50673: contig of 749 bp in length
* 50674 50773: gap of 100 bp
* 50774 51516: contig of 743 bp in length
* 51517 51616: gap of 100 bp
* 51617 52339: contig of 723 bp in length
* 52340 52439: gap of 100 bp
* 52440 53187: contig of 748 bp in length
* 53188 53288: gap of 100 bp
* 53288 54048: contig of 761 bp in length
* 54049 54149: gap of 100 bp
* 54149 54901: contig of 753 bp in length
* 54902 55001: gap of 100 bp
* 55002 55712: contig of 711 bp in length
* 55713 55812: gap of 100 bp
* 55813 56604: contig of 792 bp in length
* 56605 56704: gap of 100 bp
* 56705 57465: contig of 761 bp in length
* 57466 57565: gap of 100 bp
* 57566 58314: contig of 749 bp in length
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Query Match
Best Local Similarity 92.3% Score 13; DB 2; Length 65199;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGNNNNNN 18
Db 38829 CCTGGAGNNNNNN 38841

RESULT 158
AC090157
LOCUS Homo sapiens chromosome 11 clone RP11-223K12 map 11, LOW-PASS
DEFINITION SEQUENCE SAMPLING.
ACCESSION AC090157.2 GI:13431020
VERSION
KEYWORDS HTG; HTGS_PHASEO.
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 (bases 1 to 65259)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
TITLE Barna,N., Baclen,V., Boguslavsky,L., Boukhalter,B., Brown,A.,
JOURNAL Camarata,J., Campoliano,A., Choepel,Y., Colangelo,M., Collins,S.,
REFERENCE Collamore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
AUTHORS Dodge,S., Faro,S., Ferreira,F., Fitzhugh,W., Gage,D., Galagan,J.,
```

TITLE  
JOURNAL  
COMMENT

Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hago, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., Laroque, K., Lamazares, R., Landers, T., Lenock, J., Levine, R., Liu, G., Maclean, C., McDonald, P., Marquis, N., Mathew, C., McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrum, J., Meneu, L., Mhova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkiang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Ribbeck, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Sougnaz, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strausz, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 22, 2001 this sequence version replaced gi:1257786.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WtBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [submit@genome.wi.mit.edu](mailto:submit@genome.wi.mit.edu)  
Project Information  
Center project name: L11791  
Center clone name: 223\_K\_12

\* NOTE: This record contains 81 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allow  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 682: contig of 682 bp in length  
683 782: gap of 100 bp  
783 1487: contig of 705 bp in length  
1488 1587: gap of 100 bp  
1588 2310: contig of 723 bp in length  
2311 2410: gap of 100 bp  
2411 3102: contig of 692 bp in length  
3103 3202: gap of 100 bp  
3203 3906: contig of 704 bp in length  
3907 4006: gap of 100 bp  
4007 4705: contig of 699 bp in length  
4706 4805: gap of 100 bp  
4806 5499: contig of 694 bp in length  
5500 5599: gap of 100 bp  
5600 6293: contig of 694 bp in length  
6294 6393: gap of 100 bp  
6394 7101: contig of 708 bp in length  
7102 7201: gap of 100 bp  
7202 7913: contig of 712 bp in length  
7914 8013: gap of 100 bp  
8014 8730: contig of 717 bp in length  
8731 8830: gap of 100 bp  
8831 9543: contig of 713 bp in length  
9544 9643: gap of 100 bp  
9644 10358: contig of 715 bp in length  
10359 10458: gap of 100 bp  
10459 11146: contig of 688 bp in length  
11147 11246: gap of 100 bp  
11247 11960: contig of 714 bp in length  
11961 12060: gap of 100 bp

12061 12767: contig of 707 bp in length  
12768 12867: gap of 100 bp  
12868 13567: contig of 700 bp in length  
13568 13667: gap of 100 bp  
13668 14369: contig of 702 bp in length  
14370 14469: gap of 100 bp  
14470 15195: contig of 726 bp in length  
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16930 17633: contig of 704 bp in length  
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17734 18450: contig of 717 bp in length  
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19276 19375: gap of 100 bp  
19376 20078: contig of 703 bp in length  
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20879 20978: gap of 100 bp  
20979 21670: contig of 692 bp in length  
21671 21770: gap of 100 bp  
21771 22459: contig of 689 bp in length  
22460 22559: gap of 100 bp  
22560 23278: contig of 719 bp in length  
23279 23378: gap of 100 bp  
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27451 28144: contig of 694 bp in length  
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33085 33770: contig of 686 bp in length  
33771 33870: gap of 100 bp  
33871 34620: contig of 750 bp in length  
34621 34720: gap of 100 bp  
34721 35430: contig of 710 bp in length  
35431 35530: gap of 100 bp  
35531 36223: contig of 693 bp in length  
36224 36323: gap of 100 bp  
36324 37013: contig of 690 bp in length  
37014 37113: gap of 100 bp  
37114 37786: contig of 673 bp in length  
37787 37886: gap of 100 bp  
37887 38596: contig of 710 bp in length  
38597 38696: gap of 100 bp  
38697 39400: contig of 704 bp in length  
39401 39500: gap of 100 bp  
39501 40224: contig of 724 bp in length  
40225 40324: gap of 100 bp  
40325 41025: contig of 701 bp in length  
41026 41125: gap of 100 bp  
41126 41875: contig of 750 bp in length

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* 41876 41975: gap of 100 bp
* 41976 42703: contig of 734 bp in length
* 42710 42809: gap of 100 bp
* 42810 43526: contig of 717 bp in length
* 43527 43626: gap of 100 bp
* 43627 44329: contig of 703 bp in length
* 44330 44429: gap of 100 bp
* 44430 45129: contig of 700 bp in length
* 45130 45229: gap of 100 bp
* 45230 45913: contig of 684 bp in length
* 45914 46013: gap of 100 bp
* 46014 46700: contig of 687 bp in length
* 46701 46800: gap of 100 bp
* 46801 47505: contig of 705 bp in length
* 47506 47605: gap of 100 bp
* 47606 48303: contig of 698 bp in length
* 48304 48403: gap of 100 bp
* 48404 49121: contig of 718 bp in length
* 49122 49221: gap of 100 bp
* 49222 49899: contig of 678 bp in length
* 49900 49999: gap of 100 bp
* 50000 50750: contig of 751 bp in length
* 50751 50850: gap of 100 bp
* 50851 51574: contig of 724 bp in length
* 51575 51674: gap of 100 bp
* 51675 52381: contig of 707 bp in length
* 52382 52481: gap of 100 bp
* 52482 53183: contig of 702 bp in length
* 53184 53283: gap of 100 bp
* 53284 53961: contig of 678 bp in length
* 53962 54061: gap of 100 bp
* 54062 54789: contig of 728 bp in length
* 54790 54889: gap of 100 bp
* 54890 55571: contig of 682 bp in length

```

```

Query Match 72.2% Score 13; DB 2; Length 65259;
Best Local Similarity 92.3% Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 6 CCUGAGANNNNNN 18
Db 60406 CCTGAGANNNNNN 60418

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RESULT 159
AC012249
LOCUS Homo sapiens clone RP11-16N23, LOW-PASS SEQUENCE SAMPLING.
AC012249
AC012249.2 GI:7144955
VERSION HTG; HTGS PHASE0.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 66086)
AUTHORS Birren, B., Linton, L., Nussbaum, C. and Lander, E.
JOURNAL Unpublished
TITLE 2 (bases 1 to 66086)
AUTHORS Birren, B., Linton, L., Nussbaum, C., Lander, E., Allen, N., Anderson, M.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., Dearlano, K., Dewar, K., Domino, M., Donegan, L., Doyle, M.,
Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,
Galsagan, J., Gardyna, S., Grant, G., Hagos, B., Heath, A., Horton, L.,
Howard, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Lien, C., Locke, K., MacDonald, P., Marquis, N.,
McEwan, P., McGuirk, A., McKernan, K., McLaughlin, J., Meltrill, J.,
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Testaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,

```

# TITLE JOURNAL COMMENT

```

Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (21-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 3, 2000 this sequence version replaced gi:6091795.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L3591
Center clone name: 16_N23
-----
* NOTE: This record contains 78 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
800 799: contig of 799 bp in length
900 899: gap of 100 bp
1637 1636: contig of 737 bp in length
1737 1736: gap of 100 bp
2466 2465: gap of 100 bp
3273 3272: contig of 707 bp in length
3373 3372: gap of 100 bp
4126 4125: contig of 753 bp in length
4226 4225: gap of 100 bp
4426 4425: contig of 750 bp in length
4976 4975: gap of 100 bp
5076 5075: gap of 100 bp
5847 5846: contig of 772 bp in length
5848 5947: gap of 100 bp
5948 6692: contig of 745 bp in length
6693 6792: gap of 100 bp
6793 7530: contig of 738 bp in length
7531 7530: gap of 100 bp
7631 8374: contig of 744 bp in length
8375 8474: gap of 100 bp
8475 9210: contig of 736 bp in length
9211 9310: gap of 100 bp
9311 10028: contig of 718 bp in length
10029 10128: gap of 100 bp
10129 10840: contig of 712 bp in length
10841 10940: gap of 100 bp
10941 11687: contig of 747 bp in length
11688 11787: gap of 100 bp
11788 12520: contig of 733 bp in length
12521 12620: gap of 100 bp
12621 13379: contig of 759 bp in length
13380 13479: gap of 100 bp
13480 14248: contig of 769 bp in length
14249 14348: gap of 100 bp
14349 15141: contig of 793 bp in length
15142 15241: gap of 100 bp
15242 16000: contig of 759 bp in length
16001 16100: gap of 100 bp
16101 16836: contig of 736 bp in length
16837 16936: gap of 100 bp
16937 17720: contig of 784 bp in length
17721 17820: gap of 100 bp
17821 18504: contig of 684 bp in length
18505 18604: gap of 100 bp
18605 19321: contig of 717 bp in length

```



```

* 19322 19421: gap of 100 bp
* 19432 20147: contig of 726 bp in length
* 20148 20247: gap of 100 bp
* 20248 21001: contig of 754 bp in length
* 21002 21101: gap of 100 bp
* 21102 21816: contig of 715 bp in length
* 21817 21916: gap of 100 bp
* 21917 22658: contig of 742 bp in length
* 22659 22758: gap of 100 bp
* 22759 23487: contig of 729 bp in length
* 23488 23588: gap of 100 bp
* 23589 24318: contig of 731 bp in length
* 24319 24418: gap of 100 bp
* 24419 25154: contig of 736 bp in length
* 25155 25254: gap of 100 bp
* 25255 26015: contig of 761 bp in length
* 26016 26115: gap of 100 bp
* 26116 26837: contig of 722 bp in length
* 26838 26937: gap of 100 bp
* 26938 27653: contig of 716 bp in length
* 27654 27753: gap of 100 bp
* 27754 28482: contig of 729 bp in length
* 28483 28582: gap of 100 bp
* 28583 29337: contig of 755 bp in length
* 29338 29437: gap of 100 bp
* 29438 30183: contig of 746 bp in length
* 30184 30283: gap of 100 bp
* 30284 31031: contig of 748 bp in length
* 31032 31131: gap of 100 bp
* 31132 31879: contig of 748 bp in length
* 31880 32741: contig of 762 bp in length
* 32742 32841: gap of 100 bp
* 32842 33567: contig of 726 bp in length
* 33568 33667: gap of 100 bp
* 33668 34386: contig of 719 bp in length
* 34387 34486: gap of 100 bp
* 34487 35205: contig of 719 bp in length
* 35206 35305: gap of 100 bp
* 35306 36089: contig of 784 bp in length
* 36090 36189: gap of 100 bp
* 36190 36943: contig of 754 bp in length
* 36944 37043: gap of 100 bp
* 37044 37822: contig of 779 bp in length
* 37823 37922: gap of 100 bp
* 37923 38669: contig of 747 bp in length
* 38670 38769: gap of 100 bp
* 38770 39501: contig of 732 bp in length
* 39502 39601: gap of 100 bp
* 39602 40343: contig of 742 bp in length
* 40344 40443: gap of 100 bp
* 40444 41203: contig of 760 bp in length
* 41204 41303: gap of 100 bp
* 41304 42019: contig of 716 bp in length
* 42020 42119: gap of 100 bp
* 42120 42831: contig of 712 bp in length
* 42832 42931: gap of 100 bp
* 42932 43655: contig of 724 bp in length
* 43656 43755: gap of 100 bp
* 43756 44532: contig of 777 bp in length
* 44533 44632: gap of 100 bp
* 44633 45430: contig of 798 bp in length
* 45431 45530: gap of 100 bp
* 45531 46291: contig of 761 bp in length
* 46292 46391: gap of 100 bp
* 46392 47129: contig of 738 bp in length
* 47130 47229: gap of 100 bp
* 47230 47972: contig of 743 bp in length
* 47973 48072: gap of 100 bp
* 48073 48856: contig of 784 bp in length
* 48857 48956: gap of 100 bp
* 48957 49689: contig of 733 bp in length
* 49690 49789: gap of 100 bp

```

```

* 49790 50510: contig of 721 bp in length
* 50611 50610: gap of 100 bp
* 50611 51411: contig of 801 bp in length
* 51412 51511: gap of 100 bp
* 51512 52277: contig of 766 bp in length
* 52278 52377: gap of 100 bp
* 52378 53140: contig of 763 bp in length
* 53141 53240: gap of 100 bp
* 53241 54011: contig of 771 bp in length
* 54012 54111: gap of 100 bp
* 54112 54862: contig of 751 bp in length
* 54863 54962: gap of 100 bp
* 54963 55758: contig of 796 bp in length
* 55759 55858: gap of 100 bp
* 55859 56604: contig of 746 bp in length
* 56605 56704: gap of 100 bp
* 56705 57481: contig of 777 bp in length
* 57482 57581: gap of 100 bp
* 57582 58287: contig of 706 bp in length
* 58288 58387: gap of 100 bp
* 58388 59099: contig of 712 bp in length
* 59100 59199: gap of 100 bp
* 59200 59928: contig of 729 bp in length
* 59929 60028: gap of 100 bp
* 60029 60836: contig of 808 bp in length
* 60837 60936: gap of 100 bp
* 60937 61747: contig of 811 bp in length

Query Match      72.2%; Score 13; DB 2; Length 66086;
Best Local Similarity 92.3%; Pred. No. 4,6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY      6 CCGGAGGANNNNNN 18
Db      11681 CCTGGAGANNNNNN 11693

RESULT 160
AC120428
LOCUS      AC120428
DEFINITION Mus musculus clone RP24-542F4, LOW-PASS SEQUENCE SAMPLING.
ACCESSION  AC120428
VERSION    AC120428.1 GI:20455762
KEYWORDS   HTG; HTGS PHASE0.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 67572)
AUTHORS    Birren, B., Linton, L., Nuebaum, C., Lander, E., Ali, A., Allen, N.,
            Borkgatter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
            Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
            Cook, A., Cooke, P., Deatrelano, K., Dewar, K., Diaz, J.S., Dodge, S.,
            Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
            Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
            Hager, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
            Kamat, A., Karakas, A., Kells, C., Labrecque, K., Lamazates, R.,
            Landers, T., Lenocksky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
            Maclean, C., Macdonald, P., Major, J., Margulis, N., Matthews, C.,
            McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Menne, L.,
            Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
            North, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
            Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
            Raymond, C., Recta, R., Rieback, W., Riley, R., Rise, C., Rogov, P.,
            Roman, J., Rossetti, M., Roy, A., Santos, R., Schauer, N., Schupbach, R.,
            Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
            Strauss, N., Subramanian, A., Talame, J., Tesfaye, S., Theodore, J.,
            Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,

```

TITLE  
JOURNAL

## COMMENT

Viel.R., Vo.A., Wilson.B., Wu.X., Wyman.D., Ye.W.J., Young.G.,  
Zainoun.J., Zemek.L., Zimmer.A. and Zody.M.  
Direct Submission  
Submitted (06-MAY-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)

Project Information  
Project name: L26045  
Center project name: 542\_F\_4

\* NOTE: This record contains 81 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1  
737: contig of 737 bp in length  
738  
837: gap of 100 bp  
838  
1583: contig of 746 bp in length  
1584  
1683: gap of 100 bp  
1684  
2434: contig of 751 bp in length  
2435  
2534: gap of 100 bp  
2535  
3271: contig of 737 bp in length  
3272  
3371: gap of 100 bp  
3372  
4120: contig of 749 bp in length  
4121  
4220: gap of 100 bp  
4221  
4959: contig of 739 bp in length  
4960  
5059: gap of 100 bp  
5060  
5803: contig of 744 bp in length  
5804  
5903: gap of 100 bp  
5904  
6629: contig of 726 bp in length  
6630  
6729: gap of 100 bp  
6730  
7468: contig of 739 bp in length  
7469  
7568: gap of 100 bp  
7569  
8294: contig of 726 bp in length  
8295  
8394: gap of 100 bp  
8395  
9156: contig of 762 bp in length  
9157  
9256: gap of 100 bp  
9257  
10002: contig of 746 bp in length  
10003  
10102: gap of 100 bp  
10103  
10850: contig of 748 bp in length  
10851  
10950: gap of 100 bp  
10951  
11682: contig of 732 bp in length  
11683  
11782: gap of 100 bp  
11784  
12522: contig of 740 bp in length  
12523  
12622: gap of 100 bp  
12624  
13323: contig of 701 bp in length  
13324  
13423: gap of 100 bp  
13424  
14147: contig of 724 bp in length  
14148  
14247: gap of 100 bp  
14249  
14974: contig of 727 bp in length  
14975  
15074: gap of 100 bp  
15075  
15804: contig of 730 bp in length  
15805  
15904: gap of 100 bp  
15906  
16646: contig of 742 bp in length  
16647  
16746: gap of 100 bp  
16747  
17497: contig of 751 bp in length  
17498  
17597: gap of 100 bp  
17599  
18332: contig of 735 bp in length  
18333  
18432: gap of 100 bp  
18433  
19165: contig of 733 bp in length

19166  
19266  
20012: contig of 747 bp in length  
20013  
20112: gap of 100 bp  
20113  
20821: contig of 709 bp in length  
20822  
20921: gap of 100 bp  
20922  
21652: contig of 731 bp in length  
21653  
21752: gap of 100 bp  
21753  
22467: contig of 715 bp in length  
22468  
22567: gap of 100 bp  
22568  
23295: contig of 728 bp in length  
23296  
23395: gap of 100 bp  
23396  
24120: contig of 725 bp in length  
24121  
24220: gap of 100 bp  
24221  
24955: contig of 735 bp in length  
24956  
25055: gap of 100 bp  
25056  
25815: contig of 760 bp in length  
25816  
25915: gap of 100 bp  
25916  
26671: contig of 756 bp in length  
26672  
26771: gap of 100 bp  
26772  
27510: contig of 739 bp in length  
27511  
27610: gap of 100 bp  
27611  
28353: contig of 743 bp in length  
28354  
28453: gap of 100 bp  
28454  
29188: contig of 735 bp in length  
29189  
29288: gap of 100 bp  
29289  
30030: contig of 742 bp in length  
30031  
30130: gap of 100 bp  
30131  
30858: contig of 728 bp in length  
30859  
30958: gap of 100 bp  
30959  
31677: contig of 719 bp in length  
31678  
31777: gap of 100 bp  
31778  
32500: contig of 723 bp in length  
32501  
32600: gap of 100 bp  
32601  
33328: contig of 728 bp in length  
33329  
33428: gap of 100 bp  
33429  
34172: contig of 744 bp in length  
34173  
34272: gap of 100 bp  
34273  
35029: contig of 757 bp in length  
35029  
35129: gap of 100 bp  
35130  
35865: contig of 736 bp in length  
35866  
35965: gap of 100 bp  
35966  
36710: contig of 745 bp in length  
36710  
36810: gap of 100 bp  
36811  
37668: contig of 758 bp in length  
37669  
37668: gap of 100 bp  
37669  
38364: contig of 656 bp in length  
38365  
38464: gap of 100 bp  
38465  
39196: contig of 732 bp in length  
39196  
39296: gap of 100 bp  
39297  
39993: contig of 637 bp in length  
39993  
40093: gap of 100 bp  
40094  
40824: contig of 731 bp in length  
40824  
40924: gap of 100 bp  
40925  
41652: contig of 728 bp in length  
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41752: gap of 100 bp  
41753  
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42485  
42585: gap of 100 bp  
42586  
43113: contig of 728 bp in length  
43113  
43413: gap of 100 bp  
43414  
44176: contig of 763 bp in length  
44176  
44276: gap of 100 bp  
44277  
45024: contig of 748 bp in length  
45024  
45124: gap of 100 bp  
45125  
45851: contig of 727 bp in length  
45851  
45951: gap of 100 bp  
45952  
46678: contig of 727 bp in length  
46678  
46778: gap of 100 bp  
46779  
47516: contig of 738 bp in length  
47516  
47615: gap of 100 bp  
47617  
48344: contig of 728 bp in length  
48344  
48444: gap of 100 bp  
48445  
49177: contig of 733 bp in length  
49177  
49277: gap of 100 bp

```

* 49278 49986: contig of 709 bp in length
* 49987 50086: contig of 100 bp
* 50087 50818: contig of 732 bp in length
* 50819 50918: gap of 100 bp
* 50919 51674: contig of 756 bp in length
* 51675 51774: gap of 100 bp
* 51775 52516: contig of 742 bp in length
* 52517 52617: gap of 100 bp
* 52617 53363: contig of 747 bp in length
* 53364 53463: gap of 100 bp
* 53464 54212: contig of 748 bp in length
* 54212 54311: gap of 100 bp
* 54311 55040: contig of 729 bp in length
* 55040 55140: gap of 100 bp
* 55140 55880: contig of 740 bp in length
* 55881 55980: gap of 100 bp
* 55981 56725: contig of 745 bp in length
* 56726 56825: gap of 100 bp
* 56826 57551: contig of 726 bp in length
* 57552 57651: gap of 100 bp

Query Match 72.24; Score 13; DB 2; Length 67572;
Best Local Similarity 92.34; Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGGAGNNNNNN 18
DB 46672 CCTGGAGNNNNNN 46684

RESULT 161
AC117553
LOCUS AC117553 68315 bp DNA linear HTG 05-JUL-2002
DEFINITION Mus musculus clone RP23-374E23, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC117553.3 GI:21699553
VERSION HTG: HTG PHASE0.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 68315)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-374E23
Unpublished
2 (bases 1 to 68315)
Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N.,
Anderson,S., Barna,N., Baetien,V., Bloom,T., Boguslavsky,L.,
Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Dearrellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Fairo,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Lacroque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,
Maclean,C., MacDonald,P., Major,J., Margulis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meiditum,J., Menes,L.,
Mhova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Oliver,J., Peterson,K., Phunhthang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R.,
Seaman,S., Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 68315)
Birren,B., Nusbaum,C., Lander,E., All,A., Allen,N., Anderson,S.,

```

# TITLE JOURNAL COMMENT

Barna,N., Baetien,V., Bloom,T., Boguslavsky,L., Boukhalter,B.,  
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,  
Cook,A., Cooke,P., Dearrellano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
Fairo,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,  
Gardyna,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B.,  
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,  
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,  
Liu,G., Maclean,C., MacDonald,P., Major,J., Matthews,C.,  
McCarthy,M., Meiditum,J., Menes,L., Mhova,T., Mlenga,V.,  
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,  
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,  
Phunhthang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
Roman,J., Roy,A., Schauer,S., Schupack,R., Seaman,S., Severy,P.,  
Smith,C., Spencer,B., Strange-Thomann,N., Stojanovic,N., Talamas,J.,  
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,  
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,  
Zembek,L., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (05-JUL-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 5, 2002 this sequence version replaced gi:21426362.  
All repeats were identified using RepeatMasker:  
Smit,A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L17962  
Center clone name: 374\_E\_23  
-----

\* NOTE: This record contains 82 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 680: contig of 680 bp in length  
\* 681 780: gap of 100 bp  
\* 781 1525: contig of 745 bp in length  
\* 1526 1625: gap of 100 bp  
\* 1626 2364: contig of 739 bp in length  
\* 2365 2464: gap of 100 bp  
\* 2465 3185: contig of 721 bp in length  
\* 3186 3285: gap of 100 bp  
\* 3286 4018: contig of 733 bp in length  
\* 4019 4118: gap of 100 bp  
\* 4119 4862: contig of 744 bp in length  
\* 4863 4962: gap of 100 bp  
\* 4963 5709: contig of 747 bp in length  
\* 5710 5809: gap of 100 bp  
\* 5810 6556: contig of 747 bp in length  
\* 6557 7380: gap of 100 bp  
\* 7381 7480: contig of 724 bp in length  
\* 7481 8223: contig of 743 bp in length  
\* 8224 8323: gap of 100 bp  
\* 8324 9071: contig of 748 bp in length  
\* 9072 9171: gap of 100 bp  
\* 9172 9884: contig of 713 bp in length  
\* 9885 9984: gap of 100 bp  
\* 9985 10709: contig of 725 bp in length  
\* 10710 10809: gap of 100 bp  
\* 10810 11548: contig of 739 bp in length  
\* 11549 11649: gap of 100 bp  
\* 11650 12370: contig of 722 bp in length

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* 12371 12470: gap of 100 bp
* 12471 13194: contig of 724 bp in length
* 13195 13294: gap of 100 bp
* 13295 14031: contig of 737 bp in length
* 14032 14131: gap of 100 bp
* 14132 14850: contig of 719 bp in length
* 14851 14950: gap of 100 bp
* 14951 15695: contig of 745 bp in length
* 15696 15795: gap of 100 bp
* 15796 16539: contig of 744 bp in length
* 16540 17395: contig of 756 bp in length
* 17396 17495: gap of 100 bp
* 17496 18207: contig of 711 bp in length
* 18207 18306: gap of 100 bp
* 18307 19021: contig of 715 bp in length
* 19022 19121: gap of 100 bp
* 19122 19856: contig of 735 bp in length
* 19857 19956: gap of 100 bp
* 19957 20664: contig of 708 bp in length
* 20665 20764: gap of 100 bp
* 20765 21514: contig of 750 bp in length
* 21515 22357: contig of 743 bp in length
* 22358 22457: gap of 100 bp
* 22458 23203: contig of 746 bp in length
* 23204 24031: gap of 100 bp
* 24032 24131: gap of 100 bp
* 24132 24870: contig of 739 bp in length
* 24871 25723: contig of 753 bp in length
* 25724 25823: gap of 100 bp
* 25824 26579: contig of 756 bp in length
* 26580 26679: gap of 100 bp
* 26680 27406: contig of 727 bp in length
* 27407 27507: gap of 100 bp
* 27507 28233: contig of 727 bp in length
* 28234 29065: gap of 100 bp
* 29066 29165: gap of 100 bp
* 29166 29898: contig of 733 bp in length
* 29899 30735: contig of 737 bp in length
* 30736 30835: gap of 100 bp
* 30836 31561: contig of 726 bp in length
* 31562 31661: gap of 100 bp
* 31662 32380: contig of 719 bp in length
* 32381 32480: gap of 100 bp
* 32481 33226: contig of 746 bp in length
* 33227 33326: gap of 100 bp
* 33327 34072: contig of 746 bp in length
* 34073 34172: gap of 100 bp
* 34173 34922: contig of 750 bp in length
* 34923 35022: gap of 100 bp
* 35023 35736: contig of 714 bp in length
* 35737 35836: gap of 100 bp
* 35837 36562: contig of 726 bp in length
* 36563 37394: gap of 100 bp
* 37395 37494: gap of 100 bp
* 37495 38201: contig of 707 bp in length
* 38202 39021: contig of 720 bp in length
* 39022 39121: gap of 100 bp
* 39122 39860: contig of 733 bp in length
* 39861 39960: gap of 100 bp
* 39961 40702: contig of 742 bp in length
* 40703 40802: gap of 100 bp
* 40803 41542: contig of 740 bp in length
* 41543 41642: gap of 100 bp
* 41643 42394: contig of 752 bp in length
* 42395 42494: gap of 100 bp

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```

Query Match          72.2%; Score 13; DB 2; Length 68315;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 CCGGAGNNNNNN 18
Db       12364 CCGGAGNNNNNN 12376

```

```

RESULT 162
AC100130
LOCUS      AC100130
DEFINITION Mus musculus clone RP23-41A2, LOW-PASS SEQUENCE SAMPLING.
ACCESSION  AC100130
VERSION    AC100130.1 GI:17047496
KEYWORDS   HTG: HTGS PHASE0.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus

```

```

REFERENCE 1 (bases 1 to 68316)
AUTHORS   Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE     Mus musculus, clone RP23-41A2
JOURNAL   Unpublished
AUTHORS

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2 (bases 1 to 68316)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barina, N., Bastien, V., Boguslavsky, L., Boukhalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Choepel, Y., Collangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., DeRellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fato, S.,
Ferreira, P., Fitzhugh, W., Gage, D., Gellagan, J., Gadda, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Jones, C., Kamat, A., Karatas, A., Kelle, C., Laroque, K.,
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,
Maclean, C., Macdonald, P., Major, J., Marguis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrum, J.,
Menues, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
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Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R.,
Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, D.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliou, H.,
Viel, R., Vo, A., Wilson, D., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

```

```

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WtBR
Web site: http://www-seg.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information

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Center project name: L14000  
Center clone name: 41\_A\_2

NOTE: This record contains 66 individual  
sequencing reads that have not been assembled into  
contigs. Runs of N are used to separate the reads  
and the order in which they appear is completely  
arbitrary. Low-pass sequence sampling is useful for  
identifying clones that may be gene-rich and allows  
overlap relationships among clones to be deduced.  
However, it should not be assumed that this clone  
will be sequenced to completion. In the event that  
the record is updated, the accession number will  
be preserved.

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918 917: contig of 917 bp in length  
1018 1017: gap of 100 bp  
1972 1971: contig of 954 bp in length  
2072 2071: gap of 100 bp  
2985 2984: contig of 913 bp in length  
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3989 3988: contig of 904 bp in length  
4089 4088: gap of 100 bp  
4991 4990: contig of 902 bp in length  
5091 5090: gap of 100 bp  
6121 6121: contig of 1031 bp in length  
6122 6121: gap of 100 bp  
7176 7176: contig of 955 bp in length  
7276 7276: gap of 100 bp  
8203 8203: contig of 927 bp in length  
8204 8203: gap of 100 bp  
9182 9182: contig of 879 bp in length  
9183 9182: gap of 100 bp  
9283 9282: contig of 930 bp in length  
10212 10212: gap of 100 bp  
10213 10212: gap of 100 bp  
11268 11267: contig of 955 bp in length  
11368 11367: gap of 100 bp  
12370 12369: contig of 1002 bp in length  
12470 12469: gap of 100 bp  
13387 13387: contig of 918 bp in length  
13388 13387: gap of 100 bp  
14478 14478: contig of 991 bp in length  
14479 14478: gap of 100 bp  
15479 15493: contig of 915 bp in length  
15493 15493: gap of 100 bp  
15584 15597: contig of 804 bp in length  
16397 16397: gap of 100 bp  
16398 16497: gap of 100 bp  
17419 17419: contig of 922 bp in length  
17420 17519: gap of 100 bp  
18461 18461: contig of 942 bp in length  
18462 18561: gap of 100 bp  
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19478 19577: gap of 100 bp  
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21635 21635: gap of 100 bp  
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22573 22672: gap of 100 bp  
23643 23643: contig of 971 bp in length  
23743 23743: gap of 100 bp  
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24722 24821: gap of 100 bp  
24822 25774: contig of 953 bp in length  
25775 25874: gap of 100 bp  
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26834 26933: gap of 100 bp  
27852 27852: contig of 919 bp in length  
27953 27953: gap of 100 bp  
28932 28932: contig of 980 bp in length  
29032 29032: gap of 100 bp  
29933 29933: contig of 901 bp in length  
30033 30033: gap of 100 bp  
30939 30939: contig of 906 bp in length

## FEATURES

30940 31039: gap of 100 bp  
31040 31953: contig of 914 bp in length  
31954 32053: gap of 100 bp  
32054 33021: contig of 968 bp in length  
33022 33121: gap of 100 bp  
33122 34030: contig of 909 bp in length  
34031 34130: gap of 100 bp  
34131 35106: contig of 976 bp in length  
35107 35206: gap of 100 bp  
35207 36123: contig of 917 bp in length  
36124 36223: gap of 100 bp  
36224 37138: contig of 915 bp in length  
37139 37238: gap of 100 bp  
37239 38209: contig of 971 bp in length  
38210 38309: gap of 100 bp  
38310 39381: contig of 1072 bp in length  
39382 39481: gap of 100 bp  
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40379 40478: gap of 100 bp  
40479 41424: contig of 946 bp in length  
41425 41524: gap of 100 bp  
41525 42481: contig of 957 bp in length  
42482 42581: gap of 100 bp  
43529 43529: contig of 948 bp in length  
43530 43629: gap of 100 bp  
43630 44561: contig of 932 bp in length  
44562 44661: gap of 100 bp  
44662 45633: contig of 972 bp in length  
45634 45733: gap of 100 bp  
45734 46556: contig of 923 bp in length  
46557 46756: gap of 100 bp  
46757 47661: contig of 905 bp in length  
47662 47761: gap of 100 bp  
47762 48736: contig of 975 bp in length  
48737 48836: gap of 100 bp  
49794 49794: contig of 958 bp in length  
49795 49894: gap of 100 bp  
49895 50797: contig of 903 bp in length  
50798 50897: gap of 100 bp  
50898 51858: contig of 961 bp in length  
51859 51958: gap of 100 bp  
51959 52881: contig of 923 bp in length  
52882 52981: gap of 100 bp  
52982 53950: contig of 965 bp in length  
53951 54050: gap of 100 bp  
54051 54989: contig of 939 bp in length  
54990 55089: gap of 100 bp  
55090 56043: contig of 954 bp in length  
56044 56143: gap of 100 bp  
56144 57042: contig of 899 bp in length  
57043 57142: gap of 100 bp  
57143 58137: contig of 995 bp in length  
58138 58237: gap of 100 bp  
58238 59145: contig of 908 bp in length  
59146 59245: gap of 100 bp  
59246 60209: contig of 964 bp in length  
60210 60309: gap of 100 bp  
60310 61234: contig of 925 bp in length  
61235 61334: gap of 100 bp  
61335 62290: contig of 956 bp in length  
62291 62390: gap of 100 bp  
62391 63347: contig of 957 bp in length  
63348 63447: gap of 100 bp  
63448 64429: contig of 982 bp in length  
64430 64529: gap of 100 bp  
64530 65437: contig of 908 bp in length  
65438 65537: gap of 100 bp  
65538 66485: contig of 948 bp in length  
66486 66585: gap of 100 bp  
66586 67458: contig of 873 bp in length  
67459 67558: gap of 100 bp  
67559 68536: contig of 978 bp in length.

Location/Qualifiers

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="RP23-41A2"  
/clone\_lib="RPCI-23 Female Mouse BAC"

Query Match 72.2%; Score 13; DB 2; Length 68536;  
Best Local Similarity 92.3%; Pred. No. 4.6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGAGNNNNN 18  
||:|||||||  
46650 CCTGAGAGNNNN 46662

RESULT 163  
AC091036 68732 bp DNA linear HTG 24-MAR-2001  
LOCUS Homo sapiens chromosome 15 clone RP11-79J21 map 15, LOW-PASS  
DEFINITION AC091036  
AC091036  
AC091036.1 GI:13443198  
HTG: HTGS PHASEO.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 68732)  
Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
Homo sapiens chromosome 15, clone RP11-79J21  
Unpublished  
2 (bases 1 to 68732)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S., Barnes,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A., Camarata,J., Camporeale,A., Chang,D., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardina,S., Glade,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Karatas,A., Lacroque,K., Lamarats,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., Maclean,C., MacDonald,P., Marquis,N., Matthews,C., McCarthy,M., McKernan,K., McPheters,R., Meldrum,J., Menus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retter,R., Riebeck,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P., Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Straus,N., Subramanian,A., Talamas,J., Tefaye,S., Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zaitoun,J., Zembek,L., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (24-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit,A.F.A. & Green,P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: LJ156  
Center clone name: 79\_J\_21

\* NOTE: This record contains 82 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely

arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overall relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 677: contig of 677 bp in length  
678 777: gap of 100 bp  
778 1552: contig of 775 bp in length  
1553 1652: gap of 100 bp  
1653 2364: contig of 712 bp in length  
2365 2464: gap of 100 bp  
2465 3177: contig of 713 bp in length  
3178 3277: gap of 100 bp  
3278 3988: contig of 711 bp in length  
3989 4088: gap of 100 bp  
4089 4791: contig of 703 bp in length  
4792 4891: gap of 100 bp  
4892 5599: contig of 708 bp in length  
5600 5699: gap of 100 bp  
5700 6489: contig of 790 bp in length  
6490 6589: gap of 100 bp  
6590 7362: contig of 773 bp in length  
7363 7462: gap of 100 bp  
7463 8237: contig of 775 bp in length  
8238 8337: gap of 100 bp  
8338 9049: contig of 712 bp in length  
9050 9149: gap of 100 bp  
9150 9898: contig of 749 bp in length  
9899 10746: gap of 100 bp  
10747 10846: contig of 748 bp in length  
10847 11580: contig of 734 bp in length  
11581 11680: gap of 100 bp  
11681 12390: contig of 710 bp in length  
12391 12490: gap of 100 bp  
12491 13197: contig of 707 bp in length  
13198 13297: gap of 100 bp  
13298 14006: contig of 709 bp in length  
14007 14106: gap of 100 bp  
14107 14875: contig of 769 bp in length  
14876 14975: gap of 100 bp  
14976 15743: contig of 768 bp in length  
15744 15843: gap of 100 bp  
15844 16642: contig of 799 bp in length  
16643 16742: gap of 100 bp  
16743 17473: contig of 731 bp in length  
17474 17573: gap of 100 bp  
17573 18383: contig of 810 bp in length  
18384 18483: gap of 100 bp  
18484 19228: contig of 745 bp in length  
19229 19328: gap of 100 bp  
19329 20115: contig of 787 bp in length  
20116 20215: gap of 100 bp  
20216 20930: contig of 715 bp in length  
20931 21030: gap of 100 bp  
21031 21743: contig of 713 bp in length  
21744 21843: gap of 100 bp  
21844 22547: contig of 704 bp in length  
22548 22647: gap of 100 bp  
22648 23411: contig of 764 bp in length  
23412 23511: gap of 100 bp  
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24360 25159: contig of 800 bp in length  
25160 26031: gap of 100 bp  
26032 26131: contig of 772 bp in length  
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* 2769 28543: contig of 775 bp in length
* 28544 28643: gap of 100 bp
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* 30401 31099: contig of 699 bp in length
* 31100 31199: gap of 100 bp
* 31200 31951: contig of 752 bp in length
* 31952 32051: gap of 100 bp
* 32052 32802: contig of 751 bp in length
* 32803 32902: gap of 100 bp
* 32903 33598: contig of 696 bp in length
* 33599 33698: gap of 100 bp
* 33699 34333: contig of 735 bp in length
* 34334 34533: gap of 100 bp
* 34534 35243: contig of 710 bp in length
* 35244 35343: gap of 100 bp
* 35344 36105: contig of 762 bp in length
* 36106 36305: gap of 100 bp
* 36306 36934: contig of 729 bp in length
* 36935 37034: gap of 100 bp
* 37035 37577: contig of 723 bp in length
* 37578 38570: gap of 100 bp
* 38571 38670: contig of 713 bp in length
* 38671 39423: gap of 100 bp
* 39424 39523: gap of 100 bp
* 39524 40281: contig of 758 bp in length
* 40282 40381: gap of 100 bp
* 40382 41121: contig of 740 bp in length
* 41122 41221: gap of 100 bp
* 41222 41953: contig of 732 bp in length
* 41954 42053: gap of 100 bp
* 42054 42808: contig of 755 bp in length
* 42809 42908: gap of 100 bp
* 42909 43680: contig of 772 bp in length
* 43681 43780: gap of 100 bp
* 43781 44476: contig of 696 bp in length
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* 45390 46138: contig of 749 bp in length
* 46139 46238: gap of 100 bp
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* 47813 47912: gap of 100 bp
* 47913 48668: contig of 756 bp in length
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```

Query Match          72.2% Score 13; DB 2; Length 68732;
Best Local Similarity 92.3%; Pred. No. 4.6e+07;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 6 CCGGAGNNNNNN 18
Db 5593 CCTGAGNNNNNN 5605

RESULT 164
AC100065
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DEFINITION
AC100065
AC100065.1 GI:17047431
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

1 (bases 1 to 68951)
Mus musculus, clone RP23-33F9, LOW-PASS SEQUENCE SAMPLING.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

2 (bases 1 to 68951)
Unpublished
Mus musculus, clone RP23-33F9
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Bouknight, B.,
Brown, A., Camarata, J., Campoliano, A., Chang, J., Chazaro, B.,
Cooper, Y., Collangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S.,
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Haeftord, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Jones, C., Kamat, A., Karatas, A., Kellis, C., Labocque, K.,
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,
Maclean, C., MacDonald, P., Major, J., Margulis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrum, J.,
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Strauss, N., Subramanian, A., Talmas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigglio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A. F. A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WITB
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L13892
Center clone name: 33_F_9

-----
* NOTE: This record contains 86 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

```

1 674: contig of 674 bp in length  
675 774: gap of 100 bp  
775 1499: contig of 725 bp in length  
1500 1599: gap of 100 bp  
1600 2324: contig of 725 bp in length  
2325 2424: gap of 100 bp  
2425 3122: contig of 698 bp in length  
3123 3222: gap of 100 bp  
3223 3907: contig of 685 bp in length  
3908 4007: gap of 100 bp  
4008 4695: contig of 688 bp in length  
4696 4795: gap of 100 bp  
4796 5513: contig of 718 bp in length  
5514 5613: gap of 100 bp  
5614 6333: contig of 720 bp in length  
6334 6433: gap of 100 bp  
6434 7108: contig of 675 bp in length  
7109 7208: gap of 100 bp  
7209 7933: contig of 725 bp in length  
7934 8033: gap of 100 bp  
8034 8753: contig of 720 bp in length  
8754 8853: gap of 100 bp  
8854 9569: contig of 716 bp in length  
9570 9669: gap of 100 bp  
9670 10363: contig of 694 bp in length  
10364 10463: gap of 100 bp  
10464 11151: contig of 688 bp in length  
11152 11251: gap of 100 bp  
11252 11946: contig of 695 bp in length  
11947 12046: gap of 100 bp  
12047 12739: contig of 693 bp in length  
12740 12839: gap of 100 bp  
12840 13543: contig of 704 bp in length  
13544 13643: gap of 100 bp  
13644 14352: contig of 709 bp in length  
14353 14452: gap of 100 bp  
14453 15165: contig of 713 bp in length  
15166 15265: gap of 100 bp  
15266 15995: contig of 730 bp in length  
15996 16095: gap of 100 bp  
16096 16830: contig of 735 bp in length  
16831 16930: gap of 100 bp  
16931 17624: contig of 694 bp in length  
17625 17724: gap of 100 bp  
17725 18448: contig of 724 bp in length  
18449 18548: gap of 100 bp  
18549 19238: contig of 690 bp in length  
19239 19338: gap of 100 bp  
19339 20028: contig of 690 bp in length  
20029 20128: gap of 100 bp  
20129 20815: contig of 687 bp in length  
20816 20915: gap of 100 bp  
20916 21731: contig of 816 bp in length  
21732 21831: gap of 100 bp  
21832 22542: contig of 691 bp in length  
22543 22642: gap of 100 bp  
22623 23329: contig of 707 bp in length  
23330 23429: gap of 100 bp  
23430 24156: contig of 727 bp in length  
24157 24256: gap of 100 bp  
24257 24931: contig of 675 bp in length  
24932 25031: gap of 100 bp  
25032 25762: contig of 731 bp in length  
25763 25862: gap of 100 bp  
25863 26581: contig of 719 bp in length  
26582 27387: gap of 100 bp  
27388 27497: contig of 716 bp in length  
27498 28187: contig of 690 bp in length  
28188 28287: gap of 100 bp  
28289 28957: contig of 670 bp in length  
28958 29057: gap of 100 bp  
29059 29752: contig of 695 bp in length

29753 29853: gap of 100 bp  
29854 30536: contig of 684 bp in length  
30537 30637: gap of 100 bp  
30638 31342: contig of 706 bp in length  
31343 31442: gap of 100 bp  
31443 32145: contig of 703 bp in length  
32146 32246: gap of 100 bp  
32247 32944: contig of 699 bp in length  
32945 33044: gap of 100 bp  
33045 33772: contig of 728 bp in length  
33773 34555: contig of 683 bp in length  
34556 34656: gap of 100 bp  
34657 35365: contig of 710 bp in length  
35366 35465: gap of 100 bp  
35466 36193: contig of 728 bp in length  
36194 36293: gap of 100 bp  
36294 37013: contig of 720 bp in length  
37014 37113: gap of 100 bp  
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39353 39452: gap of 100 bp  
39453 40140: contig of 688 bp in length  
40141 40240: gap of 100 bp  
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41737 41836: gap of 100 bp  
41837 42552: contig of 716 bp in length  
42553 42652: gap of 100 bp  
42653 43365: contig of 713 bp in length  
43366 43465: gap of 100 bp  
43466 44162: contig of 697 bp in length  
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44997 45096: gap of 100 bp  
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45826 45925: gap of 100 bp  
45926 46633: contig of 708 bp in length  
46634 46733: gap of 100 bp  
46734 47422: contig of 689 bp in length  
47423 47522: gap of 100 bp  
47522 48210: contig of 688 bp in length  
48211 48310: gap of 100 bp  
48311 48982: contig of 672 bp in length  
48983 49082: gap of 100 bp  
49083 49774: contig of 692 bp in length  
49775 49874: gap of 100 bp  
49875 50596: contig of 722 bp in length  
50597 50696: gap of 100 bp  
50697 51425: contig of 729 bp in length  
51426 51525: gap of 100 bp  
51526 52260: contig of 735 bp in length  
52261 52360: gap of 100 bp  
52361 53084: contig of 724 bp in length  
53085 53184: gap of 100 bp  
53185 53897: contig of 713 bp in length  
53898 53997: gap of 100 bp  
53998 54670: contig of 673 bp in length  
54671 54771: gap of 100 bp  
54772 55462: contig of 692 bp in length  
55463 55562: gap of 100 bp

Query Match 72.2%; Score 13; DB 2; Length 68951;  
Best Local Similarity 92.3%; Pred. No. 4.6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CCUGAGNNNNNN 18  
DB 60965 CCTGGAGNNNNNN 60977



RESULT 165  
AC090143  
LOCUS  
DEFINITION  
AC090143  
Homo sapiens chromosome 8 clone RP11-263C6 map 8, LOW-PASS SEQUENCE  
AC090143  
AC090143.4 GI:17047108  
VERSION  
HTG: HTGS PHASE0  
KEYWORDS  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 70557)  
Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
Homo sapiens chromosome 8, clone RP11-263C6  
Unpublished  
2 (bases 1 to 70557)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,  
Barna, N., Baeten, V., Boguslavsky, L., Boukhalter, B., Brown, A.,  
Camarta, J., Campiano, A., Choepel, Y., Colangelo, M., Collins, S.,  
Collamore, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J.S.,  
Dodg, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J.,  
Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,  
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,  
Jones, C., Karatas, A., Lakoque, K., Lamazares, R., Landers, T.,  
Lenczky, J., Levine, R., Liu, G., Maclean, C., Macdonald, P.,  
Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K.,  
McNeeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,  
Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H.,  
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Phunkiang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,  
Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Roselli, M.,  
Roy, A., Santos, R., Schauer, S., Schupack, R., Seaman, S., Severy, P.,  
Sougnaz, C., Spencer, B., Strange-Thomann, N., Stojanovic, N.,  
Strauss, N., Subramanian, A., Talamas, J., Teafaye, S., Theodore, J.,  
Travers, M., Travis, N., Trigilio, J., Vasilev, H., Viel, R., Vo, A.,  
Wilson, B., Wu, X., Wyman, D., Ye, W.-J., Young, G., Zaitoun, J.,  
Zemke, L., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Nov 22, 2001 this sequence version replaced gi:14029927.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WITR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L1676  
Center clone name: 263\_C\_6  
-----  
\* NOTE: This record contains 90 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
\* 1  
\* 637: contig of 637 bp in length  
\* 638 737: gap of 100 bp  
\* 738 1410: contig of 673 bp in length  
\* 1411 1510: gap of 100 bp  
\* 1511 2179: contig of 669 bp in length  
\* 2180 2279: gap of 100 bp

2280 2951: contig of 672 bp in length  
\* 2952 3051: gap of 100 bp  
\* 3052 3751: contig of 700 bp in length  
\* 3752 3851: gap of 100 bp  
\* 3852 4543: contig of 692 bp in length  
\* 4544 4643: gap of 100 bp  
\* 4644 5335: contig of 692 bp in length  
\* 5336 5435: gap of 100 bp  
\* 5436 6130: contig of 695 bp in length  
\* 6131 6230: gap of 100 bp  
\* 6231 6916: contig of 686 bp in length  
\* 6917 7017: gap of 100 bp  
\* 7017 7693: contig of 677 bp in length  
\* 7694 7793: gap of 100 bp  
\* 7794 8475: contig of 682 bp in length  
\* 8476 8575: gap of 100 bp  
\* 8576 9244: contig of 669 bp in length  
\* 9245 9344: gap of 100 bp  
\* 9345 10033: contig of 689 bp in length  
\* 10034 10133: gap of 100 bp  
\* 10134 10821: contig of 688 bp in length  
\* 10822 10921: gap of 100 bp  
\* 10922 11604: contig of 683 bp in length  
\* 11605 11704: gap of 100 bp  
\* 11705 12386: contig of 682 bp in length  
\* 12387 12486: gap of 100 bp  
\* 12487 13175: contig of 689 bp in length  
\* 13176 13275: gap of 100 bp  
\* 13275 13964: contig of 689 bp in length  
\* 13965 14064: gap of 100 bp  
\* 14065 14761: contig of 697 bp in length  
\* 14762 14861: gap of 100 bp  
\* 14862 15557: contig of 696 bp in length  
\* 15558 15657: gap of 100 bp  
\* 15658 16342: contig of 685 bp in length  
\* 16343 17135: gap of 100 bp  
\* 16443 17235: contig of 693 bp in length  
\* 17236 17235: gap of 100 bp  
\* 17236 17894: contig of 659 bp in length  
\* 17895 17994: gap of 100 bp  
\* 17995 18680: contig of 686 bp in length  
\* 18681 18780: gap of 100 bp  
\* 18781 19469: contig of 689 bp in length  
\* 19470 19569: gap of 100 bp  
\* 19570 20257: contig of 688 bp in length  
\* 20258 20357: gap of 100 bp  
\* 20358 21033: contig of 676 bp in length  
\* 21034 21133: gap of 100 bp  
\* 21134 21840: contig of 707 bp in length  
\* 21841 21940: gap of 100 bp  
\* 21941 22625: contig of 685 bp in length  
\* 22626 22725: gap of 100 bp  
\* 22726 23415: contig of 690 bp in length  
\* 23416 23515: gap of 100 bp  
\* 23516 24186: contig of 671 bp in length  
\* 24187 24286: gap of 100 bp  
\* 24287 24976: contig of 690 bp in length  
\* 24977 25076: gap of 100 bp  
\* 25077 25766: contig of 690 bp in length  
\* 25767 25866: gap of 100 bp  
\* 25867 26550: contig of 684 bp in length  
\* 26551 26650: gap of 100 bp  
\* 26651 27317: contig of 667 bp in length  
\* 27318 27417: gap of 100 bp  
\* 27418 28106: contig of 689 bp in length  
\* 28107 28206: gap of 100 bp  
\* 28207 28897: contig of 691 bp in length  
\* 28898 28997: gap of 100 bp  
\* 28998 29691: contig of 694 bp in length  
\* 29692 29791: gap of 100 bp  
\* 29792 30469: contig of 678 bp in length  
\* 30470 30569: gap of 100 bp  
\* 30570 31234: contig of 665 bp in length

```

* 31235 31334: gap of 100 bp
* 31235 32019: contig of 685 bp in length
* 32020 32119: gap of 100 bp
* 32120 32809: contig of 690 bp in length
* 32810 32909: gap of 100 bp
* 32910 33576: contig of 667 bp in length
* 33577 33676: gap of 100 bp
* 33677 34370: contig of 694 bp in length
* 34371 34470: gap of 100 bp
* 34471 35139: contig of 669 bp in length
* 35140 35239: gap of 100 bp
* 35240 35935: contig of 696 bp in length
* 35936 36035: gap of 100 bp
* 36036 36706: contig of 671 bp in length
* 36707 36806: gap of 100 bp
* 36807 37489: contig of 683 bp in length
* 37490 37589: gap of 100 bp
* 37590 38276: contig of 687 bp in length
* 38277 38376: gap of 100 bp
* 38377 39046: contig of 670 bp in length
* 39047 39146: gap of 100 bp
* 39147 39822: contig of 676 bp in length
* 39823 39922: gap of 100 bp
* 39923 40583: contig of 661 bp in length
* 40584 40684: gap of 100 bp
* 40684 41381: contig of 698 bp in length
* 41382 41482: gap of 100 bp
* 41482 42179: contig of 698 bp in length
* 42180 42279: gap of 100 bp
* 42280 42971: contig of 692 bp in length
* 42972 43071: gap of 100 bp
* 43072 43768: contig of 697 bp in length
* 43769 43868: gap of 100 bp
* 43869 44559: contig of 691 bp in length
* 44560 44659: gap of 100 bp
* 44660 45328: contig of 669 bp in length
* 45329 45428: gap of 100 bp
* 45429 46121: contig of 693 bp in length
* 46122 46221: gap of 100 bp
* 46222 46911: contig of 690 bp in length
* 46912 47011: gap of 100 bp
* 47012 47704: contig of 693 bp in length
* 47705 47804: gap of 100 bp
* 47805 48487: contig of 683 bp in length
* 48488 48587: gap of 100 bp
* 48588 49280: contig of 693 bp in length
* 49281 49380: gap of 100 bp
* 49381 50070: contig of 690 bp in length
* 50071 50170: gap of 100 bp
* 50171 50866: contig of 696 bp in length
* 50867 50966: gap of 100 bp
* 50967 51654: contig of 688 bp in length
* 51655 51754: gap of 100 bp
* 51755 52441: contig of 687 bp in length
* 52442 52541: gap of 100 bp
* 52542 53220: contig of 679 bp in length
* 53221 53320: gap of 100 bp
* 53321 54016: contig of 696 bp in length

```

Query Match Best Local Similarity 92.3%; Score 13; DB 2; Length 70557; Pred. No. 4.6e+02; Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGAGNNNNN 18  
Db 44553 CCTGAGAGNNNNN 44565

RESULT 166  
AC100674  
LOCUS  
DEFINITION Mus musculus clone RP23-167K24, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC100674

# VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

AC100674.1 GI:117048040  
HTG; HTGS PHASE0.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 71396)  
Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
Mus musculus, clone RP23-167K24  
Unpublished  
2 (bases 1 to 71396)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,  
Anderson, S., Barna, N., Bastien, V., Boguski, L., Bookbinder, B.,  
Brown, A., Camarata, J., Chang, J., Chazotte, B.,  
Choquel, Y., Colangelo, M., Collins, S., Collumore, A., Cook, A.,  
Cooke, P., Dearlano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,  
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardina, S.,  
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-pierre, N.,  
Hagos, B., Heaford, A., Horton, L., Hulme, W., Illie, I., Johnson, R.,  
Jones, C., Kamat, A., Karatas, A., Kells, C., Larocque, K.,  
Lamazares, R., Landers, T., Lehotzky, J., Levine, R., Liu, G.,  
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McCarthy, M., McEwan, P., McKernan, K., McPherson, R., Meldrum, J.,  
Menus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C.,  
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,  
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,  
Raymond, C., Rella, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,  
Roman, J., Roselli, M., Roy, A., Santos, R., Schauer, S., Schupack, R.,  
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stanovic, N.,  
Straus, N., Subramanian, A., Talamas, J., Teefay, S., Theodore, J.,  
Topham, K., Travers, M., Travis, N., Triggilio, J., Vasilev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G.,  
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIRB  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submission@genome.wi.mit.edu  
----- Project Information  
Center project name: 167\_K\_24  
Center clone name: 167\_K\_24

\* NOTE: This record contains 71 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

```

* 1 789 888: gap of 100 bp in length
* 889 1702: contig of 814 bp in length
* 1703 1803 1802: gap of 100 bp in length
* 1803 2642: contig of 840 bp in length
* 2643 2743 2742: gap of 100 bp
* 2743 3637: contig of 895 bp in length
* 3638 3737: gap of 100 bp
* 3738 4635: contig of 898 bp in length
* 4636 4735: gap of 100 bp
* 4736 5657: contig of 922 bp in length
* 5658 5757: gap of 100 bp
* 5758 6692: contig of 935 bp in length
* 6693 6792: gap of 100 bp

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6793 7703: contig of 911 bp in length  
7804 7803: gap of 100 bp in length  
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8743 8842: gap of 100 bp in length  
8843 9787: contig of 945 bp in length  
9788 9887: gap of 100 bp in length  
9888 10819: contig of 932 bp in length  
10820 10919: gap of 100 bp in length  
10920 11808: contig of 889 bp in length  
11809 11908: gap of 100 bp in length  
11909 12830: contig of 922 bp in length  
12831 12930: gap of 100 bp in length  
12931 13847: contig of 917 bp in length  
13848 13947: gap of 100 bp in length  
13948 14886: contig of 939 bp in length  
14887 14986: gap of 100 bp in length  
14987 15911: contig of 925 bp in length  
15912 16011: gap of 100 bp in length  
16012 16903: contig of 892 bp in length  
16904 17003: gap of 100 bp in length  
17004 17906: contig of 903 bp in length  
17907 18006: gap of 100 bp in length  
18007 18931: contig of 925 bp in length  
18932 19031: gap of 100 bp in length  
19032 19945: contig of 914 bp in length  
19946 20045: gap of 100 bp in length  
20046 20951: contig of 906 bp in length  
20952 21051: gap of 100 bp in length  
21052 21949: contig of 898 bp in length  
21950 22049: gap of 100 bp in length  
22050 22950: contig of 901 bp in length  
22951 23945: gap of 100 bp in length  
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24956 25055: gap of 100 bp in length  
25056 25980: contig of 925 bp in length  
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27053 28067: contig of 915 bp in length  
28068 28167: gap of 100 bp in length  
28168 29076: contig of 909 bp in length  
29077 29176: gap of 100 bp in length  
29177 30093: contig of 917 bp in length  
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30194 31099: contig of 906 bp in length  
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32098 32197: gap of 100 bp in length  
32198 33113: contig of 916 bp in length  
33114 34125: contig of 912 bp in length  
34126 34225: gap of 100 bp in length  
34226 35133: contig of 908 bp in length  
35134 35233: gap of 100 bp in length  
35234 36150: contig of 917 bp in length  
36151 36250: gap of 100 bp in length  
36251 37171: contig of 921 bp in length  
37172 37271: gap of 100 bp in length  
37272 38159: contig of 888 bp in length  
38160 38259: gap of 100 bp in length  
38260 39156: contig of 897 bp in length  
39157 39256: gap of 100 bp in length  
39257 40188: contig of 932 bp in length  
40189 40288: gap of 100 bp in length  
40289 41210: contig of 922 bp in length  
41211 41310: gap of 100 bp in length  
41311 42222: contig of 912 bp in length  
42223 42322: gap of 100 bp in length  
42323 43218: contig of 896 bp in length  
43219 43318: gap of 100 bp in length  
43319 44233: contig of 915 bp in length

44234 44334: gap of 100 bp in length  
44334 45245: contig of 913 bp in length  
45245 45346: gap of 100 bp in length  
45347 46261: contig of 915 bp in length  
46262 46361: gap of 100 bp in length  
46362 47279: contig of 918 bp in length  
47280 47379: gap of 100 bp in length  
47380 48275: contig of 897 bp in length  
48277 48376: gap of 100 bp in length  
48377 49282: contig of 906 bp in length  
49283 49382: gap of 100 bp in length  
49383 50305: contig of 923 bp in length  
50306 50405: gap of 100 bp in length  
50406 51314: contig of 909 bp in length  
51315 51414: gap of 100 bp in length  
51415 52335: contig of 921 bp in length  
52336 52436: gap of 100 bp in length  
52436 53163: contig of 728 bp in length  
53164 53263: gap of 100 bp in length  
53264 54210: contig of 947 bp in length  
54211 54310: gap of 100 bp in length  
54311 55199: contig of 889 bp in length  
55200 55299: gap of 100 bp in length  
55300 56212: contig of 913 bp in length  
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56313 57287: contig of 975 bp in length  
57288 57387: gap of 100 bp in length  
57388 58245: contig of 858 bp in length  
58246 58345: gap of 100 bp in length  
58346 59236: contig of 891 bp in length  
59237 59336: gap of 100 bp in length  
59337 60272: contig of 936 bp in length  
60273 60372: gap of 100 bp in length  
60373 61289: contig of 917 bp in length  
61290 61389: gap of 100 bp in length  
61390 62299: contig of 910 bp in length  
62300 62399: gap of 100 bp in length  
62400 63322: contig of 923 bp in length  
63323 63422: gap of 100 bp in length  
63423 64336: contig of 914 bp in length  
64337 64436: gap of 100 bp in length  
64437 65354: contig of 918 bp in length  
65355 65454: gap of 100 bp in length  
65455 66352: contig of 898 bp in length  
66353 66452: gap of 100 bp in length  
66453 67362: contig of 910 bp in length  
67363 67462: gap of 100 bp in length  
67463 68370: contig of 908 bp in length  
68371 68470: gap of 100 bp in length  
68471 69379: contig of 909 bp in length  
69380 69479: gap of 100 bp in length

Query Match 72.2%; Score 13; DB 2; Length 71396;  
Best Local Similarity 92.3%; Pred. No. 4.6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGANNNNN 18  
Db 68364 CCTGAGANNNNN 68376

RESULT 167  
AC026581 72969 bp DNA linear HTG 22-MAR-2000  
LOCUS Homo sapiens clone RP11-67804, LOW-PASS SEQUENCE SAMPLING.  
DEFINITION AC026581  
VERSION AC026581.1 GI:7294166  
KEYWORDS HTG; HTGS\_PHASE0.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 72969)

# AUTHORS TITLE JOURNAL REFERENCE AUTHORS

Birtren, B., Linton, L., Nusbaum, C. and Lander, E.  
Homo sapiens, clone RP11-67804

2 (bases 1 to 72969)

Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bada, F.,  
Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,  
Campoliano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,  
Collamore, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S.,  
Dodgson, S., Domingo, M., Doyle, M., Ferreira, P., Fitzhugh, M., Gage, D.,  
Gardner, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,  
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatae, A.,  
Klein, J., Lacroque, K., Lamazares, R., Landers, T., Lehoczy, J.,  
Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Margulis, N.,  
McCarthy, M., McGowan, P., McGuck, A., McKernan, K., McPheters, R.,  
Melidrim, J., Menus, L., Mihova, T., Miranda, C., Mlangi, V., Morrow, J.,  
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,  
O'Neil, D., Ollivar, T.M., Oliver, J., Peterson, K., Pierre, N.,  
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,  
Roy, A., Santos, R., Schauer, S., Severy, F., Spencer, B.,  
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Tessier, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J.,  
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,  
Young, G., Zainoun, D., Zimmer, A. and Zody, M.

## TITLE

## JOURNAL

## COMMENT

Submitted (22-MAR-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:  
Smit, A.P.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WITB

Web site: http://www-seq.wi.mit.edu

Contact: sequence\_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L8363

Center clone name: 678\_O\_4

\* NOTE: This record contains 88 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 716: contig of 716 bp in length  
\* 717 816: gap of 100 bp  
\* 817 1560: contig of 744 bp in length  
\* 1561 1660: gap of 100 bp  
\* 1661 2397: contig of 737 bp in length  
\* 2398 2497: gap of 100 bp  
\* 2498 3221: contig of 724 bp in length  
\* 3222 3321: gap of 100 bp  
\* 3322 4046: contig of 725 bp in length  
\* 4047 4146: gap of 100 bp  
\* 4147 4863: contig of 717 bp in length  
\* 4864 4963: gap of 100 bp  
\* 4964 5694: contig of 731 bp in length  
\* 5695 5794: gap of 100 bp  
\* 5795 6515: contig of 721 bp in length  
\* 6516 6615: gap of 100 bp  
\* 6616 7343: contig of 728 bp in length  
\* 7344 7443: gap of 100 bp  
\* 7444 8179: contig of 736 bp in length  
\* 8180 8279: gap of 100 bp  
\* 8280 9017: contig of 738 bp in length  
\* 9018 9117: gap of 100 bp

9118 9846: contig of 729 bp in length  
\* 9847 9946: gap of 100 bp  
\* 9947 10676: contig of 730 bp in length  
\* 10677 10776: gap of 100 bp  
\* 10777 11512: contig of 736 bp in length  
\* 11513 11613: gap of 100 bp  
\* 11613 12343: contig of 730 bp in length  
\* 12343 12443: gap of 100 bp  
\* 12443 13171: contig of 729 bp in length  
\* 13171 13271: gap of 100 bp  
\* 13271 13372: contig of 707 bp in length  
\* 13372 13979: gap of 100 bp  
\* 13979 14079: gap of 100 bp  
\* 14079 14792: contig of 714 bp in length  
\* 14792 14892: gap of 100 bp  
\* 14892 14993: contig of 701 bp in length  
\* 14993 15593: gap of 100 bp  
\* 15593 15693: contig of 733 bp in length  
\* 15693 16426: gap of 100 bp  
\* 16426 16526: gap of 100 bp  
\* 16526 17261: contig of 735 bp in length  
\* 17261 17361: gap of 100 bp  
\* 17361 18099: contig of 738 bp in length  
\* 18099 18199: gap of 100 bp  
\* 18199 18942: contig of 743 bp in length  
\* 18942 19042: gap of 100 bp  
\* 19042 19775: contig of 733 bp in length  
\* 19775 19875: gap of 100 bp  
\* 19875 20595: contig of 720 bp in length  
\* 20595 20695: gap of 100 bp  
\* 20695 21432: contig of 737 bp in length  
\* 21432 21532: gap of 100 bp  
\* 21532 22263: contig of 731 bp in length  
\* 22263 22363: gap of 100 bp  
\* 22363 23085: contig of 722 bp in length  
\* 23085 23185: gap of 100 bp  
\* 23185 23902: contig of 717 bp in length  
\* 23902 24002: gap of 100 bp  
\* 24002 24717: contig of 715 bp in length  
\* 24717 24817: gap of 100 bp  
\* 24817 25549: contig of 732 bp in length  
\* 25549 25649: gap of 100 bp  
\* 25649 26395: contig of 746 bp in length  
\* 26395 26495: gap of 100 bp  
\* 26495 27238: contig of 743 bp in length  
\* 27238 27338: gap of 100 bp  
\* 27338 28076: contig of 738 bp in length  
\* 28076 28176: gap of 100 bp  
\* 28176 28894: contig of 718 bp in length  
\* 28894 29735: contig of 741 bp in length  
\* 29735 29835: gap of 100 bp  
\* 29835 30573: contig of 728 bp in length  
\* 30573 30673: gap of 100 bp  
\* 30673 31392: contig of 719 bp in length  
\* 31392 31492: gap of 100 bp  
\* 31492 32223: contig of 731 bp in length  
\* 32223 32323: gap of 100 bp  
\* 32323 33046: contig of 723 bp in length  
\* 33046 33146: gap of 100 bp  
\* 33146 33853: contig of 707 bp in length  
\* 33853 33953: gap of 100 bp  
\* 33953 34691: contig of 728 bp in length  
\* 34691 34791: gap of 100 bp  
\* 34791 35522: contig of 721 bp in length  
\* 35522 35622: gap of 100 bp  
\* 35622 36364: contig of 742 bp in length  
\* 36364 37066: contig of 742 bp in length  
\* 37066 37306: gap of 100 bp  
\* 37306 38052: contig of 746 bp in length  
\* 38052 38152: gap of 100 bp  
\* 38152 38878: contig of 726 bp in length  
\* 38878 38978: gap of 100 bp  
\* 38978 39707: contig of 729 bp in length

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* 39708 39807: gap of 100 bp
* 39808 40529: contig of 722 bp in length
* 40530 40629: gap of 100 bp
* 40630 41363: contig of 734 bp in length
* 41364 41463: gap of 100 bp
* 41464 42185: contig of 722 bp in length
* 42186 42285: gap of 100 bp
* 42286 43013: contig of 728 bp in length
* 43014 43113: gap of 100 bp
* 43114 43823: contig of 710 bp in length
* 43824 43923: gap of 100 bp
* 43924 44657: contig of 734 bp in length
* 44658 44757: gap of 100 bp
* 44758 45502: contig of 745 bp in length
* 45503 45602: gap of 100 bp
* 45603 46323: contig of 721 bp in length
* 46324 46423: gap of 100 bp
* 46424 47167: contig of 744 bp in length
* 47168 47267: gap of 100 bp
* 47268 47993: contig of 726 bp in length
* 47994 48093: gap of 100 bp
* 48094 48810: contig of 717 bp in length
* 48811 48910: gap of 100 bp
* 48911 49639: contig of 729 bp in length
* 49640 49739: gap of 100 bp
* 49740 50468: contig of 729 bp in length
* 50469 50568: gap of 100 bp
* 50569 51284: contig of 716 bp in length
* 51285 51384: gap of 100 bp
* 51385 52109: contig of 725 bp in length
* 52110 52209: gap of 100 bp
* 52210 52945: contig of 736 bp in length
* 52946 53045: gap of 100 bp
* 53046 53783: contig of 738 bp in length
* 53784 53883: gap of 100 bp
* 53884 54621: contig of 738 bp in length
* 54622 54721: gap of 100 bp
* 54722 55447: contig of 726 bp in length
* 55448 55547: gap of 100 bp
* 55548 56291: contig of 744 bp in length
* 56292 56391: gap of 100 bp
* 56392 57110: contig of 719 bp in length
* 57111 57210: gap of 100 bp
* 57211 57938: contig of 728 bp in length

```

```

Query Match 72.2%; Score 13; DB 2; Length 72969;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 6 CUCGAGNNNNNN 18
Db 18936 CUCGAGNNNNNN 18948

```

```

RESULT 168
AC025146
LOCUS Homo sapiens chromosome 1 clone RP11-27H21 map 1, LOW-PASS SEQUENCE
DEFINITION AC025146.1 GI:7158957
ACCESSION AC025146
VERSION AC025146.1
KEYWORDS HTG; HTGS-PHASED.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 73173)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Homo sapiens chromosome 1, clone RP11-27H21
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 73173)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,

```

# TITLE JOURNAL COMMENT

```

Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G.,
Campiano, A., Casle, A., Choe, Y., Colangelo, M., Collins, S.,
Collamore, A., Cooke, P., DeArle, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Gagan, J., Gardina, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hago, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karata, A.,
Klein, J., LaRoque, K., Lamazara, R., Landers, T., Lehotzky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrum, J., Menes, L., Mihova, T., Miranda, C., Menga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rotman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talama, J.,
Tessier, S., Theodore, J., Tirrell, A., Travers, M., Trigglio, J.,
Vassiliev, H., Vse, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zaitoun, J., Zimmer, A. and Zody, M.
Direct Submission (05-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L7962
Center clone name: 27_H_21
-----
* NOTE: This record contains 84 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1
* 801 800: contig of 800 bp in length
* 901 900: gap of 100 bp
* 1680 1680: contig of 780 bp in length
* 1681 1780: gap of 100 bp
* 1781 2570: contig of 790 bp in length
* 2571 2670: gap of 100 bp
* 2671 3445: contig of 775 bp in length
* 3446 3545: gap of 100 bp
* 3546 4328: contig of 783 bp in length
* 4329 4428: gap of 100 bp
* 4429 5197: contig of 769 bp in length
* 5198 5297: gap of 100 bp
* 5298 6047: contig of 750 bp in length
* 6048 6147: gap of 100 bp
* 6148 6927: contig of 780 bp in length
* 6928 7027: gap of 100 bp
* 7028 7806: contig of 779 bp in length
* 7807 7906: gap of 100 bp
* 7907 8702: contig of 796 bp in length
* 8703 8803: gap of 100 bp
* 8803 9572: contig of 770 bp in length
* 9573 9672: gap of 100 bp
* 9673 10454: contig of 782 bp in length
* 10455 10554: gap of 100 bp
* 10555 11340: contig of 786 bp in length
* 11341 11440: gap of 100 bp
* 11441 12218: contig of 778 bp in length
* 12219 12318: gap of 100 bp

```

```

* 12319 13100: contig of 782 bp in length
* 13101 13200: gap of 100 bp
* 13201 13969: contig of 769 bp in length
* 13970 14069: gap of 100 bp
* 14070 14797: contig of 728 bp in length
* 14798 14897: gap of 100 bp
* 14898 15664: contig of 767 bp in length
* 15665 15764: gap of 100 bp
* 15765 16525: contig of 761 bp in length
* 16526 16625: gap of 100 bp
* 16626 17422: contig of 797 bp in length
* 17423 17522: gap of 100 bp
* 17523 18305: contig of 783 bp in length
* 18306 18405: gap of 100 bp
* 18406 19167: contig of 761 bp in length
* 19167 19266: gap of 100 bp
* 19267 20044: contig of 778 bp in length
* 20045 20144: gap of 100 bp
* 20145 20925: contig of 781 bp in length
* 20926 21025: gap of 100 bp
* 21026 21904: contig of 779 bp in length
* 21905 22634: gap of 100 bp
* 22635 22734: gap of 100 bp
* 22735 23484: contig of 749 bp in length
* 23484 24345: gap of 100 bp
* 24346 24445: gap of 100 bp
* 24446 25194: contig of 749 bp in length
* 25195 25294: gap of 100 bp
* 25295 26059: contig of 764 bp in length
* 26059 26158: gap of 100 bp
* 26159 26925: contig of 767 bp in length
* 26926 27025: gap of 100 bp
* 27026 27783: contig of 758 bp in length
* 27784 27883: gap of 100 bp
* 27884 28664: contig of 781 bp in length
* 28665 28764: gap of 100 bp
* 28765 29545: contig of 781 bp in length
* 29546 30422: gap of 100 bp
* 30423 30522: contig of 777 bp in length
* 30523 31299: gap of 100 bp
* 31299 31398: contig of 776 bp in length
* 31399 32159: contig of 761 bp in length
* 32160 32259: gap of 100 bp
* 32260 33040: contig of 781 bp in length
* 33041 33140: gap of 100 bp
* 33141 33912: contig of 772 bp in length
* 33913 34012: gap of 100 bp
* 34013 34794: contig of 782 bp in length
* 34795 34894: gap of 100 bp
* 34895 35664: contig of 769 bp in length
* 35664 35763: gap of 100 bp
* 35764 36536: contig of 773 bp in length
* 36537 37409: contig of 773 bp in length
* 37410 37509: gap of 100 bp
* 37510 38248: contig of 739 bp in length
* 38249 38348: gap of 100 bp
* 38349 39153: contig of 805 bp in length
* 39154 39253: gap of 100 bp
* 39254 40034: contig of 781 bp in length
* 40035 40134: gap of 100 bp
* 40135 40918: contig of 784 bp in length
* 40919 41018: gap of 100 bp
* 41019 41803: contig of 784 bp in length
* 41803 41902: gap of 100 bp
* 41903 42670: contig of 768 bp in length
* 42671 42770: gap of 100 bp
* 42771 43542: contig of 772 bp in length
* 43543 43642: gap of 100 bp
* 43643 44407: contig of 765 bp in length

```

```

* 44408 44507: gap of 100 bp
* 44508 45268: contig of 761 bp in length
* 45269 45368: gap of 100 bp
* 45369 46141: contig of 773 bp in length
* 46142 46241: gap of 100 bp
* 46242 47013: contig of 772 bp in length
* 47014 47113: gap of 100 bp
* 47114 47891: contig of 778 bp in length
* 47892 47991: gap of 100 bp
* 47992 48772: contig of 781 bp in length
* 48773 48872: gap of 100 bp
* 48873 49647: contig of 775 bp in length
* 49648 49747: gap of 100 bp
* 49748 50520: contig of 773 bp in length
* 50521 50620: gap of 100 bp
* 50621 51395: contig of 775 bp in length
* 51396 51495: gap of 100 bp
* 51496 52281: contig of 786 bp in length
* 52282 52381: gap of 100 bp
* 52382 53162: contig of 781 bp in length
* 53163 53262: gap of 100 bp
* 53263 54030: contig of 768 bp in length
* 54031 54130: gap of 100 bp
* 54131 54916: contig of 786 bp in length
* 54917 55016: gap of 100 bp
* 55017 55767: contig of 751 bp in length
* 55768 55867: gap of 100 bp
* 55868 56639: contig of 771 bp in length
* 56639 56738: gap of 100 bp
* 56739 57511: contig of 773 bp in length
* 57512 57611: gap of 100 bp
* 57612 58384: contig of 773 bp in length
* 58385 58484: gap of 100 bp
* 58485 59271: contig of 787 bp in length
* 59272 59371: gap of 100 bp
* 59372 60141: contig of 770 bp in length
* 60142 60241: gap of 100 bp

```

```

Query Match      72.2%; Score 13; DB 2; Length 73173;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      6 CCUGAGNNNNN 18
Db      69671 CCTGAGNNNNN 69683

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```

RESULT 169
AC090991
LOCUS      75974 bp DNA linear HTG-22-MAR-2001
DEFINITION Homo sapiens chromosome 15 clone RP11-100A21 map 15, LOW-PASS
SEQUENCE SAMPLING.
ACCESSION AC090991.1 GI:13431041
VERSION AC090991.1
KEYWORDS HTG; HTGS PHASE0.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 75974)
Birtren,B., Linton,L., Nusbaum,C. and Lander,E.
2 (bases 1 to 75974)
REFERENCE 1
AUTHORS Birtren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 15, clone RP11-100A21
JOURNAL Unpublished
REFERENCE 2
AUTHORS Birtren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Batnra,N., Bastien,V., Boguslavsky,L., Boukhalter,B., Brown,A.,
Cammarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,
Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K.,
Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D.,
Gallagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Heatford,A., Horton,L., Hulme,W.,
Iliev,I., Johnson,R., Jones,C., Karatas,A., Larocque,K.,
Lamazares,R., Landers,T., Lenoczky,J., Levine,R., Liu,G.,

```

TITLE  
JOURNAL  
COMMENT

MacLean, C., Macdonald, P., Marguis, N., Matthews, C., McCarthy, M.,  
McGowan, P., McKernan, K., McPheters, R., Meldrum, J., Meneus, L.,  
Milnova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C.,  
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,  
Peterson, K., Phunhkhang, P., Pierre, N., Pollara, V., Raymond, C.,  
Retta, R., Ribback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,  
Roretci, P., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S.,  
Severy, P., Sougnuez, C., Spencer, B., Stange-Thomann, N.,  
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,  
Theodore, J., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,  
Zainoun, J., Zemбек, L., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (22-MAR-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

## ----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

## ----- Project Information

Center project name: 100\_A\_21

Center clone name: 100\_A\_21

\* NOTE: This record contains 92 individual

\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1  
739: contig of 739 bp in length  
740  
839: gap of 100 bp  
840  
1561: contig of 722 bp in length  
1562  
1661: gap of 100 bp  
1662  
2385: contig of 724 bp in length  
2386  
2485: gap of 100 bp  
2486  
3207: contig of 722 bp in length  
3208  
3307: gap of 100 bp  
3308  
4035: contig of 728 bp in length  
4036  
4135: gap of 100 bp  
4136  
4880: contig of 745 bp in length  
4881  
4980: gap of 100 bp  
4981  
5707: contig of 727 bp in length  
5708  
5807: gap of 100 bp  
5808  
6534: contig of 727 bp in length  
6535  
7374: gap of 100 bp  
7375  
7474: contig of 740 bp in length  
7475  
8179: gap of 100 bp  
8180  
8279: gap of 100 bp  
8280  
9015: contig of 736 bp in length  
9016  
9115: gap of 100 bp  
9116  
9832: contig of 717 bp in length  
9833  
9932: gap of 100 bp  
9933  
10672: contig of 740 bp in length  
10673  
10772: gap of 100 bp  
10773  
11493: contig of 721 bp in length  
11494  
11593: gap of 100 bp  
11594  
12319: contig of 726 bp in length  
12320  
12419: gap of 100 bp  
12420  
13148: contig of 729 bp in length  
13149  
13248: gap of 100 bp  
13249  
13955: contig of 707 bp in length  
13956  
14055: gap of 100 bp  
14056  
14796: contig of 741 bp in length

14797  
14897  
15625  
15724: gap of 100 bp in length  
15725  
15725  
16437: gap of 100 bp in length  
16437  
16537: gap of 100 bp in length  
16537  
17258: contig of 722 bp in length  
17259  
17358: gap of 100 bp in length  
17359  
18075: contig of 717 bp in length  
18076  
18175: gap of 100 bp in length  
18176  
18913: contig of 738 bp in length  
18914  
19013: gap of 100 bp in length  
19014  
19724: contig of 711 bp in length  
19725  
19824: gap of 100 bp in length  
19825  
20541: contig of 717 bp in length  
20542  
20641: gap of 100 bp in length  
20642  
21378: contig of 737 bp in length  
21379  
21478: gap of 100 bp in length  
21479  
22226: contig of 748 bp in length  
22227  
22325: gap of 100 bp in length  
22327  
22337  
23062: contig of 736 bp in length  
23063  
23162: gap of 100 bp in length  
23163  
23897: contig of 735 bp in length  
23898  
23997: gap of 100 bp in length  
23998  
24728: contig of 731 bp in length  
24729  
24828: gap of 100 bp in length  
24829  
25555: contig of 728 bp in length  
25557  
25656: gap of 100 bp in length  
25657  
26385: contig of 729 bp in length  
26386  
26485: gap of 100 bp in length  
26486  
27210: contig of 725 bp in length  
27211  
27310: gap of 100 bp in length  
27311  
28029: contig of 715 bp in length  
28030  
28123: gap of 100 bp in length  
28130  
28858: contig of 729 bp in length  
28859  
28955: gap of 100 bp in length  
28959  
29672: contig of 714 bp in length  
29673  
29772: gap of 100 bp in length  
29773  
30497: contig of 725 bp in length  
30498  
30597: gap of 100 bp in length  
30598  
31314: contig of 717 bp in length  
31315  
31415: gap of 100 bp in length  
31415  
32154: contig of 740 bp in length  
32155  
32254: gap of 100 bp in length  
32255  
32980: contig of 726 bp in length  
32981  
33080: gap of 100 bp in length  
33081  
33814: contig of 734 bp in length  
33815  
33915: gap of 100 bp in length  
33915  
34646: contig of 732 bp in length  
34647  
34745: gap of 100 bp in length  
34747  
35475: contig of 729 bp in length  
35476  
35575: gap of 100 bp in length  
35576  
36283: contig of 708 bp in length  
36284  
36384: gap of 100 bp in length  
36384  
37116: contig of 733 bp in length  
37117  
37215: gap of 100 bp in length  
37217  
37935: contig of 715 bp in length  
37936  
38035: gap of 100 bp in length  
38036  
38777: contig of 742 bp in length  
38778  
38877: gap of 100 bp in length  
38878  
39600: contig of 723 bp in length  
39601  
39700: gap of 100 bp in length  
39701  
40414: contig of 714 bp in length  
40415  
40514: gap of 100 bp in length  
40515  
41248: contig of 734 bp in length  
41249  
41349: gap of 100 bp in length  
41349  
42089: contig of 741 bp in length  
42090  
42189: gap of 100 bp in length  
42190  
42932: contig of 743 bp in length  
42933  
43032: gap of 100 bp in length  
43033  
43765: contig of 733 bp in length  
43766  
43865: gap of 100 bp in length  
43866  
44581: contig of 716 bp in length  
44582  
44681: gap of 100 bp in length

```

* 44682 45412: contig of 721 bp in length
* 45413 45512: gap of 100 bp
* 45513 46239: contig of 727 bp in length
* 46240 46339: gap of 100 bp
* 46340 47063: contig of 724 bp in length
* 47064 47163: gap of 100 bp
* 47164 47883: contig of 720 bp in length
* 47884 47983: gap of 100 bp
* 47984 48718: contig of 735 bp in length
* 48719 48818: gap of 100 bp
* 48819 49535: contig of 717 bp in length
* 49536 49635: gap of 100 bp
* 49636 50359: contig of 724 bp in length
* 50360 50459: gap of 100 bp
* 50460 51195: contig of 736 bp in length
* 51196 51295: gap of 100 bp
* 51296 52032: contig of 737 bp in length
* 52033 52132: gap of 100 bp
* 52133 52837: contig of 705 bp in length
* 52838 52937: gap of 100 bp
* 52938 53648: contig of 711 bp in length
* 53649 53748: gap of 100 bp
* 53749 54477: contig of 729 bp in length
* 54478 54577: gap of 100 bp
* 54578 55313: contig of 736 bp in length
* 55314 56129: contig of 716 bp in length
* 56130 56229: gap of 100 bp
* 56230 56945: contig of 716 bp in length
* 56946 57045: gap of 100 bp

```

```

Query Match 72.2% Score 13; DB 2; Length 75974;
Best Local Similarity 92.3%; Pred. No. 4,6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 6 CCTGAGAGNNNNNN 18
DB 12313 CCTGAGAGNNNNNN 12325

```

```

RESULT 170
AC023453
LOCUS Homo sapiens clone RP11-734K12, LOW-PASS SEQUENCE SAMPLING.
AC023453
DEFINITION Homo sapiens clone RP11-734K12, LOW-PASS SEQUENCE SAMPLING.
AC023453
VERSION AC023453.2 GI:9164172
KEYWORDS HTG; HTGS PHASEO.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 76113)
Birren,B., Linton,L., Nuebaum,C. and Lander,E.
Homo sapiens, clone RP11-734K12
Unpublished
2 (bases 1 to 76113)
Birren,B., Linton,L., Nuebaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavsky,L.,
Boukagaiter,B., Brown,A., Burkett,G., Campolano,A., Castle,A.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
Dearellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M.,
Fenster,J., Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heatford,A., Horton,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heatford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kam,L., Karatas,A.,
Klein,J., Landers,T., Laroque,K., Lehoczy,J., Levine,R.,
Lieu,C., Liu,G., Locke,K., MacDonald,P., Marquis,N., McCarthy,M.,
McEwan,P., McGurk,A., McKernan,K., McNeeters,R., Meltrim,J.,
Meneus,L., Minova,T., Miranda,C., Mlenga,V., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T.M.,
Peterson,K., Pierre,N., Pisanl,C., Pollara,V., Raymond,C.,
Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,

```

# TITLE JOURNAL COMMENT

Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A.,  
Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,  
Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and  
Zody,M.

Direct Submission  
Submitted (14-FEB-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced gi:6970673.  
All repeats were identified using RepeatMasker:  
Smit,A.F.A. & Green,P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information -----  
Center project name: L6552  
Center clone name: 734\_K\_12

\* NOTE: This record contains 79 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

```

1 867: contig of 867 bp in length
868 967: gap of 100 bp
968 1914: contig of 947 bp in length
1915 2014: gap of 100 bp
2015 2863: contig of 849 bp in length
2864 2963: gap of 100 bp
2964 3820: contig of 857 bp in length
3821 3920: gap of 100 bp
3921 4780: contig of 860 bp in length
4781 4880: gap of 100 bp
4881 5781: contig of 901 bp in length
5782 5881: gap of 100 bp
5882 6775: contig of 884 bp in length
6776 6875: gap of 100 bp
6876 7736: contig of 861 bp in length
7737 7836: gap of 100 bp
7837 8724: contig of 888 bp in length
8725 8824: gap of 100 bp
8825 9701: contig of 877 bp in length
9702 9801: gap of 100 bp
9802 10667: contig of 866 bp in length
10668 10767: gap of 100 bp
10768 11614: contig of 847 bp in length
11615 11714: gap of 100 bp
11715 12575: contig of 861 bp in length
12576 12675: gap of 100 bp
12676 13577: contig of 902 bp in length
13578 13677: gap of 100 bp
13678 14570: contig of 893 bp in length
14571 14670: gap of 100 bp
14671 15519: contig of 849 bp in length
15520 15619: gap of 100 bp
15620 16480: contig of 861 bp in length
16481 16580: gap of 100 bp
16581 17433: contig of 851 bp in length
17434 17531: gap of 100 bp
17532 18410: contig of 879 bp in length
18411 18510: gap of 100 bp
18511 19381: contig of 871 bp in length
19382 19481: gap of 100 bp
19482 20311: contig of 830 bp in length
20312 20411: gap of 100 bp

```



```

* 20412 21240: contig of 829 bp in length
* 21241 21340: gap of 100 bp
* 21341 22202: contig of 862 bp in length
* 22203 22302: gap of 100 bp
* 22303 23176: contig of 874 bp in length
* 23177 23277: gap of 100 bp
* 23277 24127: contig of 851 bp in length
* 24128 24227: gap of 100 bp
* 24228 25090: contig of 863 bp in length
* 25091 25190: gap of 100 bp
* 25191 26066: contig of 876 bp in length
* 26067 26166: gap of 100 bp
* 26167 27042: contig of 876 bp in length
* 27043 27143: gap of 100 bp
* 27143 27989: contig of 847 bp in length
* 27990 28089: gap of 100 bp
* 28090 28965: contig of 876 bp in length
* 28966 29065: gap of 100 bp
* 29066 29936: contig of 871 bp in length
* 29937 30036: gap of 100 bp
* 30037 30884: contig of 848 bp in length
* 30885 30984: gap of 100 bp
* 30985 31837: contig of 853 bp in length
* 31838 31937: gap of 100 bp
* 31938 32777: contig of 840 bp in length
* 32778 32877: gap of 100 bp
* 32878 33770: contig of 893 bp in length
* 33771 33770: gap of 100 bp
* 33771 34711: contig of 841 bp in length
* 33871 34711: gap of 100 bp
* 34712 35671: contig of 860 bp in length
* 34812 35771: gap of 100 bp
* 35672 35627: contig of 856 bp in length
* 35772 36227: gap of 100 bp
* 36228 36728: gap of 100 bp
* 36728 37574: contig of 847 bp in length
* 37575 37674: gap of 100 bp
* 37675 38567: contig of 893 bp in length
* 38568 38667: gap of 100 bp
* 38668 39551: contig of 884 bp in length
* 39552 39651: gap of 100 bp
* 39652 40511: contig of 860 bp in length
* 40512 40611: gap of 100 bp
* 40612 41450: contig of 839 bp in length
* 41451 41550: gap of 100 bp
* 41551 42411: contig of 861 bp in length
* 42412 42511: gap of 100 bp
* 42512 43395: contig of 884 bp in length
* 43396 43495: gap of 100 bp
* 43496 44334: contig of 839 bp in length
* 44335 44434: gap of 100 bp
* 44435 45285: contig of 851 bp in length
* 45286 45385: gap of 100 bp
* 45386 46221: contig of 836 bp in length
* 46222 46321: gap of 100 bp
* 46322 47154: contig of 833 bp in length
* 47155 47254: gap of 100 bp
* 47255 48088: contig of 834 bp in length
* 48089 48188: gap of 100 bp
* 48189 49072: contig of 884 bp in length
* 49073 49172: gap of 100 bp
* 49173 50028: contig of 856 bp in length
* 50029 50128: gap of 100 bp
* 50129 50991: contig of 863 bp in length
* 50992 51091: gap of 100 bp
* 51092 51942: contig of 851 bp in length
* 51943 52042: gap of 100 bp
* 52043 52927: contig of 885 bp in length
* 52928 53027: gap of 100 bp
* 53028 53916: contig of 889 bp in length
* 53917 54016: gap of 100 bp
* 54017 54864: contig of 848 bp in length
* 54865 54964: gap of 100 bp
* 54965 55825: contig of 861 bp in length

```

```

* 55826 55925: gap of 100 bp
* 55926 56793: contig of 868 bp in length
* 56794 56893: gap of 100 bp
* 56894 57757: contig of 864 bp in length
* 57758 57857: gap of 100 bp
* 57858 58724: contig of 867 bp in length
* 58725 58824: gap of 100 bp
* 58825 59703: contig of 879 bp in length
* 59704 59803: gap of 100 bp
* 59804 59804: gap of 100 bp
* 60641 60740: gap of 100 bp
* 60741 61624: contig of 884 bp in length
* 61625 61724: gap of 100 bp
* 61725 62603: contig of 879 bp in length
* 62604 62703: gap of 100 bp
* 62704 63574: contig of 871 bp in length
* 63575 63674: gap of 100 bp
* 63675 64546: contig of 872 bp in length
* 64547 64646: gap of 100 bp
* 64647 65519: contig of 873 bp in length
* 65520 65619: gap of 100 bp
* 65620 66487: contig of 868 bp in length
* 66488 66587: gap of 100 bp

```

```

Query Match 72.2% Score 13; DB 2; Length 76113;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 6 CCUCGAGNNNNNN 18
Db 54858 CCTCGAGNNNNNN 54870

```

```

RESULT 171
AC021526 76856 bp DNA linear HTG 13-JUL-2000
LOCUS Homo sapiens clone RP11-351F2, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC021526
AC021526.2 GI:9148724
VERSION HTG; HTGS_PHASE0.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (Bases 1 to 76856)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abrahams, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckert, R., Bida, F.,
Boguslavsky, L., Bouckhalter, B., Brown, A., Burkett, G., Castle, A.,
Choepe, Y., Collangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeBartolo, K., Dewar, K., Domingo, M., Doyle, M., Fenebor, J.,
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J., C., Johnson, R., Jones, C., Kann, U., Karatas, A., Klein, J.,
Landers, T., Lehoczek, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
Mcdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
McPheters, R., Meldrum, J., Meneus, L., Morrow, J., Naylor, J.,
Norman, C. H., O'Connor, T., O'Donnell, P., Olivari, T. M., Peterson, K.,
Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Roachman, D.,
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Vasilev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,
Zimmer, A., and Zody, M.
Direct Submission
TITLE Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

```

```
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 15513
Center clone name: 351_F_2

* NOTE: This record contains 79 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1
873: contig of 872 bp in length
973: gap of 100 bp
973: contig of 882 bp in length
1854: gap of 100 bp
1855: contig of 836 bp in length
2791: gap of 100 bp
2891: contig of 872 bp in length
3763: gap of 100 bp
3863: contig of 873 bp in length
4736: gap of 100 bp
4836: contig of 853 bp in length
5689: gap of 100 bp
5789: contig of 874 bp in length
6663: gap of 100 bp
6763: contig of 828 bp in length
7581: gap of 100 bp
7691: contig of 855 bp in length
8546: gap of 100 bp
8646: contig of 901 bp in length
9547: gap of 100 bp
9647: contig of 882 bp in length
10529: gap of 100 bp
10629: contig of 887 bp in length
11516: gap of 100 bp
12501: contig of 886 bp in length
12601: gap of 100 bp
13503: contig of 902 bp in length
13504: gap of 100 bp
13604: contig of 863 bp in length
14467: gap of 100 bp
14567: contig of 864 bp in length
15431: gap of 100 bp
15531: contig of 866 bp in length
16397: gap of 100 bp
16497: contig of 876 bp in length
17373: gap of 100 bp
17473: contig of 862 bp in length
18335: gap of 100 bp
18435: contig of 873 bp in length
19307: gap of 100 bp
19407: contig of 890 bp in length
20398: gap of 100 bp
20998: contig of 819 bp in length
21217: gap of 100 bp
21317: contig of 857 bp in length
22174: gap of 100 bp
22274: contig of 904 bp in length
23178: gap of 100 bp
23278: contig of 896 bp in length
24173: gap of 100 bp
24274: contig of 888 bp in length
25161: gap of 100 bp
25261: contig of 890 bp in length
26151: gap of 100 bp in length

26152: gap of 100 bp
26252: contig of 867 bp in length
27119: gap of 100 bp
27219: contig of 870 bp in length
28089: gap of 100 bp
28189: contig of 845 bp in length
29034: gap of 100 bp
29134: contig of 878 bp in length
30012: gap of 100 bp
30112: contig of 885 bp in length
30997: gap of 100 bp
31097: contig of 882 bp in length
31979: gap of 100 bp
32079: contig of 916 bp in length
32995: gap of 100 bp
33095: contig of 899 bp in length
33994: gap of 100 bp
34094: contig of 882 bp in length
34976: gap of 100 bp
35076: contig of 899 bp in length
35975: gap of 100 bp
36075: contig of 893 bp in length
36968: gap of 100 bp
37068: contig of 870 bp in length
37937: gap of 100 bp
38037: contig of 854 bp in length
38891: gap of 100 bp
38991: contig of 885 bp in length
39876: gap of 100 bp
39976: contig of 885 bp in length
40861: gap of 100 bp
40961: contig of 869 bp in length
41830: gap of 100 bp
41930: contig of 853 bp in length
42789: gap of 100 bp
42889: contig of 882 bp in length
43771: gap of 100 bp
43871: contig of 882 bp in length
44753: gap of 100 bp
44853: contig of 882 bp in length
45694: gap of 100 bp
45794: contig of 841 bp in length
46661: gap of 100 bp
46761: contig of 867 bp in length
47643: gap of 100 bp
47743: contig of 882 bp in length
48627: gap of 100 bp
48727: contig of 884 bp in length
49557: gap of 100 bp
49657: contig of 830 bp in length
50518: gap of 100 bp
50618: contig of 861 bp in length
51463: gap of 100 bp
51563: contig of 845 bp in length
52443: gap of 100 bp
52543: contig of 880 bp in length
53420: gap of 100 bp
53520: contig of 877 bp in length
54413: gap of 100 bp
54513: contig of 893 bp in length
55406: gap of 100 bp
55506: contig of 893 bp in length
56384: gap of 100 bp
56484: contig of 878 bp in length
57375: gap of 100 bp
57475: contig of 891 bp in length
58321: gap of 100 bp
58421: contig of 846 bp in length
59302: gap of 100 bp
59402: contig of 881 bp in length
60234: gap of 100 bp
60334: contig of 832 bp in length
61204: gap of 100 bp
61304: contig of 870 bp in length
```

\* 61305 62206: contig of 902 bp in length  
\* 62207 62306: contig of 100 bp in length  
\* 62307 63206: contig of 900 bp in length  
\* 63207 63306: gap of 100 bp  
\* 63307 64152: contig of 846 bp in length  
\* 64152 64252: gap of 100 bp  
\* 64252 65126: contig of 874 bp in length  
\* 65126 65227 65226: gap of 100 bp  
\* 65227 66109: contig of 883 bp in length  
\* 66109 66210 66209: gap of 100 bp  
\* 66210 67083: contig of 874 bp in length  
\* 67083 67183: gap of 100 bp  
\* 67183 68039: contig of 856 bp in length  
\* 68039 68139: gap of 100 bp  
\* 68139 69001: contig of 862 bp in length  
\* 69001 69101: gap of 100 bp  
\* 69101 69002

Query Match 72.2%; Score 13; DB 2; Length 76856;  
Best Local Similarity 92.3%; Pred. No. 4.6e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNN 18  
11:|||||  
41824 CCTGAGANNNNN 41836

RESULT 172  
AC015735  
LOCUS AC015735 84680 bp DNA linear HTG 13-JUL-2000  
DEFINITION Homo sapiens clone RP11-1D9, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC015735  
VERSION AC015735.2 GI:9108760  
KEYWORDS HTG; HTGS\_PHASE0.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 84680)  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 84680)  
Homo sapiens chromosome, clone RP11-1D9  
Unpublished  
2 (bases 1 to 84680)  
Britten, B., Linton, L., Nuebaum, C., Lander, E., Allen, N., Anderson, M.,  
Baldwin, J., Barne, N., Beckery, R., Boguslawski, L., Boukhalter, B.,  
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,  
Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,  
Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,  
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
Howland, J., Johnson, R., Jones, C., Kann, L., Karatae, A., Klein, J.,  
Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,  
McGowan, P., McGuck, A., McKernan, K., McLaughlin, J., Meldrum, J.,  
Mortow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,  
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,  
Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Thesfaye, S., Tirrell, A., Vassiliou, H., Vo, A., Wheeler, J., Wu, X.,  
Wyman, D., Ye, W. J., Zimmer, A. and Zoody, M.  
Direct Submission  
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome  
Research, 330 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced gi:6446952.  
All repeats were identified using RepeatMasker:  
Sait, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIRB  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
Project Information  
Center project name: L1435  
Center clone name: L\_D\_9  
\* NOTE: This record contains 86 individual

\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
1  
\* 862: contig of 862 bp in length  
\* 863 962: gap of 100 bp  
\* 962 1864: contig of 902 bp in length  
\* 1864 1964: gap of 100 bp  
\* 1964 2847: contig of 883 bp in length  
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\* 3924 4807: contig of 883 bp in length  
\* 4807 4907: gap of 100 bp  
\* 4907 5781: contig of 874 bp in length  
\* 5781 5881: gap of 100 bp  
\* 5881 6769: contig of 888 bp in length  
\* 6769 6869: gap of 100 bp  
\* 6869 7741: contig of 872 bp in length  
\* 7741 7841: gap of 100 bp  
\* 7841 8717: contig of 876 bp in length  
\* 8717 8817: gap of 100 bp  
\* 8817 9687: contig of 870 bp in length  
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\* 9787 10674: contig of 887 bp in length  
\* 10674 10774: gap of 100 bp  
\* 10774 11628: contig of 854 bp in length  
\* 11628 11728: gap of 100 bp  
\* 11728 12605: contig of 877 bp in length  
\* 12605 12705: gap of 100 bp  
\* 12705 13603: contig of 898 bp in length  
\* 13603 13703: gap of 100 bp  
\* 13703 14623: contig of 920 bp in length  
\* 14623 14723: gap of 100 bp  
\* 14723 15615: contig of 892 bp in length  
\* 15615 15715: gap of 100 bp  
\* 15715 16713: contig of 898 bp in length  
\* 16713 16714: gap of 100 bp  
\* 16714 17532: contig of 879 bp in length  
\* 17532 17692: gap of 100 bp  
\* 17692 18593: contig of 901 bp in length  
\* 18593 18693: gap of 100 bp  
\* 18693 19575: contig of 882 bp in length  
\* 19575 19576: gap of 100 bp  
\* 19576 20562: contig of 887 bp in length  
\* 20562 20662: gap of 100 bp  
\* 20662 21529: contig of 867 bp in length  
\* 21529 21629: gap of 100 bp  
\* 21629 22538: contig of 909 bp in length  
\* 22538 22638: gap of 100 bp  
\* 22638 23494: contig of 856 bp in length  
\* 23494 23594: gap of 100 bp  
\* 23594 24475: contig of 881 bp in length  
\* 24475 24575: gap of 100 bp  
\* 24575 25454: contig of 879 bp in length  
\* 25454 25544: gap of 100 bp  
\* 25544 26449: contig of 895 bp in length  
\* 26449 27417: contig of 868 bp in length  
\* 27417 27517: gap of 100 bp  
\* 27517 28399: contig of 882 bp in length  
\* 28399 28499: gap of 100 bp  
\* 28499 29382: contig of 883 bp in length  
\* 29382 29482: gap of 100 bp  
\* 29482 30389: contig of 907 bp in length  
\* 30389 30489: gap of 100 bp  
\* 30489 31354: contig of 865 bp in length

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* 31355 31454: gap of 100 bp
* 31455 32330: contig of 876 bp in length
* 32331 32430: gap of 100 bp
* 32431 33318: contig of 888 bp in length
* 33319 33418: gap of 100 bp
* 33419 34297: contig of 879 bp in length
* 34298 34397: gap of 100 bp
* 34398 35286: contig of 889 bp in length
* 35287 35387: gap of 100 bp
* 35387 36297: contig of 911 bp in length
* 36298 37301: contig of 904 bp in length
* 37302 37401: gap of 100 bp
* 37402 38302: contig of 901 bp in length
* 38303 38402: gap of 100 bp
* 38403 39297: contig of 895 bp in length
* 39298 39397: gap of 100 bp
* 39398 40303: contig of 906 bp in length
* 40304 40403: gap of 100 bp
* 40404 41298: contig of 895 bp in length
* 41299 41398: gap of 100 bp
* 41399 42273: contig of 875 bp in length
* 42274 42373: gap of 100 bp
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* 43258 43357: gap of 100 bp
* 43358 44276: contig of 919 bp in length
* 44277 44376: gap of 100 bp
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* 45243 45342: gap of 100 bp
* 45343 46228: contig of 886 bp in length
* 46229 47212: gap of 100 bp
* 47213 47312: contig of 884 bp in length
* 47313 48218: gap of 100 bp
* 48219 49203: contig of 885 bp in length
* 49204 49303: gap of 100 bp
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* 50201 50301: gap of 100 bp
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* 51197 51296: gap of 100 bp
* 51297 52191: contig of 895 bp in length
* 52192 52292: gap of 100 bp
* 52293 53163: contig of 872 bp in length
* 53164 53263: gap of 100 bp
* 53264 54112: contig of 845 bp in length
* 54113 54212: gap of 100 bp
* 54213 55083: contig of 871 bp in length
* 55084 55183: gap of 100 bp
* 55184 56091: contig of 908 bp in length
* 56092 56191: gap of 100 bp
* 56192 57072: contig of 881 bp in length
* 57073 57172: gap of 100 bp
* 57173 58086: contig of 914 bp in length
* 58087 58186: gap of 100 bp
* 58187 59075: contig of 889 bp in length
* 59076 59175: gap of 100 bp
* 59176 60054: contig of 879 bp in length
* 60055 60154: gap of 100 bp
* 60155 61041: contig of 887 bp in length
* 61042 61141: gap of 100 bp
* 61142 62035: contig of 894 bp in length
* 62036 62135: gap of 100 bp
* 62136 63027: contig of 892 bp in length
* 63028 63127: gap of 100 bp
* 63128 64018: contig of 891 bp in length
* 64019 64118: gap of 100 bp
* 64119 65012: contig of 894 bp in length
* 65013 65112: gap of 100 bp
* 65113 65992: contig of 880 bp in length
* 65993 66092: gap of 100 bp
* 66093 66959: contig of 867 bp in length
* 67059: gap of 100 bp

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Query Match      72.2%  Score 13;  D8 2;  Length 84680;
Best Local Similarity 92.3%  Pred. No. 4,6e+02;
Matches 12;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;
Qy      6  CCUGAGAGNNNNNN 18
Db      50194  CCTGAGAGNNNNN 50206

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RESULT 173
AC140498
LOCUS
DEFINITION
Homosapiens chromosome 8 clone CTD-3029615 map 8, LOW-PASS
SEQUENCE SAMPLING.
AC140498
VERSION
AC140498.1 GI:28475780
KEYWORDS
HTG; HTGS PHASE0.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 87463)
REFERENCE
Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone CTD-3029615
JOURNAL
Unpublished
2 (bases 1 to 87463)
AUTHORS
Birren,B., Nusbaum,C., Lander,E., Abouelella,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barina,N., Bastien,Y., Bloom,T.,
Boguslavsky,L., Bouknight,B., Camarata,J., Chang,J., Choepel,Y.,
Collins,A., Cook,A., Cooke,P., Corum,B., Deaellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamc,A., Karatas,A., Kelis,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrum,J., Menus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,J., Peterson,K., Phunhang,P., Pierre,N.,
Rachupka,A., Ramsamy,U., Raymond,C., Rette,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schnupack,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zemek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-FEB-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02144, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

```

TITLE  
JOURNAL  
COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
Project Information  
Center project name: L29357  
Center clone name: 3029\_6\_15

\* NOTE: This record contains 80 individual  
\* sequencing reads that have not been assembled into

```
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*
* 1
* 963: contig of 963 bp in length
* 964
* 1063: gap of 100 bp
* 1064
* 2039: contig of 976 bp in length
* 2040
* 2139: gap of 100 bp
* 2140
* 3099: contig of 960 bp in length
* 3100
* 3199: gap of 100 bp
* 3200
* 4183: contig of 984 bp in length
* 4184
* 4283: gap of 100 bp
* 4284
* 5281: contig of 998 bp in length
* 5282
* 5381: gap of 100 bp
* 5382
* 6395: contig of 1014 bp in length
* 6396
* 6495: gap of 100 bp
* 6496
* 7501: contig of 1006 bp in length
* 7502
* 8626: contig of 1025 bp in length
* 8627
* 8726: gap of 100 bp
* 8727
* 9727: contig of 1001 bp in length
* 9728
* 9827: gap of 100 bp
* 9828
* 10826: contig of 999 bp in length
* 10827
* 10926: gap of 100 bp
* 10927
* 11899: contig of 973 bp in length
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* 11999: gap of 100 bp
* 12000
* 12952: contig of 953 bp in length
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* 13052: gap of 100 bp
* 13053
* 14016: contig of 964 bp in length
* 14017
* 14116: gap of 100 bp
* 14117
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* 15120
* 15219: gap of 100 bp
* 15220
* 16221: contig of 1002 bp in length
* 16222
* 16321: gap of 100 bp
* 16322
* 17311: contig of 990 bp in length
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* 17411: gap of 100 bp
* 17412
* 18416: contig of 1005 bp in length
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* 18516: gap of 100 bp
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* 21789: gap of 100 bp
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* 22912: gap of 100 bp
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* 23901: contig of 989 bp in length
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* 34862
* 34961: gap of 100 bp
*
*
* 34962
* 35944
* 36044
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* 42484: contig of 1005 bp in length
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* 42584: gap of 100 bp
* 42585
* 43605: contig of 1021 bp in length
* 43606
* 43705: gap of 100 bp
* 43706
* 44734: contig of 1029 bp in length
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* 44834: gap of 100 bp
* 44835
* 45838: contig of 1004 bp in length
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* 45938: gap of 100 bp
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* 46923: contig of 985 bp in length
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* 47023: gap of 100 bp
* 47024
* 48048: contig of 1025 bp in length
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* 48148: gap of 100 bp
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* 49137: contig of 989 bp in length
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* 49237: gap of 100 bp
* 49238
* 50219: contig of 982 bp in length
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* 51411: gap of 100 bp
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* 53538: contig of 1024 bp in length
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* 53638: gap of 100 bp
* 53639
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* 54745
* 55759: contig of 1015 bp in length
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* 55859: gap of 100 bp
* 55860
* 56852: contig of 993 bp in length
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* 56953
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* 58964: contig of 934 bp in length
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* 60183: gap of 100 bp
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* 61175: contig of 992 bp in length
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* 61276
* 62294: contig of 1019 bp in length
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* 62394: gap of 100 bp
* 62395
* 63406: contig of 1012 bp in length
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* 63506: gap of 100 bp
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* 64496: contig of 990 bp in length
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* 64596: gap of 100 bp
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* 65587: contig of 991 bp in length
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* 65687: gap of 100 bp
* 65688
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* 66774: gap of 100 bp
* 66775
* 67752: contig of 978 bp in length
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* 67853
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* 72253
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* 75459: contig of 993 bp in length
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* 70629 71576: contig of 948 bp in length
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* 72731 73669: contig of 939 bp in length
* 73670 73769: gap of 100 bp

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 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 6 CCTGGAGNNNNNN 18
Db 7252 CCTGGAGNNNNNN 7264

RESULT 175
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LOCUS AX695818 92726 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1445 from Patent WO03008583.
ACCESSION AX695818
VERSION AX695818.1 GI:29418972
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Morris, D.W. and Engelhard, E.K.
TITLE Novel compositions and methods for cancer
JOURNAL Patent: WO 03008583-A 1445 30-JUN-2003;
FEATURES
source Location/Qualifiers
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/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

ORIGIN
Query Match 72.2% Score 13; DB 6; Length 92726;
Best Local Similarity 92.3%; Pred. No. 4.6e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCTGGAGNNNNNN 18
Db 155 CCTGGAGNNNNNN 143

RESULT 176
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LOCUS AC013392
DEFINITION Homo sapiens chromosome 2 clone RP11-429N24 map 2, LOW-PASS
SEQUENCE SAMPLING.
AC013392
AC013392.3 GI:9123920
VERSION HTG; HTGS_PHASE0.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
TITLE Baldwin, J., Batra, N., Becker, R., Boguslavsky, L., Bouckgeater, B.,
JOURNAL Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
REFERENCE Cooke, P., Dearielano, K., Dewar, C., Domingo, M., Donelan, L., Doyle, M.,
AUTHORS Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,
JOURNAL Galagan, J., Gardyna, S., Grant, G., Hages, B., Heaford, A., Horton, L.,
AUTHORS Hawland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
REFERENCE Lehoczy, J., Lieu, C., Locke, K., Macdonald, P., Marguis, N.,
AUTHORS McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,
TITLE Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
JOURNAL Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
REFERENCE Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talmas, J.,
AUTHORS Testfaye, S., Tittell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
JOURNAL Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
TITLE Direct Substitution
JOURNAL Submitted (09-NOV-1999) Whitehead Institute/MIT Center for Genome
COMMENT Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:6425709.
All repeats were identified using RepeatMasker.

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Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
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Center: Whitehead Institute/ MIT Center for Genome Research  
Genome Center  
Center code: MIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence.submissions@genome.wi.mit.edu  
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Project Information  
Center project name: L3805  
Center clone name: 429\_N\_24  
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\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
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Query Match 72.2% Score 13; DB 2; Length 99591;
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Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 6 CCGGAGNNNNNN 18
Db 35233 CCGGAGNNNNNN 35245

RESULT 177
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50 unordered pieces.
AC142060.1 GI:29135531
HTG: HTGS_PHASE1.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 99630)
REFERENCE
AUTHORS Wuzny,D.,Watte,M.,Metzker,M.,Lee,A.,Abramson,S.,Adams,C.,Alder,J.,
Allen,C.,Allen,H.,Albrooks,S.,Amth,A.,Angiano,D.,
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TITLE
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AUTHORS
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COMMENT

Morris,S.,Mundasa,M.,Murphy,M.,Nair,L.,Nankervis,C.,Neal,D.,
Newton,N.,Nguyen,N.,Norris,S.,Nwaekelam,O.,Okonji,G.,
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Waldron,L.,Walker,B.,Wang,J.,Wang,Q.,Wang,S.,Warren,J.,
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Zhao,S.,Dunn,D.,von Niederhausern,A.,Weiss,R.,Smith,D.R.,
Holt,R.A.,Smith,H.O.,Weinstock,G. and Gibbs,R.A.

Direct Submission
Unpublished
2 (bases 1 to 99630)
Submitted (21-MAR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GM02
Center clone name: CH230-21H3
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 69017 bases at least Q40
Consensus quality: 78942 bases at least Q30
Consensus quality: 85937 bases at least Q20
Estimated insert size: 76134; sum-of-contigs estimation
Quality coverage: 1x in Q20 bases; sum-of-contigs estimation

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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 50 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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## FEATURES

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 Db 73973 CCTGAGANNNNNN 73985

RESULT 178  
AC091367.0/c  
WPCOMMENT

Sequence split into 6 fragments LOCUS AC091367 Accession AC091367

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AC091367_5	500001	519219

LOCUS AC091367  
 DEFINITION Rattus norvegicus clone CH230-unknown, \*\*\* SEQUENCING IN PROGRESS  
 \*\*\* 77 unordered pieces.

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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE  
AUTHORS

1 (bases 1 to 519219)  
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,  
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Nguyen, N., Nickerson, E., Nwokweto, S., Ogun, M., Okunolu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L., Qureshi, M., Ren, Y., Rivera, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Sawyer, G., Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I., Soederstrom, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Swalek, A., Taber, P., Tameris, A., Tameris, K., Tang, H., Tansley, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Uman, K., Vazquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wlezyk, R., Woodson, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.

Unpublished  
Direct Submission  
2 (bases 1 to 519219)  
Worley, K.C.  
Submitted (18-APR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 519219)  
Worley, K.C.  
Submitted (26-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Sep 26, 2002 this sequence version replaced gi:13661933.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: TUEX  
Center clone name: CH230-unknown  
----- Summary Statistics  
Assembly program: Phrap, version 0.990329  
Consensus quality: 167367 bases at least Q40  
Consensus quality: 178727 bases at least Q30  
Consensus quality: 187406 bases at least Q20  
Estimated insert size: 261798; sum-of-contigs estimation  
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

----- NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html))  
\* NOTE: This sequence may represent more than one clone.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 77 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 10492: contig of 10492 bp in length  
\* 10493 10592: gap of unknown length  
\* 10593 22069: contig of 11477 bp in length  
\* 22070 22169: gap of unknown length  
\* 22170 25007: contig of 2838 bp in length  
\* 25008 25107: gap of unknown length  
\* 25108 27865: contig of 2758 bp in length  
\* 27866 27965: gap of unknown length  
\* 27966 253152: contig of 225187 bp in length  
\* 253153 253252: gap of unknown length  
\* 253253 256213: contig of 2961 bp in length

256214 256313: gap of unknown length  
\* 256314 322664: contig of 66351 bp in length  
\* 322665 332765: gap of unknown length  
\* 332766 335240: contig of 12476 bp in length  
\* 335241 335340: gap of unknown length  
\* 335341 348395: contig of 13055 bp in length  
\* 348396 348495: gap of unknown length  
\* 348496 359045: contig of 10551 bp in length  
\* 359047 359146: gap of unknown length  
\* 359147 370030: contig of 10884 bp in length  
\* 370031 370130: gap of unknown length  
\* 370131 381017: contig of 10887 bp in length  
\* 381018 381117: gap of unknown length  
\* 381118 391885: contig of 10766 bp in length  
\* 391886 391985: gap of unknown length  
\* 391986 407863: contig of 15878 bp in length  
\* 407864 407963: gap of unknown length  
\* 407964 419853: contig of 11890 bp in length  
\* 419854 419953: gap of unknown length  
\* 419954 423130: contig of 3177 bp in length  
\* 423131 423230: gap of unknown length  
\* 423231 427402: contig of 4172 bp in length  
\* 427403 427502: gap of unknown length  
\* 427503 428519: contig of 1017 bp in length  
\* 428520 428619: gap of unknown length  
\* 428620 429743: contig of 1124 bp in length  
\* 429744 429843: gap of unknown length  
\* 429844 431152: contig of 1309 bp in length  
\* 431153 431252: gap of unknown length  
\* 431253 432285: contig of 1032 bp in length  
\* 432286 432385: gap of unknown length  
\* 432386 433461: contig of 1076 bp in length  
\* 433462 433560: gap of unknown length  
\* 433561 434982: contig of 1422 bp in length  
\* 434983 435082: gap of unknown length  
\* 435083 436447: contig of 1365 bp in length  
\* 436448 436547: gap of unknown length  
\* 436548 437572: contig of 1025 bp in length  
\* 437573 437672: gap of unknown length  
\* 437673 438994: contig of 1322 bp in length  
\* 438995 439094: gap of unknown length  
\* 439095 440323: contig of 1229 bp in length  
\* 440324 440423: gap of unknown length  
\* 440424 441494: contig of 1071 bp in length  
\* 441495 441594: gap of unknown length  
\* 441595 443035: contig of 1441 bp in length  
\* 443036 443135: gap of unknown length  
\* 443136 444199: contig of 1064 bp in length  
\* 444200 444299: gap of unknown length  
\* 444300 445615: contig of 1316 bp in length  
\* 445616 445715: gap of unknown length  
\* 445716 447329: contig of 1614 bp in length  
\* 447330 447429: gap of unknown length  
\* 447430 448522: contig of 1093 bp in length  
\* 448523 448622: gap of unknown length  
\* 448623 449996: contig of 1374 bp in length  
\* 449997 450096: gap of unknown length  
\* 450097 451111: contig of 1015 bp in length  
\* 451112 452216: contig of 1005 bp in length  
\* 452217 452316: gap of unknown length  
\* 452317 453405: contig of 1089 bp in length  
\* 453406 453505: gap of unknown length  
\* 453506 454758: contig of 1253 bp in length  
\* 454759 454859: gap of unknown length  
\* 454860 456425: contig of 1567 bp in length  
\* 456426 456525: gap of unknown length  
\* 456526 457806: contig of 1281 bp in length  
\* 457807 457906: gap of unknown length  
\* 457907 459589: contig of 1683 bp in length  
\* 459590 459690: gap of unknown length  
\* 459691 460963: contig of 1274 bp in length  
\* 460964 461063: gap of unknown length

\* 461064 462922: contig of 1859 bp in length  
\* 462923 463022: gap of unknown length  
\* 463023 464760: contig of 1738 bp in length  
\* 464761 464860: gap of unknown length  
\* 464861 466416: contig of 1556 bp in length  
\* 466417 466516: gap of unknown length

Query Match 72.2%; Score 13; DB 2; Length 110000;  
Best Local Similarity 92.3%; Pred. No. 4.5e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
Db 10599 CCTGGAGAGNNNNNN 10587

RESULT 179  
AC107099\_2  
WPCOMMENT  
Sequence split into 6 fragments LOCUS AC107099 Accession AC107099  
Fragment Name Begin End  
AC107099\_0 1 110000  
AC107099\_1 100001 210000  
AC107099\_2 200001 310000  
AC107099\_3 300001 410000  
AC107099\_4 400001 510000  
AC107099\_5 500001 541716  
Continuation (3 of 6) of AC107099 from base 200001 (AC107099 Rattus norvegicus clone CH2)

Query Match 72.2%; Score 13; DB 2; Length 110000;  
Best Local Similarity 92.3%; Pred. No. 4.5e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
Db 26513 CCTGGAGAGNNNNNN 26525

RESULT 180  
AC130665\_1/c  
WPCOMMENT  
Sequence split into 4 fragments LOCUS AC130665 Accession AC130665  
Fragment Name Begin End  
AC130665\_0 1 110000  
AC130665\_1 100001 210000  
AC130665\_2 200001 310000  
AC130665\_3 300001 389215  
Continuation (2 of 4) of AC130665 from base 100001 (AC130665 Mus musculus clone RP23-369)

Query Match 72.2%; Score 13; DB 2; Length 110000;  
Best Local Similarity 92.3%; Pred. No. 4.5e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
Db 72266 CCTGGAGAGNNNNNN 72254

RESULT 181  
AC145312\_0/c  
WPCOMMENT  
Sequence split into 4 fragments LOCUS AC145312 Accession AC145312  
Fragment Name Begin End  
AC145312\_0 1 110000  
AC145312\_1 100001 210000  
AC145312\_2 200001 310000  
AC145312\_3 300001 408009  
AC145312 408009 bp DNA linear HTG 23-JUN-2003  
DEFINITION Homo sapiens chromosome 16 clone RP11-1398M15, WORKING DRAFT  
ACCESSION AC145312  
VERSION AC145312.1 GI:32141371  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.

SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE  
AUTHORS  
DOE Joint Genome Institute.  
TITLE  
Sequencing of Human Chromosome 16  
JOURNAL  
Unpublished  
REFERENCE  
AUTHORS  
DOE Joint Genome Institute.  
TITLE  
Direct Submission  
Submitted (23-JUN-2003) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: <http://www.jgi.doe.gov>

Project Information  
Center Project Name: 2756769  
Center Clone Name: RPCI-11\_1398M15

Summary Statistics  
Consensus quality: 367259 bases at least Q40  
Consensus quality: 376423 bases at least Q30  
Consensus quality: 383403 bases at least Q20  
Estimated insert size: 175000; agarose-gel estimation  
Estimated insert size: 399709; sum-of-contigs estimation  
Quality coverage: 12.41 in Q20 bases; agarose-gel estimation  
Quality coverage: 5.43 in Q20 bases; sum-of-contigs estimation.  
NOTE: This is a 'working draft' sequence. It currently  
\* consists of 84 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1  
1197 1196: contig of 1196 bp in length  
1297 1296: gap of unknown length  
2412 2412: contig of 1116 bp in length  
2413 2512: gap of unknown length  
2513 4010: contig of 1498 bp in length  
4011 4110: gap of unknown length  
4111 5217: contig of 1107 bp in length  
5218 5317: gap of unknown length  
5318 6752: contig of 1435 bp in length  
6753 6852: gap of unknown length  
6853 8157: contig of 1305 bp in length  
8158 8257: gap of unknown length  
8258 9436: gap of unknown length  
9437 9536: contig of 1179 bp in length  
9537 10665: contig of 1129 bp in length  
10666 10765: gap of unknown length  
10766 12233: contig of 1368 bp in length  
12134 12233: gap of unknown length  
12234 13334: contig of 1101 bp in length  
13335 13434: gap of unknown length  
13435 14783: contig of 1349 bp in length  
14784 14883: gap of unknown length  
14884 16159: contig of 1276 bp in length  
16160 16259: gap of unknown length  
16260 17298: contig of 1039 bp in length  
17299 17398: gap of unknown length  
17399 18565: contig of 1167 bp in length  
18566 18665: gap of unknown length  
18666 19866: contig of 1201 bp in length  
19867 19966: gap of unknown length  
19967 21434: contig of 1467 bp in length  
21434 21533: contig of 1467 bp in length  
21534 23000: gap of unknown length  
23001 23100: contig of 1467 bp in length  
23101 24648: contig of 1548 bp in length

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* 24649 24748: gap of unknown length
* 24749 26165: contig of 1417 bp in length
* 26166 26265: gap of unknown length
* 26266 27599: contig of 1334 bp in length
* 27600 27699: gap of unknown length
* 27700 29089: contig of 1390 bp in length
* 29090 29189: gap of unknown length
* 29190 30621: contig of 1432 bp in length
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* 30722 32172: contig of 1451 bp in length
* 32173 32272: gap of unknown length
* 32273 33761: contig of 1489 bp in length
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* 33862 35038: contig of 1177 bp in length
* 35039 35138: gap of unknown length
* 35139 36681: contig of 1543 bp in length
* 36682 36781: gap of unknown length
* 36782 38327: contig of 1546 bp in length
* 38328 38427: gap of unknown length
* 38428 39450: contig of 1023 bp in length
* 39451 39550: gap of unknown length
* 39551 40681: contig of 1131 bp in length
* 40682 40781: gap of unknown length
* 40782 42221: contig of 1440 bp in length
* 42222 42321: gap of unknown length
* 42322 43385: contig of 1064 bp in length
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* 43486 45081: contig of 1596 bp in length
* 45082 45181: gap of unknown length
* 45182 46279: contig of 1098 bp in length
* 46280 46379: gap of unknown length
* 46380 47437: contig of 1058 bp in length
* 47438 47537: gap of unknown length
* 47538 48993: contig of 1456 bp in length
* 48994 49093: gap of unknown length
* 49094 50562: contig of 1469 bp in length
* 50563 50662: gap of unknown length
* 50663 52415: contig of 1753 bp in length
* 52416 52515: gap of unknown length
* 52516 54065: contig of 1550 bp in length
* 54066 54165: gap of unknown length
* 54166 55666: contig of 1501 bp in length
* 55667 55766: gap of unknown length
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* 57875 57974: gap of unknown length
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* 59803 59902: gap of unknown length
* 59904 62008: contig of 2106 bp in length
* 62009 62108: gap of unknown length
* 62109 64347: contig of 2239 bp in length
* 64348 64447: gap of unknown length
* 64448 66153: contig of 1706 bp in length
* 66154 66253: gap of unknown length
* 66254 68873: contig of 2620 bp in length
* 68874 68973: gap of unknown length
* 68975 71129: contig of 2156 bp in length
* 71130 71229: gap of unknown length
* 71230 73183: contig of 1954 bp in length
* 73184 73283: gap of unknown length
* 73284 75892: contig of 2609 bp in length
* 75893 75992: gap of unknown length
* 75993 78233: contig of 2241 bp in length
* 78234 78333: gap of unknown length
* 78334 80553: contig of 2220 bp in length
* 80554 80653: gap of unknown length
* 80654 82812: contig of 2159 bp in length
* 82813 82912: gap of unknown length
* 82913 84728: contig of 1816 bp in length
* 84729 84828: gap of unknown length
* 84829 87233: contig of 2405 bp in length
* 87234 87333: gap of unknown length
* 87334 90139: contig of 2806 bp in length
* 90140 90239: gap of unknown length

```

```

* 90240 92563: contig of 2324 bp in length
* 92564 92663: gap of unknown length
* 92664 95367: contig of 2704 bp in length
* 95368 95467: gap of unknown length
* 95468 98282: contig of 2815 bp in length
* 98283 98382: gap of unknown length
* 98383 100819: contig of 2437 bp in length
* 100820 100919: gap of unknown length
* 100920 103443: contig of 2524 bp in length
* 103444 103543: gap of unknown length
* 103544 106164: contig of 2621 bp in length
* 106165 106264: gap of unknown length
* 106265 109600: contig of 3336 bp in length
* 109601 109700: gap of unknown length
* 109701 112652: contig of 2952 bp in length
* 112653 112752: gap of unknown length
* 112753 115031: contig of 2279 bp in length
* 115032 115131: gap of unknown length
* 115132 118017: contig of 2886 bp in length
* 118018 118117: gap of unknown length
* 118118 120779: contig of 2662 bp in length
* 120780 120879: gap of unknown length
* 120880 124557: contig of 3678 bp in length
* 124558 124657: gap of unknown length
* 124659 128048: contig of 4392 bp in length
* 128049 129050: gap of unknown length
* 129051 129150: contig of 4648 bp in length
* 129151 133797: gap of unknown length
* 133798 133897: gap of unknown length
* 133898 139769: contig of 5872 bp in length
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* 139870 145264: contig of 5395 bp in length
* 145265 145364: gap of unknown length
* 145365 151079: contig of 5715 bp in length
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* 151180 156310: contig of 5131 bp in length
* 156311 156410: gap of unknown length
* 156411 162615: contig of 6205 bp in length
* 162616 162715: gap of unknown length
* 162716 163903: contig of 1188 bp in length
* 163904 163904: gap of unknown length
* 164004 173562: contig of 9559 bp in length

Query Match 72.2% Score 13; DB 2; Length 110000;
Beet Local Similarity 92.3%; Pred. No. 4.5e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18
Db 19973 CCTGAGAGNNNNNN 19961

RESULT 182
AC055726 0/c
WPCOMMENT
Sequence split into 5 fragments LOCUS AC055726 Accession AC055726
Fragment Name Begin End
AC055726_0 1 110000
AC055726_1 100001 210000
AC055726_2 200001 310000
AC055726_3 300001 410000
AC055726_4 400001 456720
LOCUS AC055726 456720 bp DNA linear HTG 27-JAN-2002
DEFINITION Homo sapiens chromosome 3 clone Rpl1-98J5, WORKING DRAFT SEQUENCE.
ACCESSION AC055726
VERSION AC055726.13 GI:18377140
KEYWORDS HTG; HTGS_Phasel; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 456720)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

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Albrooks, S.L., Amaralunge, H.C., Are, J.R., Ayale, M., Banks, T.,  
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 Williams, G., Williamson, A., Wleczek, R., Woodson, S., Worley, K.,  
 Wu, C., Wu, Y., Wu, Y.F., Zhou, D., Zorrilla, S., Nelson, D.,  
 Weinstein, G. and Gibbs, R.

Unpublished  
 Direct Submission  
 2 (bases 1 to 456720)  
 Worley, K.C.

Direct Submission  
 Submitted (18-APR-2000) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On Jan 27, 2002 this sequence version replaced gi:11128115.

----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu

----- Project Information  
 Center project name: HAVU  
 Center clone name: RP11-98J5  
 Sequencing vector: M13; L08821  
 Chemistry: Dye-terminator Big Dye 738 of reads  
 Assembly program: Phrap; version 0.990329First call to  
 findPhrapList

Consensus quality: 369571 bases at least Q40  
 Consensus quality: 395345 bases at least Q30  
 Consensus quality: 411294 bases at least Q20  
 Estimated insert size: 393000; sum-of-contigs estimation  
 Quality coverage: 0x in Q20 bases; agarose-tp estimation  
 Quality coverage: 4.4x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html))  
 \* NOTE: This sequence may represent more than one clone.  
 \* NOTE: This is a 'working draft' sequence. It currently

\* consists of 101 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1  
 794  
 894  
 1673  
 1773  
 2797  
 2897  
 3756  
 3856  
 5009  
 5109  
 6182  
 6282  
 7039  
 7139  
 7400  
 7440  
 7853  
 7953  
 8688  
 8788  
 9927  
 10027  
 11424  
 11524  
 12033  
 12133  
 12771  
 12872  
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 13881  
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 14907  
 16194  
 16294  
 17499  
 17599  
 18314  
 18414  
 18415  
 19366  
 19466  
 19880  
 19881  
 19981  
 20826  
 20827  
 20926  
 22068  
 22069  
 22169  
 22862  
 22962  
 24198  
 24298  
 25124  
 25224  
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 26260  
 27343  
 27443  
 28283  
 28383  
 29113  
 29213  
 29673  
 29773  
 30857  
 30957  
 32196  
 32296  
 33297  
 33357

793: contig of 793 bp in length  
 893: gap of unknown length  
 1672: contig of 779 bp in length  
 1772: gap of unknown length  
 2796: contig of 1024 bp in length  
 2896: gap of unknown length  
 3755: contig of 859 bp in length  
 3855: gap of unknown length  
 5008: contig of 1153 bp in length  
 5108: gap of unknown length  
 6181: contig of 1073 bp in length  
 6281: gap of unknown length  
 7039: contig of 758 bp in length  
 7139: gap of unknown length  
 7400: contig of 713 bp in length  
 7440: gap of unknown length  
 7852: contig of 735 bp in length  
 7952: gap of unknown length  
 8687: contig of 735 bp in length  
 8787: gap of unknown length  
 9926: contig of 1139 bp in length  
 10026: gap of unknown length  
 11423: contig of 1397 bp in length  
 11523: gap of unknown length  
 12032: contig of 509 bp in length  
 12132: gap of unknown length  
 12771: contig of 639 bp in length  
 12871: gap of unknown length  
 13780: contig of 909 bp in length  
 13880: gap of unknown length  
 13881: contig of 926 bp in length  
 14806: gap of unknown length  
 14906: contig of 1287 bp in length  
 16193: gap of unknown length  
 16293: gap of unknown length  
 17498: contig of 1205 bp in length  
 17598: gap of unknown length  
 18313: contig of 715 bp in length  
 18413: gap of unknown length  
 18414: contig of 952 bp in length  
 19365: gap of unknown length  
 19465: gap of unknown length  
 19880: contig of 415 bp in length  
 19881: gap of unknown length  
 20826: contig of 846 bp in length  
 20926: gap of unknown length  
 22068: contig of 1142 bp in length  
 22069: gap of unknown length  
 22169: contig of 694 bp in length  
 22862: gap of unknown length  
 22962: gap of unknown length  
 24198: contig of 1236 bp in length  
 24298: gap of unknown length  
 25124: contig of 826 bp in length  
 25224: gap of unknown length  
 26160: contig of 936 bp in length  
 26260: gap of unknown length  
 27343: contig of 1083 bp in length  
 27443: gap of unknown length  
 28283: contig of 840 bp in length  
 28383: gap of unknown length  
 29113: contig of 730 bp in length  
 29213: gap of unknown length  
 29673: contig of 460 bp in length  
 29773: gap of unknown length  
 30857: contig of 1084 bp in length  
 30957: gap of unknown length  
 32196: contig of 1239 bp in length  
 32296: gap of unknown length  
 33297: contig of 961 bp in length  
 33357: gap of unknown length



Query Match 72.2%, Score 13, DB 2, Length 116585;  
Best Local Similarity 92.3%, Pred. No. 4.5e+02;  
Matches 12, Conservative 1, Mismatches 0, Indels 0, Gaps 0;

6 CCUGAGNNNNNN 18  
||:|||||||  
97382 CCTGAGNNNNNN 97394

Db

RESULT 184  
AC013324/c  
LOCUS  
DEFINITION  
AC013324 118540 bp DNA linear HTG 13-JUL-2000  
Homo sapiens chromosome 2 clone RP11-388K24 map 2, LOW-PASS  
SEQUENCE SAMPLING.  
AC013324  
AC013324.3 GI:9123914  
HTG; HTGS PHASE0.  
KEYWORDS  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 118540)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,  
Baldwin, J., Barne, N., Becker, R., Boguslavsky, L., Bouckgalter, B.,  
Brown, A., Castle, A., Collins, S., Collins, S., Collymore, A.,  
Cook, P., Dearlano, K., Dewar, K., Domingo, M., Donelan, L., Doyle, M.,  
Ferris, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,  
Galland, J., Gaidyna, S., Grant, G., Haggis, B., Harford, A., Horton, L.,  
Howland, J., Johnson, K., Jones, C., Kann, L., Karstad, A., Horton, L.,  
Lehoczky, J., Lien, C., Locke, K., MacDonald, P., Margulis, A.,  
McEwan, P., McGuirk, A., McKernan, K., McLaughlin, J., Meldrum, J.,  
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,  
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,  
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Teste, S., Tetrell, A., Vasilev, H., Vo, A., Wheeler, J., Wu, X.,  
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (06-NOV-1999) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced gi:6289165.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L3787  
Center clone name: 388\_K\_24

\* NOTE: This record contains 125 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 856: contig of 856 bp in length  
\* 857 956: gap of 100 bp  
\* 957 1821: contig of 865 bp in length  
\* 1822 1921: gap of 100 bp  
\* 1922 2776: contig of 855 bp in length

2777 2876: gap of 100 bp  
\* 2877 3767: contig of 891 bp in length  
\* 3768 3867: gap of 100 bp  
\* 3868 4709: contig of 842 bp in length  
\* 4710 4809: gap of 100 bp  
\* 4810 5655: contig of 846 bp in length  
\* 5656 5755: gap of 100 bp  
\* 5756 6627: contig of 872 bp in length  
\* 6628 6727: gap of 100 bp  
\* 6728 7587: contig of 859 bp in length  
\* 7588 7687: gap of 100 bp  
\* 7687 8541: contig of 855 bp in length  
\* 8542 8641: gap of 100 bp  
\* 8642 9524: contig of 883 bp in length  
\* 9525 9624: gap of 100 bp  
\* 9625 10509: contig of 885 bp in length  
\* 10510 10609: gap of 100 bp  
\* 10610 11474: contig of 865 bp in length  
\* 11475 11574: gap of 100 bp  
\* 11575 12441: contig of 867 bp in length  
\* 12442 12541: gap of 100 bp  
\* 12542 13409: contig of 868 bp in length  
\* 13410 13509: gap of 100 bp  
\* 13510 14439: contig of 930 bp in length  
\* 14440 14539: gap of 100 bp  
\* 14540 15433: contig of 894 bp in length  
\* 15434 15533: gap of 100 bp  
\* 15534 16442: contig of 909 bp in length  
\* 16443 16542: gap of 100 bp  
\* 16543 17521: contig of 879 bp in length  
\* 17522 18380: contig of 859 bp in length  
\* 18381 18480: gap of 100 bp  
\* 18481 19345: contig of 865 bp in length  
\* 19346 19445: gap of 100 bp  
\* 19446 20327: contig of 882 bp in length  
\* 20328 21297: gap of 100 bp  
\* 21298 21397: contig of 870 bp in length  
\* 21398 22055: contig of 658 bp in length  
\* 22056 22155: gap of 100 bp  
\* 22156 23005: contig of 850 bp in length  
\* 23006 23105: gap of 100 bp  
\* 23106 24016: contig of 911 bp in length  
\* 24017 24116: gap of 100 bp  
\* 24117 24972: contig of 856 bp in length  
\* 24973 25072: gap of 100 bp  
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\* 25978 26078: gap of 100 bp  
\* 26079 26952: contig of 875 bp in length  
\* 26953 27052: gap of 100 bp  
\* 27053 27911: contig of 859 bp in length  
\* 27912 28011: gap of 100 bp  
\* 28012 28868: contig of 857 bp in length  
\* 28869 29624: gap of 100 bp  
\* 29625 29724: contig of 656 bp in length  
\* 29725 30574: gap of 100 bp  
\* 30575 30674: contig of 850 bp in length  
\* 30675 31530: contig of 856 bp in length  
\* 31531 31630: gap of 100 bp  
\* 31631 32491: contig of 861 bp in length  
\* 32492 32591: gap of 100 bp  
\* 32592 33467: contig of 876 bp in length  
\* 33468 33567: gap of 100 bp  
\* 33568 34437: contig of 870 bp in length  
\* 34438 34537: gap of 100 bp  
\* 34538 35404: contig of 867 bp in length  
\* 35405 35504: gap of 100 bp  
\* 35505 36368: contig of 864 bp in length  
\* 36369 36468: gap of 100 bp  
\* 36469 37353: contig of 885 bp in length  
\* 37354 37453: gap of 100 bp



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* 37454 38310: contig of 857 bp in length
* 38311 38410: gap of 100 bp
* 38411 38267: contig of 857 bp in length
* 39268 39367: gap of 100 bp
* 39368 40217: contig of 850 bp in length
* 40218 40317: gap of 100 bp
* 40318 41226: contig of 909 bp in length
* 41227 41326: gap of 100 bp
* 41327 41995: contig of 869 bp in length
* 42196 42295: gap of 100 bp
* 42296 43180: contig of 885 bp in length
* 43181 43280: gap of 100 bp
* 43281 44143: contig of 863 bp in length
* 44144 44243: gap of 100 bp
* 44244 45131: contig of 888 bp in length
* 45132 45231: gap of 100 bp
* 45232 46149: contig of 918 bp in length
* 46150 46249: gap of 100 bp
* 46250 47122: contig of 873 bp in length
* 47123 48101: contig of 879 bp in length
* 48102 48201: gap of 100 bp
* 48202 49041: contig of 840 bp in length
* 49042 49141: gap of 100 bp
* 49142 50059: contig of 918 bp in length
* 50060 50159: gap of 100 bp
* 50160 51029: contig of 870 bp in length
* 51030 51129: gap of 100 bp
* 51130 51995: contig of 866 bp in length
* 51996 52095: gap of 100 bp
* 52096 52971: contig of 876 bp in length
* 52972 53071: gap of 100 bp
* 53072 53942: contig of 871 bp in length
* 53943 54042: gap of 100 bp
* 54043 54923: contig of 881 bp in length
* 54924 55023: gap of 100 bp
* 55024 55977: contig of 854 bp in length
* 55978 56851: gap of 100 bp
* 56852 56951: gap of 100 bp
* 56952 57808: contig of 857 bp in length
* 57809 58755: contig of 847 bp in length
* 58756 59709: gap of 100 bp
* 59710 59809: gap of 100 bp
* 59810 60521: contig of 712 bp in length
* 60522 60621: gap of 100 bp
* 60622 61501: contig of 880 bp in length
* 61502 61601: gap of 100 bp
* 61602 62490: contig of 889 bp in length
* 62491 62590: gap of 100 bp
* 62591 63450: contig of 860 bp in length
* 63451 63550: gap of 100 bp
* 63551 64094: contig of 544 bp in length
* 64095 64194: gap of 100 bp
* 64195 65022: contig of 828 bp in length
* 65023 65122: gap of 100 bp
* 65123 65983: contig of 861 bp in length
* 65984 66083: gap of 100 bp
* 66084 66922: contig of 839 bp in length
* 66923 67022: gap of 100 bp
* 67023 67908: contig of 886 bp in length
* 67909 68008: gap of 100 bp
* 68009 68879: contig of 871 bp in length
* 68880 68979: gap of 100 bp

```

```

Query Match 72.2% Score 13; DB 2; Length 118540;
Best Local Similarity 92.3%; Pred. No. 4.5e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
6 CCUGAGAGNNNNNN 18
||:|||||||

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Db 117737 CCTGAGAGNNNNNN 117725

RESULT 185  
ALJ55675/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

ALJ55675 132600 bp DNA linear HTG 10-JUL-2001  
Homo sapiens chromosome 1 clone RP5-1132F1, 21 unordered pieces.  
ALJ55675 GI:9863739  
HTG; HTGS PHASE1; HTGS\_CANCELLED.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Plumb, B.  
Direct Submission  
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
requests: clonerequests@sanger.ac.uk  
On Aug 21, 2000 this sequence version replaced gi:9213627.  
-----  
Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquerry@sanger.ac.uk  
-----  
Project Information  
Center project name: dj1132F1  
-----

# COMMENT

----- Summary Statistics -----  
Sequencing vector: plasmid, 108752; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Consensus quality: 122442 bases at least Q40  
Consensus quality: 126008 bases at least Q30  
Consensus quality: 128093 bases at least Q20  
Insert size: 130600; sum-of-contigs  
Quality coverage: 3.42x in Q20 bases; sum-of-contigs Quality  
coverage: 3.13x in Q20 bases; agarose-fp  
-----

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 21 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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4087: contig of 4087 bp in length  
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4188 18184: contig of 13997 bp in length  
18185 18284: gap of 100 bp  
18285 20786: contig of 2502 bp in length  
20787 20886: gap of 100 bp  
20887 32597: contig of 11711 bp in length  
32598 32697: gap of 100 bp  
32698 38951: contig of 6254 bp in length  
38952 39051: gap of 100 bp  
39052 42761: contig of 3710 bp in length  
42762 42861: gap of 100 bp  
42862 50655: contig of 7794 bp in length  
50656 50755: gap of 100 bp  
50756 50755: gap of 100 bp  
50756 60116: contig of 9361 bp in length  
60117 60216: gap of 100 bp  
60217 62824: contig of 2608 bp in length  
62825 62924: gap of 100 bp  
62925 68919: contig of 5995 bp in length  
68920 69019: gap of 100 bp  
69020 86112: contig of 17093 bp in length  
86113 86212: gap of 100 bp  
86213 90244: contig of 4032 bp in length  
90245 90344: gap of 100 bp  
90345 93814: contig of 3470 bp in length

```

* 93915 93914: gap of 100 bp
* 93915 98595: contig of 4681 bp in length
* 98595 98595: gap of 100 bp
* 98595 101439: contig of 2744 bp in length
* 98595 101440: gap of 100 bp
* 101440 101539: gap of 100 bp
* 101539 108271: contig of 6732 bp in length
* 108271 108372: gap of 100 bp
* 108372 117614: contig of 9243 bp in length
* 117614 117715: gap of 100 bp
* 117715 120384: contig of 2670 bp in length
* 120384 120485: gap of 100 bp
* 120485 122837: contig of 2353 bp in length
* 122837 122938: gap of 100 bp
* 122938 130451: contig of 7514 bp in length
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            117715..120384
            /note="assembly fragment:01167"
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            /note="assembly fragment:00803"

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ORIGIN
    Query Match          72.2%; Score 13; DB 2; Length 132600;
    Best Local Similarity 92.3%; Pred. No. 4.5e+02;
    Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 CCUGGAGNNNNNN 18
Db      122944 CCTGGAGNNNNNN 122932

RESULT 186
LOCUS      AC102359
DEFINITION Mus musculus clone RP23-22C6, LOW-PASS SEQUENCE SAMPLING.
ACCESSION  AC102359
VERSION     AC102359.2 GI:22004563
KEYWORDS    HTG; HTGS PHASE0.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 133669)
AUTHORS    Birren, B., Nusbaum, C., and Lander, E.
JOURNAL    Unpublished
TITLES     2 (bases 1 to 133669)
AUTHORS    Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, A.,
            Anderson, S., Bana, N., Bastien, V., Boguslavsky, L., Bouckgaalter, B.,
            Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
            Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
            Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
            Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
            Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
            Hagos, B., Heatford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
            Jones, C., Kamat, A., Karatas, A., Kelle, C., Labocque, K.,
            Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,
            Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
            McCarthy, M., McEwan, P., McKernan, K., McHeeters, R., Meldrim, J.,
            Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
            Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
            Oliver, J., Peterson, K., Phunhphang, P., Pierre, N., Pollara, V.,
            Raymond, C., Rector, K., Rieback, M., Riley, R., Rise, C., Rogov, P.,
            Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
            Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
            Strauss, N., Subramanian, A., Talamas, J., Testfaye, S., Theodore, J.,
            Topham, K., Travers, M., Travis, N., Triggilio, V., Vassiliev, H.,
            Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.-J., Young, G.,
            Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
            Direct Submission
            Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
            3 (bases 1 to 133669)
TITLE      JOURNAL
AUTHORS    Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
            Bana, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckgaalter, B.,
            Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
            Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
            Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
            Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
            Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
            Karatas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K.,
            Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C.,
            McCarthy, M., Meldrim, J., Menus, L., Mihova, T., Mlenga, V.,
            Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H.,
            O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
            Phunhphang, P., Pierre, N., Raymond, C., Rector, K., Rise, C., Rogov, P.,
            Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
            Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
            Testfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H.,
            Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
            Zembek, L., Zimmer, A. and Zody, M.

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TITLE  
JOURNAL  
COMMENT

Direct Submission  
Submitted (30-JUL-2002) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 30, 2002 this sequence version replaced gi:17061445.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

Project Information

Center project name: L18567

Center clone name: 22\_C\_8

NOTE: This record contains 162 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1  
710 809: contig of 709 bp in length  
810 1539: contig of 730 bp in length  
1540 1639: gap of 100 bp  
1640 2356: contig of 717 bp in length  
2357 2456: gap of 100 bp  
2457 3162: contig of 706 bp in length  
3163 3262: gap of 100 bp  
3263 3988: contig of 726 bp in length  
3989 4088: gap of 100 bp  
4089 4827: contig of 739 bp in length  
4828 4927: gap of 100 bp  
4928 5665: contig of 738 bp in length  
5666 5765: gap of 100 bp  
5766 6497: contig of 731 bp in length  
6497 6596: gap of 100 bp  
6597 7321: contig of 725 bp in length  
7322 7421: gap of 100 bp  
7422 8153: contig of 732 bp in length  
8154 8253: gap of 100 bp  
8254 8976: contig of 723 bp in length  
8977 9076: gap of 100 bp  
9077 9796: contig of 720 bp in length  
9797 9896: gap of 100 bp  
9897 10613: contig of 717 bp in length  
10614 10713: gap of 100 bp  
10714 11417: contig of 704 bp in length  
11418 11517: gap of 100 bp  
11518 12247: contig of 730 bp in length  
12247 12347: gap of 100 bp  
12348 13078: contig of 731 bp in length  
13079 13178: gap of 100 bp  
13179 13904: contig of 726 bp in length  
13905 14004: gap of 100 bp  
14005 14745: contig of 741 bp in length  
14746 14845: gap of 100 bp  
14846 15568: contig of 723 bp in length  
15569 15689: gap of 100 bp  
15690 16384: contig of 716 bp in length  
16385 16484: gap of 100 bp  
16485 17305: contig of 721 bp in length  
17306 18030: contig of 725 bp in length  
18031 18130: gap of 100 bp  
18131 18848: contig of 718 bp in length  
18849 18948: gap of 100 bp

18949 19666: contig of 718 bp in length  
19667 19766: gap of 100 bp  
19767 20477: contig of 711 bp in length  
20478 20577: gap of 100 bp  
20578 21304: contig of 727 bp in length  
21305 21404: gap of 100 bp  
21405 22138: contig of 734 bp in length  
22139 22238: gap of 100 bp  
22239 22971: contig of 733 bp in length  
22972 23072: gap of 100 bp  
23073 23796: contig of 725 bp in length  
23797 23896: gap of 100 bp  
23897 24623: contig of 726 bp in length  
24624 24723: gap of 100 bp  
24724 25446: contig of 723 bp in length  
25447 25546: gap of 100 bp  
25547 26271: contig of 726 bp in length  
26272 26371: gap of 100 bp  
26372 27099: contig of 728 bp in length  
27100 27199: gap of 100 bp  
27200 27911: contig of 712 bp in length  
27912 28011: gap of 100 bp  
28012 28727: contig of 716 bp in length  
28728 28827: gap of 100 bp  
28829 29543: contig of 716 bp in length  
29544 29643: gap of 100 bp  
29644 30377: contig of 734 bp in length  
30378 30477: gap of 100 bp  
30478 31209: contig of 732 bp in length  
31210 31309: gap of 100 bp  
31310 32045: contig of 736 bp in length  
32046 32146: gap of 100 bp  
32147 32870: contig of 725 bp in length  
32871 32970: gap of 100 bp  
32971 33690: contig of 720 bp in length  
33691 33790: gap of 100 bp  
33791 34517: contig of 727 bp in length  
34518 34617: gap of 100 bp  
34618 35334: contig of 717 bp in length  
35335 35434: gap of 100 bp  
35435 36149: contig of 715 bp in length  
36150 36249: gap of 100 bp  
36250 36965: contig of 716 bp in length  
36966 37066: gap of 100 bp  
37067 37666: contig of 701 bp in length  
37667 37866: gap of 100 bp  
37867 38584: contig of 718 bp in length  
38585 39422: gap of 100 bp  
39423 39522: gap of 100 bp  
39523 40258: contig of 736 bp in length  
40259 40358: gap of 100 bp  
40359 41090: contig of 732 bp in length  
41091 41190: gap of 100 bp  
41191 41916: contig of 726 bp in length  
41917 42016: gap of 100 bp  
42017 42740: contig of 724 bp in length  
42741 42840: gap of 100 bp  
42841 43565: contig of 725 bp in length  
43566 43665: gap of 100 bp  
43666 44385: contig of 720 bp in length  
44386 44485: gap of 100 bp  
44486 45217: contig of 732 bp in length  
45218 45317: gap of 100 bp  
45318 46035: contig of 718 bp in length  
46036 46135: gap of 100 bp  
46136 46851: contig of 716 bp in length  
46852 46951: gap of 100 bp  
46952 47682: contig of 731 bp in length

Query Match 72.2%; Score 13; DB 2; Length 133669;  
Best Local Similarity 92.3%; Pred. No. 4.5e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY      6 CCUGAGNNNNNN 18
Db      49339 CCTGAGNNNNNN 49351

RESULT 187
AC007835
LOCUS   136756 bp DNA linear HTG 21-DEC-1999
DEFINITION Drosophila melanogaster chromosome 2 clone BACR10N07 (D611) RPTI-98
            10.N.7 map 53D-54A strain Y; cn bw sp, *** SEQUENCING IN PROGRESS
            *** 95 unordered pieces.
ACCESSION AC007835
VERSION   AC007835.5 GI:66233908
KEYWORDS  HTG, HTGS, PHASE1.
SOURCE    Drosophila melanogaster (fruit fly)
ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 136756)
            Celinker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,
            Butenoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
            Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
            Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K.,
            Kearney, L., Lee, B., Lewis, S., Li, P., Lomocan, M.A., Mazda, P.,
            Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,
            Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D.,
            Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M.
            Sequencing of Drosophila melanogaster
            Unpublished
            2 (bases 1 to 136756)
            Celinker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,
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            Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
            Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,
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            Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S.,
            Pfeiffer, B., Poon, L., Sequelstra, A., Sethi, H., Smit, E.,
            Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
            Rubin, G.M.
            Direct Submission
            Submitted (16-JUN-1999) Drosophila Genome Center, Lawrence Berkeley
            Laboratory, MS 64-121, Berkeley, CA 94720, USA
            On Dec 21, 1999 this sequence version replaced gi:5554231.
            For further information about this sequence, including its location
            and relationship to other sequences, please visit our sequence
            archive Web site (http://www.fruitfly.org/sequence/) or send email
            to bugreport@fruitfly.berkeley.edu. All contigs in this submission meet
            the following cutoffs: length >= 200 bases.
            NOTE: This is a 'working draft' sequence. It currently
            * consists of 95 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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            830: contig of 830 bp in length
            831 910: gap of unknown length
            911 1857: contig of 947 bp in length
            1858 1937: gap of unknown length
            1938 2821: contig of 884 bp in length
            2822 2901: gap of unknown length
            2902 3568: contig of 667 bp in length
            3569 3648: gap of unknown length
            3649 4395: contig of 747 bp in length
            4396 4475: gap of unknown length
            4476 5457: contig of 982 bp in length
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            5538 6219: contig of 682 bp in length
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            6300 6812: contig of 513 bp in length
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            25438 26543: contig of 1106 bp in length
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\* 56201 60051: contig of 3851 bp in length  
\* 60052 60131: gap of unknown length  
\* 60132 61474: contig of 1343 bp in length  
\* 61475 61554: gap of unknown length  
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\* 67055 67134: gap of unknown length  
\* 67135 70924: contig of 3790 bp in length  
\* 70925 71005 74744: contig of 3740 bp in length  
\* 74745 74824: gap of unknown length  
\* 74825 78675: contig of 3851 bp in length  
\* 78676 78755: gap of unknown length  
\* 78756 83636: contig of 4881 bp in length  
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\* 110647 110726: gap of unknown length  
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\* 111395 111475 112199: contig of 725 bp in length  
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\* 113045 113595: contig of 551 bp in length  
\* 113596 113675: gap of unknown length  
\* 113676 114219: contig of 544 bp in length  
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\* 117677 117756: gap of unknown length  
\* 117757 118411: contig of 655 bp in length  
\* 118412 118491: gap of unknown length  
\* 118492 119125: contig of 635 bp in length  
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\* 119207 119873: contig of 667 bp in length  
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Query Match 72.2% Score 13; DB 2; Length 136756;  
Best Local Similarity 92.3% Pred. No. 4.Se+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCGGAGANNNNN 18  
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DB 30172 CCTGGAGNNNNN 30184

RESULT 188

RN374E16/c  
LOCUS RN374E16 140714 bp DNA linear HTG 13-JUN-2002  
DEFINITION Ratius norvegicus clone RPCI-31-374E16 strain Brown Norway, WORKING  
RAFT SEQUENCE, 118 unordered pieces.  
ACCESSION AL603726  
VERSION AL603726.2 GI:17154526  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE Ratius norvegicus (Norway rat)  
ORGANISM Ratius norvegicus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1  
AUTHORS Sudbrak, R., Borzym, K., Mueller, I., Klages, S., Kosiura, A.,  
Walter, L., Guenther, E., Hurt, P., Lehnach, H., Himmelbauer, H. and  
Reinhardt, R.  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 140714)  
AUTHORS MOLGENR.  
TITLE Direct Submission  
COMMENT Submitted (10-AUG-2001) MPIMG, Abt. Lehnach, Max Planck Institut  
Fuer Molekulare Genetik, Ihnestrasse 73, Berlin, 14195 Germany  
On Nov 29, 2001 this sequence version replaced gi:15149584.  
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contig 02 1352 .3264  
contig 03 3365 .4425  
contig 04 4526 .5017  
contig 05 5118 .6184  
contig 06 6285 .6954  
contig 07 7055 .9462  
contig 08 9563 .10280  
contig 09 10381 .10681  
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contig 11 12618 .13628  
contig 12 13729 .14193  
contig 13 14294 .14692  
contig 14 14793 .15257  
contig 15 15358 .15741  
contig 16 15842 .16024  
contig 17 16125 .16370  
contig 18 16471 .16826  
contig 19 16927 .19591  
contig 20 19692 .20966  
contig 21 21067 .23531  
contig 22 23632 .23905  
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contig 25 25996 .26775  
contig 26 26876 .27274  
contig 27 27375 .27751  
contig 28 27852 .28141  
contig 29 28242 .29828  
contig 30 29929 .32999  
contig 31 33100 .35425  
contig 32 35526 .36380  
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contig 45 51435 .51907  
contig 46 52008 .53006  
contig 47 53107 .53670  
contig 48 53771 .54204  
contig 49 54305 .54782  
contig 50 54883 .55445

contig 51 .55546. .56296  
contig 52 .56397. .57181  
contig 53 .57282. .57761  
contig 54 .57862. .58482  
contig 55 .58583. .59568  
contig 56 .59669. .60357  
contig 57 .60458. .61299  
contig 58 .61400. .62399  
contig 59 .62500. .63595  
contig 60 .63696. .64135  
contig 61 .64236. .65192  
contig 62 .65293. .66006  
contig 63 .66107. .67251  
contig 64 .67352. .68256  
contig 65 .68357. .69246  
contig 66 .69347. .70512  
contig 67 .70613. .71482  
contig 68 .71583. .72741  
contig 69 .72842. .73605  
contig 70 .73706. .77780  
contig 71 .77881. .77954  
contig 72 .78055. .78878  
contig 73 .78979. .80987  
contig 74 .81088. .82590  
contig 75 .82691. .83093  
contig 76 .83194. .84378  
contig 77 .84479. .85650  
contig 78 .85751. .87194  
contig 79 .87295. .87636  
contig 80 .87737. .89531  
contig 81 .89632. .90993  
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contig 84 .93634. .94070  
contig 85 .94171. .95672  
contig 86 .95773. .97862  
contig 87 .97963. .99909  
contig 88 .100010. .102482  
contig 89 .102583. .104861  
contig 90 .104962. .106935  
contig 91 .107036. .110372  
contig 92 .110473. .112722  
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contig 105 .130882. .131775  
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contig 107 .132126. .132518  
contig 108 .132619. .133046  
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contig 114 .136278. .136781  
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contig 116 .137421. .139379  
contig 117 .138480. .139590  
contig 118 .139691. .140714.  
contig 119 .14141918

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 118 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1251: contig of 1251 bp in length  
1252 1351: gap of 100 bp  
1352 3264: contig of 1913 bp in length  
3265 3364: gap of 100 bp  
3365 4425: contig of 1061 bp in length  
4426 4525: gap of 100 bp  
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5118 6184: contig of 1067 bp in length  
6185 6284: gap of 100 bp  
6285 6954: contig of 670 bp in length  
6955 7055: gap of 100 bp  
7056 9462: contig of 2408 bp in length  
9463 9563: gap of 100 bp  
9564 10280: contig of 718 bp in length  
10281 10380: gap of 100 bp  
10381 10681: contig of 301 bp in length  
10682 10781: gap of 100 bp  
10782 12517: contig of 1736 bp in length  
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12618 13628: contig of 1011 bp in length  
13629 13728: gap of 100 bp  
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14693 14792: gap of 100 bp  
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19692 20966: contig of 1275 bp in length  
20967 21066: gap of 100 bp  
21067 23531: contig of 2465 bp in length  
23532 23631: gap of 100 bp  
23632 23905: contig of 274 bp in length  
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Query Match 72.2% Score 13; DB 2; Length 140714;  
Best Local Similarity 92.3% Pred. No. 4.5e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
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Db 45249 CCGTGGAGNNNNNN 45237

RESULT 189  
AC141918

LOCUS AC141918 143907 bp DNA linear HTG 21-MAR-2003  
DEFINITION Rattus norvegicus clone CH230-341123, WORKING DRAFT SEQUENCE, 20  
unorderd pieces.  
ACCESSION AC141918  
VERSION AC141918.2 GI:29135393

KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.

SOURCE  
ORGANISM

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.REFERENCE  
AUTHORS

1 (bases 1 to 143907)

Munzy,D,Marie., Metzger,M, Lee., Abramzon,S., Adams,C., Alder,J.,  
Allen,C., Allen,H., Alebrooks,S., Amin,A., Angiano,D.,  
Avalanche,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,  
Baldwin,D., Bandaranaike,D., Barber,M., Barneshead,M., Benahmed,F.,  
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Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,  
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,U.,  
Davis,M., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,  
Delgado,O., Denison,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,  
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Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,  
Fraser,C.M., Gabisi,A., Gantner,R., Garcia,A., Garner,T., Garza,M.,  
Georgievski,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,  
Gunnarsson,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K.,  
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,  
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hoques,M.,  
Hollins,B., Howells,S., Hulky,S., Hume,J., Idlebird,D., Jackson,A.,  
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,  
Karpachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovac,C.,  
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,  
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,  
Lorenshewa,L., Louisedge,H., Lozada,R.J., Lu,X., Ma,J.,  
Maheshwari,M., Mahindartne,M., Mahmud,M., Malloy,K., Mangum,A.,  
Mangum,B., Mapa,P., Martin,K., Martin,R., Martinez,E.,  
Mawhinley,S., McLeod,M., McNeill,T., Meenen,E., Milosavljevic,A.,  
Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K.,  
Morris,S., Mundasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D.,  
Newton,N., Nguyen,N., Norris,S., Nwaokelimeh,O., Okunolu,G.,  
Olanunsaogun,A., Pal,S., Parks,K., Pasternak,S., Paul,H.,  
Perez,A., Perez,L., Pfennoch,C., Plopper,F., Polidexter,A.,  
Popovic,D., Primus,E., Pu,L., Puazo,M., Quito,J., Rechlin,E.,  
Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y.,  
Reuter,M., Richards,S., Riggs,F., Rivers,C., Rodkey,T., Rojes,A.,  
Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S.,  
Scott,G., Shatman,S., Shen,H., Shetty,J., Shvartsbeyn,A.,  
Sisson,I., Sitter,C.D., Smales,D., Sneed,A., Sodergren,E.,  
Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A.,  
Syatek,A., Taber,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S.,  
Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D.,  
Waldron,L., Walker,B., Wang,J., Wang,O., Wang,S., Warren,J.,  
Warren,R., Wei,X., White,F., Williams,G., Wilson,R., Wleciyk,R.,  
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Yan,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X.,  
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Holt,R.A., Smith,H.O., Weinstein,G., and Gibbs,R.A.

TITLE  
JOURNAL

Unpublished

2 (bases 1 to 143907)

REFERENCE  
AUTHORS

Worley,K.C.

TITLE  
JOURNAL

Submitted (20-MAR-2003) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 143907)

REFERENCE  
AUTHORS

Worley,K.C.

TITLE  
JOURNAL

Submitted (21-MAR-2003) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

On Mar 21, 2003 this sequence version replaced gi:29126272.

## COMMENT

Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

Project Information

Center project name: KEIG  
Center clone name: CH230-341123

Summary Statistics

Sequencing vector: Plasmid;  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 137103 bases at least Q40  
Consensus quality: 138905 bases at least Q30  
Consensus quality: 140423 bases at least Q20  
Estimated insert size: 138648; sum-of-contigs estimation  
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/Genbankdraft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbankdraft_data.html)).  
NOTE: This is a "working draft" sequence. It currently  
consists of 20 contigs. The true order of the pieces  
is not known and their order in this sequence record is  
arbitrary. Gaps between the contigs are represented as  
runs of N, but the exact sizes of the gaps are unknown.  
This record will be updated with the finished sequence  
as soon as it is available and the accession number will  
be preserved.

1	1071: contig of 1071 bp in length
1072	1171: gap of unknown length
1172	2612: contig of 1441 bp in length
2613	2712: gap of unknown length
2713	3962: contig of 1250 bp in length
3963	4062: gap of unknown length
4063	5820: contig of 1758 bp in length
5821	5920: gap of unknown length
5921	7092: contig of 1172 bp in length
7093	7192: gap of unknown length
7193	10187: contig of 2995 bp in length
10188	10287: gap of unknown length
10288	12373: contig of 2086 bp in length
12374	12473: gap of unknown length
12474	15632: contig of 3159 bp in length
15633	15732: gap of unknown length
15733	18655: contig of 2923 bp in length
18656	18755: gap of unknown length
18756	22166: contig of 3411 bp in length
22167	22266: gap of unknown length
22267	28829: contig of 6563 bp in length
28830	33920: gap of unknown length
33921	33920: contig of 4991 bp in length
34021	34020: gap of unknown length
40458	40458: contig of 6438 bp in length
40459	40558: gap of unknown length
40559	48823: contig of 8265 bp in length
48824	48923: gap of unknown length
48924	60713: contig of 11790 bp in length
60714	60813: gap of unknown length
60814	72715: contig of 11992 bp in length
72716	72815: gap of unknown length
72816	83723: contig of 10908 bp in length
83724	83823: gap of unknown length
83824	100667: contig of 16244 bp in length
100668	100167: gap of unknown length
100168	117398: contig of 17231 bp in length
117399	117498: gap of unknown length
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Location/Qualifiers

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/organism="Rattus norvegicus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10116"

/clone="CH230-341123"

## ORIGIN

Query Match 72.2%; Score 13; DB 2; Length 143907;  
Best local Similarity 92.3%; Pred. No. 4.5e+02;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 CCUGAGNNNNNN 18  
 Db 2606 CCTGAGNNNNNN 2618

RESULT 190  
 AC009555  
 LOCUS  
 DEFINITION Homo sapiens chromosome 16 clone RPL1-2409 map 16, WORKING DRAFT  
 AC009555  
 AC009555  
 AC009555.5 GI:9966258  
 HTG, HTGS, PHASE1, HTGS\_DRAFT.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 1 (bases 1 to 144832)  
 Homo sapiens chromosome 16, clone RPL1-2409  
 Unpublished  
 2 (bases 1 to 144832)  
 Birtten, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,  
 Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A.,  
 Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,  
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 Karatas, A., Lehoczy, J., Liu, C., Locke, K., Macdonald, P.,  
 Mardum, J., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J.,  
 Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B.,  
 Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P.,  
 Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A.,  
 Tsefaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A.,  
 Wheeler, J., Wu, X., Wyman, D., Ye, W. J. and Zody, M.  
 Direct Submission

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 Submitted (27-AUG-1999) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 144832)  
 Birtten, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,  
 Barna, N., Bastien, V., Boguslavsky, L., Bouhgalter, B., Brown, A.,  
 Camarata, J., Campopiano, A., Chang, J., Choepel, Y., Colangelo, M.,  
 Collins, S., Collymore, A., Cooke, P., Dekrellano, K., Dewar, K.,  
 Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D.,  
 Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,  
 Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W.,  
 Iliev, I., Johnson, R., Jones, C., Karatas, A., Laroque, K.,  
 Lamaazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,  
 Maclean, C., Macdonald, P., Marguis, N., Matthews, C., McGrath, M.,  
 McEwan, P., McKernan, K., McPheters, R., Meldrum, J., Menus, L.,  
 Mhova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C.,  
 Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,  
 Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,  
 Reiter, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,  
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 Severy, P., Sougnuez, C., Spencer, B., Stange-Thomann, N.,  
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 Zaitoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission

TITLE  
 JOURNAL  
 COMMENT  
 Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Sep 4, 2000 this sequence version replaced g1:731386.  
 All repeats were identified using RepeatMasker:  
 Smit, A. F. A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research

Center code: MIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 Project Information  
 Center project name: L1670  
 Center clone name: 24\_0\_9  
 ----- Summary Statistics  
 Sequencing vector: M13; M77815; 94% of reads  
 Sequencing vector: Plasmid; n/a; %0.0% of reads  
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 Chemistry: Dye-terminator Big Dye; 98% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 126916 bases at least Q40  
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 Insert size: 12100; agarose-gel  
 Insert size: 142432; sum-of-contigs  
 Quality coverage.  
 NOTE: This is a 'working draft' sequence. It currently  
 consists of 25 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.  
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 76459 88576: contig of 12118 bp in length  
 88577 88676: gap of 100 bp  
 88677 100732: contig of 12066 bp in length  
 100733 100832: gap of 100 bp  
 100833 119590: contig of 18758 bp in length  
 119591 119690: gap of 100 bp  
 119691 144649: contig of 24959 bp in length



\* 14450 144749: gap of 100 bp  
\* 144750 144832: contig of 83 bp in length.

## FEATURES

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Query Match 72.2%; Score 13; DB 2; Length 144832;  
Best Local Similarity 92.3%; Pred. No. 4.5e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNN 18  
DB 63765 CCTGAGNNNNN 63777

## RESULT 191

AC141949

LOCUS DEFINITION

AC141949 145009 bp DNA linear HTG 24-MAR-2003

Rattus norvegicus clone CH230-435L6, WORKING DRAFT SEQUENCE, 62

unpublished pieces.

AC141949 2 GI:29165546

HTG: HTGS\_PHASE1; HTGS\_DRAFT.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 145009)

Muzny, D., Marle, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Albrooks, S., Amin, A., Angiano, D.,

Anyalebechi, V., Aoyagi, A., Ayodeji, M., Bacc, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,

Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,

Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,

Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chu, J.,

Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,

Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Dval, B., Eaves, K.,

Egan, A., Escotto, M., Eugene, C., Evans, C.A., Faller, T., Fan, G.,

Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,

Fraser, C.M., Gabris, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,

Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guvarro, W.,

Gunnarsson, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,

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Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,

Kowic, S., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,

Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,

Lorenswald, L., Louisse, H., Lozano, R., Lu, X., Ma, J.,

Maheshwari, M., Mahindaratne, M., Mahoud, M., Malloy, K., Mangum, A.,

Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E.,

Mawhinney, S., McLeod, M., McNeill, T., Meenen, E., Mitoavljetic, A.,

Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K.,

Morrison, S., Munida, M., Murphy, M., Nait, L., Nankervis, C., Neal, D.,

Newton, N., Nguyen, N., Norris, S., Nwokilehen, O., Okwona, G.,

Olatunbosun, A., Pal, S., Parks, K., Pasternak, S., Paul, H.,

Perez, A., Perez, L., Pfankoch, C., Plopper, F., Poindexter, A.,

Popovic, D., Primus, E., Pu, L., Pu, M., Quirio, J., Rachlin, E.,

Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y.,

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Sisson, I., Sitter, C.D., Smith, D., Sneed, A., Sodergren, E.,

Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A.,

Swatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S.,

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Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X.,

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Holt, R.A., Smith, H.O., Weinstock, G., and Gibbs, R.A.

Direct Submission

Unpublished

2 (bases 1 to 145009)

Worley, K.C.

Direct Submission

Submitted (21-MAR-2003) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 145009)

Worley, K.C.

Direct Submission

## JOURNAL

## COMMENT

Submitted (24-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Mar 24, 2003 this sequence version replaced gi:29135377.

## ----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: KEJ1

Center clone name: CH230-43516

----- Summary Statistics

Sequencing vector: Plasmid

Chemistry: Dye-terminator Big Dye 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 122876 bases at least Q40

Consensus quality: 127474 bases at least Q30

Consensus quality: 131284 bases at least Q20

Estimated insert size: 121255; sum-of-contigs estimation

Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 62 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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* 1 1048: contig of 1048 bp in length
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* 15193 15292: gap of unknown length
* 15293 16100: contig of 1318 bp in length
* 16101 16710: gap of unknown length
* 16711 18179: contig of 1469 bp in length
* 18180 18279: gap of unknown length
* 18280 19439: contig of 1160 bp in length
* 19440 19539: gap of unknown length
* 19540 21054: contig of 1515 bp in length
* 21055 21154: gap of unknown length
* 21155 22263: contig of 1109 bp in length
* 22264 22363: gap of unknown length
* 22364 23594: contig of 1231 bp in length
* 23595 23694: gap of unknown length
* 23695 25739: contig of 2045 bp in length
* 25740 25839: gap of unknown length
* 25840 27682: contig of 1843 bp in length
* 27683 29322: gap of unknown length
* 29322: contig of 1540 bp in length

```

```

* 29323 29423: gap of unknown length
* 29423 30548: contig of 1126 bp in length
* 30549 30648: gap of unknown length
* 30649 31905: contig of 1257 bp in length
* 31906 32005: gap of unknown length
* 32006 33205: contig of 1199 bp in length
* 33206 33305: gap of unknown length
* 33306 34778: contig of 1474 bp in length
* 34779 34878: gap of unknown length
* 34879 35927: contig of 1049 bp in length
* 35928 36027: gap of unknown length
* 36028 37320: contig of 1233 bp in length
* 37321 37420: gap of unknown length
* 37421 38889: contig of 1469 bp in length
* 38890 38989: gap of unknown length
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* 40262 40361: gap of unknown length
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* 55259 55358: gap of unknown length
* 55359 56920: contig of 1562 bp in length
* 56921 57020: gap of unknown length
* 57021 59109: contig of 2089 bp in length
* 59110 59209: gap of unknown length
* 59210 61669: contig of 2460 bp in length
* 61670 61769: gap of unknown length
* 61770 64277: contig of 2508 bp in length
* 64278 64377: gap of unknown length
* 64378 66760: contig of 2383 bp in length
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* 66861 69304: contig of 2344 bp in length
* 69305 72908: contig of 3604 bp in length
* 72909 73008: gap of unknown length
* 73009 75798: contig of 2790 bp in length
* 75799 75898: gap of unknown length
* 75899 79161: contig of 3263 bp in length
* 79162 79261: gap of unknown length
* 79262 81697: contig of 2436 bp in length
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Best Local Similarity 92.3%; Pred. No. 4; se+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 6 CCUGAGNNNNNN 18
DB 64271 CCTGAGNNNNNN 64283

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RESULT 192
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LOCUS AC143192
DEFINITION Macaca mulatta clone CH250-263A1, *** SEQUENCING IN PROGRESS ***
ACCESSION AC143192.1 GI:29567831
VERSION AC143192.1 GI:29567831
KEYWORDS HTG; HTGS_PHASE2; HTGS_PGI.

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SOURCE  
ORGANISM  
Macaca mulatta (rhesus monkey)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca. 1 (bases 1 to 145555)  
Cauro, M. and Miosavljetic, A.  
Pooled genomic indexing (PGI): mathematical analysis and experiment design  
(in) Guigo, R. and Gusfield, D. (eds.);  
ALGORITHMS IN BIOINFORMATICS, SECOND INTERNATIONAL WORKSHOP, WABI  
SPRINGER, ITALY, SEPTEMBER 17-21, 2002, PROCEEDINGS: 10-28;  
Springer (2002)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
2 (bases 1 to 145555)  
Miosavljetic, A., Sodergren, E., Cauro, M., Li, B., Jackson, A.R., Adams, C., Adio-Oduola, B., Ali-ouman, F.R., Allen, C., Alsbrooks, S.L., Amaralunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbato, J., Benton, J., Bimaga, K., Blankenburg, K., Bonin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Dem, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Egan, A., Earhart, C., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garaciata, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, F., Hodgson, A., Hognes, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulik, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W., Louleghed, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapa, P., Marondel, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Metzger, M., Miller, A., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokwke, S., Ogun, M., Okwona, G., Otagunye, N., Oviedo, R., Pace, A., Peyton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Saverly, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shochatari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Taboi, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telitod, B., Thomas, N., Thomas, S., Usmani, K., Vaquez, L., Ver, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleciyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorilla, S., Kuchelapatti, R., Weinstein, G. and Gibbs, R.

TITLE  
JOURNAL  
Direct Submission  
Unpublished  
3 (bases 1 to 145555)  
Worley, K.C.  
Direct Submission  
Submitted (05-APR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
4 (bases 1 to 145555)  
Worley, K.C.  
Direct Submission  
Submitted (09-APR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
-----  
Genome Center  
Center: Baylor College of Medicine  
Center code: BCM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Submitted (09-APR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
-----  
Genome Center  
Center: Baylor College of Medicine  
Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
-----  
Project Information  
Center project name: LAUI  
Center clone name: CH250-269A1  
-----  
Summary Statistics  
Chemistry: Dye-terminator Big Dye; inf% of reads  
Consensus quality: 5823 bases at least Q40  
Consensus quality: 6614 bases at least Q30  
Consensus quality: 7584 bases at least Q20  
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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html))  
\* NOTE: The contigs are based on the application  
\* of the PGI method using the human genome (NCBI build 31)  
\* as the comparative genome.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 1 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 145555: contig of 145555 bp in length.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9544"  
/clone="CH250-269A1"  
1. 145555  
/note="assembly name: CH250-269A1.1A"  
CONFIDENCE: 0.83"

ORIGIN  
misc\_feature  
Query Match 72.2%; Score 13; DB 2; Length 145555;  
Best Local Similarity 92.3%; Pred. No. 4.5e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 103728 CCTGAGANNNNN 103740

Qy 6 CCUGAGANNNNN 18

RESULT 193  
AC010803  
LOCUS  
AC010803 Homo sapiens clone RP11-2024, LOW-PASS SEQUENCE SAMPLING.  
DEFINITION  
AC010803  
AC010803.3 GI:9120116  
VERSION  
AC010803.3  
KEYWORDS  
HTG; HTGS PHASE0.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 146487)  
Birren, B., Linton, L., Nuebaum, C. and Lander, E.  
Homo sapiens, clone RP11-2024  
Unpublished  
2 (bases 1 to 146487)  
Birren, B., Linton, L., Nuebaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Bouhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Donlin, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hages, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karakas, A., Klein, J., Lehoczy, J., Liu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

TITLE  
JOURNAL  
COMMENT

Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,  
Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Teasdale, S., Tirrell, A., Vasilev, H., Vo, A., Wheeler, J., Wu, X.,  
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.  
Submitted (23-SEP-1999) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced g1.6730898.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: MIBR

Web site: <http://www-seq.wi.mit.edu>Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L2687

Center clone name: 2\_O\_24

NOTE: This record contains 148 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

1 866: contig of 866 bp in length  
\* 867 966: gap of 100 bp  
\* 967 1831: contig of 865 bp in length  
\* 1832 1931: gap of 100 bp  
\* 1932 2814: contig of 883 bp in length  
\* 2815 2914: gap of 100 bp  
\* 2915 3793: contig of 879 bp in length  
\* 3794 3894: gap of 100 bp  
\* 3894 4777: contig of 884 bp in length  
\* 4778 4878: gap of 100 bp  
\* 4878 5733: contig of 856 bp in length  
\* 5734 5833: gap of 100 bp  
\* 5834 6709: contig of 876 bp in length  
\* 6710 6810: gap of 100 bp  
\* 6810 7681: contig of 872 bp in length  
\* 7682 7781: gap of 100 bp  
\* 7782 8662: contig of 881 bp in length  
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\* 8763 9643: contig of 881 bp in length  
\* 9644 9744: gap of 100 bp  
\* 9744 10613: contig of 870 bp in length  
\* 10614 10713: gap of 100 bp  
\* 10714 11570: contig of 857 bp in length  
\* 11571 11670: gap of 100 bp  
\* 11671 12555: contig of 885 bp in length  
\* 12556 12655: gap of 100 bp  
\* 12656 13508: contig of 853 bp in length  
\* 13509 13608: gap of 100 bp  
\* 13609 14490: contig of 882 bp in length  
\* 14491 14590: gap of 100 bp  
\* 14591 15479: contig of 889 bp in length  
\* 15480 15579: gap of 100 bp  
\* 15580 16444: contig of 865 bp in length  
\* 16445 17426: contig of 882 bp in length  
\* 17427 17526: gap of 100 bp  
\* 17527 18399: contig of 873 bp in length  
\* 18400 18499: gap of 100 bp  
\* 18500 19392: contig of 893 bp in length  
\* 19393 19492: gap of 100 bp  
\* 19493 20385: contig of 893 bp in length  
\* 20386 20485: gap of 100 bp

20486 21361: contig of 876 bp in length  
\* 21362 21461: gap of 100 bp  
\* 21462 22337: contig of 876 bp in length  
\* 22338 22437: gap of 100 bp  
\* 22438 23319: contig of 882 bp in length  
\* 23320 23419: gap of 100 bp  
\* 23420 24296: contig of 877 bp in length  
\* 24297 24396: gap of 100 bp  
\* 24397 25255: contig of 859 bp in length  
\* 25256 25355: gap of 100 bp  
\* 25356 26264: contig of 909 bp in length  
\* 26265 26354: gap of 100 bp  
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\* 32114 32213: gap of 100 bp  
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\* 33084 33183: gap of 100 bp  
\* 33184 34060: contig of 877 bp in length  
\* 34061 34160: gap of 100 bp  
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\* 35049 35148: gap of 100 bp  
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\* 40017 40899: contig of 883 bp in length  
\* 40900 40999: gap of 100 bp  
\* 41000 41913: contig of 914 bp in length  
\* 41914 42013: gap of 100 bp  
\* 42014 42801: contig of 888 bp in length  
\* 42902 43001: gap of 100 bp  
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```

Query Match      72.2%  Score 13; DB 2; Length 146487;
Best Local Similarity 92.3%  Pred. NO. 4.5e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 6 CCUGAGNNNNNN 18
Db 102508 CCTGAGNNNNNN 102520

```

```

RESULT 194
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LOCUS
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Rattus norvegicus clone CH230-524N23, *** SEQUENCING IN PROGRESS
***, 56 unordered pieces.
ACCESSION
AC141155
VERSION
HTG: HTGS PHASE1.
KEYWORDS
Rattus norvegicus (Norway rat)
SOURCE
Rattus norvegicus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

```

```

REFERENCE
AUTHORS
1 (bases 1 to 147352)
Muzny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alibrooks, S., Amin, A., Angiano, D.,
Ayala-Dechichi, V., Ayagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benamed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasari, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M. L., Davis, C., Davy-Carrillo, L., De Anda, C., Dederich, D.,
Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotio, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Frazer, C. M., Gabis, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gedregregis, E., Geer, K., Gill, R., Grady, W., Guerra, W., Guevara, W.,
Gutierrez, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M.,

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

```

## REFERENCE

```

AUTHORS
TITLE
JOURNAL

```

## COMMENT

Hollins, B., Howells, S., Hulik, S., Hume, J., Idlebirt, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpachy, S., Kelly, S., Khan, Z., King, L., Kovac, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshewa, L., Louisedge, H., Lozada, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartine, M., Mahmud, M., Malloy, K., Mangum, A., Mangum, B., Magnus, P., Martin, K., Martin, R., Martinec, E., Mawhinney, S., McLeod, M., McNeill, T., Meenen, E., Mitroslav, A., Miner, G., Munja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundaasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokoeleneh, O., Okunolu, G., Olarunmugbon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Polinder, A., Povevic, D., Primus, E., Pu, L., L., Puzo, M., Qutro, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Sherry, J., Shvartsbeyn, A., Slasson, I., Sitter, C. D., Smaje, D., Sneed, A., Sodergren, E., Song, X., Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uemami, K., Valas, R., Vera, V., Villaana, D., Waldron, L., Walker, B., Wang, J., Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wiczak, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstein, G. and Gibbs, R. A.

Direct Submission  
Unpublished  
2 (bases 1 to 147352)  
Worley, K. C.  
Direct Submission  
Submitted (27-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 147352)  
Worley, K. C.  
Direct Submission  
Submitted (27-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Mar 17, 2003 this sequence version replaced gi:28894510.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
----- Project Information  
Center project name: KERN  
Center clone name: CH230-524N23  
----- Summary Statistics  
Sequencing vector: Plasmid  
Chemistry: Dye-terminator Big Dye 100% of reads  
Assembly program: Phrap, version 0.990329  
Consensus quality: 134150 bases at least Q40  
Consensus quality: 140679 bases at least Q30  
Consensus quality: 145481 bases at least Q20  
Estimated insert size: 131271; sum-of-contigs estimation  
Quality coverage: 2x in Q20 bases; sum-of-contigs estimation

-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbankdraft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbankdraft_data.html)).  
\* NOTE: This is a "working draft" sequence. It currently  
\* consists of 56 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1000: contig of 1000 bp in length

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* 11001 1100: gap of unknown length
* 1101 2284: contig of 1184 bp in length
* 2285 2384: gap of unknown length
* 2385 3633: contig of 1249 bp in length
* 3634 5288: gap of unknown length
* 5289 6431: gap of unknown length
* 6431 6531: gap of unknown length
* 6531 7889: contig of 1358 bp in length
* 7889 9371: gap of unknown length
* 9371 9472: gap of unknown length
* 9472 10505: contig of 1033 bp in length
* 10505 11618: gap of unknown length
* 11618 11719: contig of 1014 bp in length
* 11719 13124: contig of 1405 bp in length
* 13124 14475: gap of unknown length
* 14475 14576: contig of 1252 bp in length
* 14576 16149: gap of unknown length
* 16149 16249: gap of unknown length
* 16250 17393: contig of 1143 bp in length
* 17393 17493: gap of unknown length
* 17493 18914: contig of 1422 bp in length
* 18914 20108: gap of unknown length
* 20108 20209: contig of 1094 bp in length
* 20209 21542: gap of unknown length
* 21542 21643: contig of 1334 bp in length
* 21643 23406: gap of unknown length
* 23406 23505: contig of 1763 bp in length
* 23505 25572: gap of unknown length
* 25572 25673: contig of 2067 bp in length
* 25673 27765: gap of unknown length
* 27765 29323: contig of 2092 bp in length
* 29323 29424: gap of unknown length
* 29424 31543: contig of 1459 bp in length
* 31543 33812: gap of unknown length
* 33812 33912: contig of 2119 bp in length
* 33912 36361: gap of unknown length
* 36361 36461: gap of unknown length
* 36461 38607: contig of 2449 bp in length
* 38607 38707: gap of unknown length
* 38707 41043: contig of 2146 bp in length
* 41043 41143: gap of unknown length
* 41143 42381: contig of 2336 bp in length
* 42381 42481: gap of unknown length
* 42481 44501: contig of 1238 bp in length
* 44501 44601: gap of unknown length
* 44601 46994: contig of 2020 bp in length
* 46994 47094: gap of unknown length
* 47094 48335: contig of 2393 bp in length
* 48335 48536: gap of unknown length
* 48536 50214: gap of unknown length
* 50214 50314: gap of unknown length
* 50314 52827: contig of 1579 bp in length
* 52827 55471: gap of unknown length
* 55471 55772: contig of 2512 bp in length
* 55772 57803: gap of unknown length
* 57803 60917: contig of 2131 bp in length
* 60917 63949: gap of unknown length
* 63949 64049: contig of 3015 bp in length
* 64049 66579: gap of unknown length
* 66579 68904: gap of unknown length
* 68904 69004: gap of unknown length

```

```

* 69005 71189: contig of 2184 bp in length
* 71189 71289: gap of unknown length
* 71289 73508: contig of 2219 bp in length
* 73508 73607: gap of unknown length
* 73607 76943: contig of 3336 bp in length
* 76943 77044: gap of unknown length
* 77044 80072: contig of 3029 bp in length
* 80072 80173: gap of unknown length
* 80173 82766: contig of 2593 bp in length
* 82766 82866: gap of unknown length
* 82866 85497: gap of unknown length
* 85497 85598: contig of 2632 bp in length
* 85598 89601: gap of unknown length
* 89601 89700: contig of 4003 bp in length
* 89700 92959: gap of unknown length
* 92959 93059: contig of 3259 bp in length
* 93059 97134: gap of unknown length
* 97134 97234: contig of 4074 bp in length
* 97234 100495: gap of unknown length
* 100495 100595: contig of 3262 bp in length
* 100595 104694: gap of unknown length
* 104694 104794: contig of 4099 bp in length
* 104794 108059: gap of unknown length
* 108059 108059: contig of 3265 bp in length

Query Match 72.2%; Score 13; DB 2; Length 147352;
Best Local Similarity 92.3%; Pred. No. 4.5e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCGGAGNNNNNN 18
Db 9365 CCTGGAGNNNNNN 9377

RESULT 195
AC080177/c
LOCUS
DEFINITION
AC080177.2 GI:11276227
VERSION
HTG; HTGS PHASE1; HTGS_DRAFT
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 147571)
Birtten,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 14, clone RP11-45F22
Unpublished
2 (bases 1 to 147571)
Birtten,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Batra,N., Baetien,V., Beda,F., Boguslavsky,L.,
Boukhallier,B., Brown,A., Burkett,G., Campolongo,A., Castle,A.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Ferreira,P.,
Fitzhugh,W., Gage,D., Galagar,J., Gardyna,S., Ginde,S., Goyette,M.,
Graham,L., Grand-pierre,N., Hagos,B., Heatford,A., Horton,L.,
Iliev,I., Johnson,R., Jones,C., Kahn,L., Karatas,A., Lakoque,K.,
Lamaze,R., Landers,T., Lehoczy,J., Levine,R., Liu,C., Liu,G.,
Macdonald,P., Margulis,N., McCarthy,M., McEwan,P., McKernan,K.,
Mcpheters,R., Meldrim,J., Menus,L., Mihova,T., Mlenga,V.,
Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T.,
O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Reback,M., Riley,R.,
Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,
Sougnaz,C., Spencer,B., Strange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zimmer,B. and Zody,M.
Direct Submission
Submitted (28-SEP-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

```

REFERENCE  
AUTHORS

3 (bases 1 to 147571)

Barren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Batra, N., Baetjen, V., Beda, F., Boguslavsky, L., Bourkhalter, B., Brown, A., Burkett, G., Campoliano, A., Castle, A., Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeRellano, K., Dewar, K., Diaz, J. S., Dodge, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Iliev, I., Johnson, R., Jones, C., Kam, L., Karacas, A., Lacroque, K., Lamasares, R., Landers, T., Lehoczy, J., Levine, R., Liu, C., Liu, G., Macdonald, P., Marguis, N., McCarthy, M., McEwan, P., McKernan, K., McHeaters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N., Pisanu, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Sougnaz, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Teafaye, S., Theodore, J., Titrell, A., Travers, M., Trigglio, J., Vasilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zairoun, D., Zimmer, A., and Zody, M.

## Direct Submission

Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Nov 22, 2000 this sequence version replaced gi:10334897.

## COMMENT

All repeats were identified using RepeatMasker:

Smith, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

## Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WITBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

## Project Information

Center project name: L1152

Center clone name: 45 F 22

## Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 121934 bases at least Q40

Consensus quality: 133474 bases at least Q30

Consensus quality: 139354 bases at least Q20

Insert size: 173000; agarose-fp

Insert size: 142971; sum-of-coverage

Quality coverage: 2.5 in Q20 bases; agarose-fp

Quality coverage: 3.0 in Q20 bases; sum-of-coverage

NOTE: This is a 'working draft' sequence. It currently consists of 47 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 230: contig of 230 bp in length  
231 330: gap of 100 bp  
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2151 2250: gap of 100 bp  
2251 3132: contig of 882 bp in length  
3133 3232: gap of 100 bp  
3232 4327: contig of 1095 bp in length  
4328 4427: gap of 100 bp  
4427 5247: contig of 820 bp in length  
5248 5347: gap of 100 bp  
5348 6772: contig of 1425 bp in length  
6773 6872: gap of 100 bp  
6873 7730: contig of 858 bp in length  
7731 7830: gap of 100 bp  
7831 8960: contig of 1130 bp in length

8961 9060: gap of 100 bp  
9061 20307: contig of 11247 bp in length  
20308 20408: gap of 100 bp  
20408 21751: contig of 1344 bp in length  
21752 21851: gap of 100 bp  
21851 23279: contig of 1428 bp in length  
23280 23379: gap of 100 bp  
23380 24916: contig of 1537 bp in length  
24917 25016: gap of 100 bp  
25017 26637: contig of 1621 bp in length  
26638 26737: gap of 100 bp  
26738 28879: contig of 2142 bp in length  
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28980 30532: contig of 1553 bp in length  
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31916 32015: gap of 100 bp  
32016 33952: contig of 1937 bp in length  
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40058 41308: contig of 1251 bp in length  
41309 41408: gap of 100 bp  
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57330 57429: gap of 100 bp  
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59824 59923: gap of 100 bp  
59924 62602: contig of 2679 bp in length  
62603 62702: gap of 100 bp  
62703 64455: contig of 1753 bp in length  
64456 64555: gap of 100 bp  
64556 67800: contig of 3245 bp in length  
67801 67900: gap of 100 bp  
67901 71123: contig of 3223 bp in length  
71124 71223: gap of 100 bp  
71224 75319: contig of 4096 bp in length  
75320 75419: gap of 100 bp  
75420 79792: contig of 4373 bp in length  
79793 79892: gap of 100 bp  
79893 82865: contig of 2973 bp in length  
82866 82965: gap of 100 bp  
82966 87249: contig of 4284 bp in length  
87250 87349: gap of 100 bp  
87350 92098: contig of 4749 bp in length  
92099 92198: gap of 100 bp  
92199 95858: contig of 3660 bp in length  
95859 95958: gap of 100 bp  
95959 100870: contig of 4912 bp in length  
100871 100970: gap of 100 bp  
100970 104153: contig of 3183 bp in length  
104154 104253: gap of 100 bp  
104254 109134: contig of 4881 bp in length  
109135 109234: gap of 100 bp  
109235 115260: contig of 6026 bp in length  
115261 115360: gap of 100 bp  
115361 124565: contig of 9205 bp in length  
124566 124665: gap of 100 bp  
124666 134844: contig of 10119 bp in length  
134845 134944: gap of 100 bp



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* 134945 146657: contig of 11713 bp in length
* 146658 146757: gap of 100 bp
* 146758 147571: contig of 814 bp in length.
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            /db_xref="taxon:9606"
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            /map="14"
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            /clone_lib="RPC1-11 Human Male BAC"
            1..230
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        misc_feature
            331..1002
            /note="assembly_fragment"
        misc_feature
            72.2%; Score 13; DB 2; Length 147571;
            Best Local Similarity 92.3%; Pred. No. 4.5e+02;
            Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy
    6 CUCGAGNNNNNN 18
    ||:|||||||
    115367 CCTGGAGNNNNNN 115355
RESULT 196
AC141654/c
LOCUS
DEFINITION
    AC141654 149652 bp DNA linear HTG 24-MAR-2003
    Rattus norvegicus clone CH230-516H6, WORKING DRAFT SEQUENCE, 19
    unoriented pieces.
AC141654
AC141654.3 GI:29165560
VERSION
    HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
    Rattus norvegicus (Norway rat)
SOURCE
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
    Rattus.
    1 (bases 1 to 149652)
REFERENCE
    AUTHORS
        Muzny, D., Marie, T., Metzker, M., Lee, S., Abramson, S., Adams, C., Alder, J.,
        Allen, C., Allen, H., Albrooks, S., Amin, A., Angiano, D.,
        Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
        Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benham, F.,
        Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
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        Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
        Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
        Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
        Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
        Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
        Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
        Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
        Frazer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
        Gebregiorgis, E., Geer, K., Gill, R., Grady, M., Guertel, W., Guayra, W.,
        Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
        Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
        Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogue, M.,
        Hollins, B., Howells, S., Hulik, S., Hume, J., Idlebird, D., Jackson, A.,
        Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
        Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
        Kows, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
        Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
        Lorensuwa, L., Louised, H., Lozano, R.J., Lu, X., Ma, J.,
        Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A.,
        Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
        Maxam, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A.,
        Minier, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K.,
        Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D.,
        Newton, N., Nguyen, N., Norris, S., Nwaekelam, O., Okunolu, G.,
        Olajunnsagoun, A., Pal, S., Parks, K., Pasternak, S., Paul, H.,
        Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A.,

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TITLE
    Unpublished
REFERENCE
    2 (bases 1 to 149652)
    Worley, K.C.
    Direct Submission
    Submitted (19-MAR-2003) Human Genome Sequencing Center, Department
    of Molecular and Human Genetics, Baylor College of Medicine, One
    Baylor Plaza, Houston, TX 77030, USA
    3 (bases 1 to 149652)
    Worley, K.C.
    Direct Submission
    Submitted (24-MAR-2003) Human Genome Sequencing Center, Department
    of Molecular and Human Genetics, Baylor College of Medicine, One
    Baylor Plaza, Houston, TX 77030, USA
    On Mar 24, 2003 this sequence version replaced gi:29135409.
COMMENT
    ----- Genome Center
    Center: Baylor College of Medicine
    Center code: BCM
    Web site: http://www.hgsc.bcm.tmc.edu/
    Contact: hgsc-help@bcm.tmc.edu
    ----- Project information
    Center project name: KSHB
    Center clone name: CH230-516H6
    ----- Summary Statistics
    Sequencing vector: Plasmid;
    Chemistry: Dye-terminator Big Dye 100% of reads
    Assembly program: Phrap; version 0.990329
    Consensus quality: 140432 bases at least Q40
    Consensus quality: 143346 bases at least Q30
    Consensus quality: 145310 bases at least Q20
    Estimated insert size: 145510; sum-of-contigs estimation
    Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

```

```

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a working draft sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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1517: gap of unknown length
1518 1517: contig of 1834 bp in length
3351: gap of unknown length
3451: gap of unknown length
3452 3451: contig of 1459 bp in length
4911 3452: gap of unknown length
5011 4911: gap of unknown length
8685: contig of 3675 bp in length
8785: gap of unknown length
8786 8685: contig of 2819 bp in length
11605 8786: gap of unknown length
11705 11605: contig of 2818 bp in length
14523 11705: gap of unknown length
14623 14523: contig of 2621 bp in length
17244 14623: gap of unknown length
17344 17244: contig of 3683 bp in length

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* 21027 21126: gap of unknown length
* 26188: contig of 5062 bp in length
* 26189 26288: gap of unknown length
* 26289 31549: contig of 5261 bp in length
* 31550 31650: gap of unknown length
* 31650 39061: contig of 7412 bp in length
* 39062 44664: gap of unknown length
* 44665 44764: gap of 5503 bp in length
* 44765 52187: gap of unknown length
* 52188 52287: contig of 7423 bp in length
* 52288 62670: gap of unknown length
* 62671 62770: contig of 10383 bp in length
* 62771 74049: gap of unknown length
* 74050 74149: gap of 11279 bp in length
* 74150 84784: gap of unknown length
* 84785 84884: gap of 10635 bp in length
* 84885 97248: gap of unknown length
* 97249 97348: gap of 12364 bp in length
* 97349 113623: gap of unknown length
* 113624 113723: gap of 16275 bp in length
* 113724 149652: gap of unknown length
* 149653: contig of 35929 bp in length.

FEATURES
    source
        1. .149652
            /organism="Rattus norvegicus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10116"
            /clone="CH230-516H6"

ORIGIN
Query Match 72.2%; Score 13; DB 2; Length 149652;
Best Local Similarity 92.3%; Pred. No. 4.5e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18
||:|||||||
||:|||||||
Db 39168 CCTGAGAGNNNNNN 39156

RESULT 197
AC091792/c
LOCUS
DEFINITION
AC091792 150967 bp DNA linear HTG 23-MAY-2002
Felis catus clone RP86-145H12, WORKING DRAFT SEQUENCE, 5 ordered
pieces.
AC091792
VERSION
AC091792.2 GI:21104895
KEYWORDS
HTG; HTGS PHASE2; HTGS_DRAFT.
SOURCE
Felis catus (cat)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
Mammalia; Felis catus (cat)
1 (bases 1 to 150967)
Abtner, N., Antocletis, A., Ayala, K., Beckstrom-Sternberg, S. M.,
Benjamin, B., Blakesley, R. W., Bouffard, G. G., Breen, K., Brinkley, C.,
Brooks, S., Dietrich, N. L., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Hansen, N., Ho, S.-L., Idol, J. R., Karlins, E., Laric, P.,
Lee-Lin, S.-Q., Legaspi, R., Maduro, Q. L., Maduro, V. B.,
Margulies, E. H., Masetto, C., Maskeri, B., Mastrian, S. D.,
McCloskey, J. C., McDowell, J., Paquirigan, C., Pearson, R.,
Portnoy, M. E., Prasad, A., Schueler, M. G., Stantip, S., Thomas, J. W.,
Thomas, P. J., Touchman, J. W., Tsugeon, C., Vogt, J. L., Walker, M. A.,
Wetherby, K. D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E. D.,
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 150967)
Green, E. D.
REFERENCE
Direct Submission
Submitted (07-JUN-2001) NIH Intramural Sequencing Center, 8717
Groveomont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 150967)
Green, E. D.
REFERENCE
Direct Submission
Submitted (23-MAY-2002) NIH Intramural Sequencing Center, 8717

```

```

COMMENT
Groveomont Circle, Gaithersburg, MD 20877, USA
On May 23, 2002 this sequence version replaced gi:14327785.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.zoo@nih.gov
----- Project Information
Center project name: ctd
Center clone name: 145H12

The sequence data in this record represents an 'enhanced'
version of a Phase 2 submission. Specifically, the indicated
order and orientation of each sequence contig has been
established using one or more of the following: read-pair
data from individual subclones, overlaps with neighboring
clones, alignment with available reference sequence (e.g.,
human), and/or confirmation by PCR testing. In addition,
the sequence assembly is based on at least 8X average
coverage in Q20 bases and has been reviewed to rule out
gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
with a Phrap-derived quality score.
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 149914 bases at least Q40
Consensus quality: 150239 bases at least Q30
Consensus quality: 150421 bases at least Q20
Insert size: 130000; agarose-fp
Insert size: 150567; sum-of-contigs
Quality coverage: 13.36x in Q20 bases; agarose-fp
Quality coverage: 11.53x in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 25568: contig of 25568 bp in length
* 25569 25668: gap of unknown length
* 25669 36116: contig of 10448 bp in length
* 36117 104093: gap of unknown length
* 36217 104093: contig of 67877 bp in length
* 104094 104193: gap of unknown length
* 104194 142495: contig of 38302 bp in length
* 142496 142595: gap of unknown length
* 142596 150967: contig of 8372 bp in length.

FEATURES
    source
        1. .150967
            /organism="Felis catus"
            /mol_type="genomic DNA"
            /db_xref="taxon:9685"
            /clone="RP86-145H12"
            /clone_1ib="RP86"
            /clone_1ib="RP86"
            /clone_1ib="RP86"
            /note="clone overlaps with GenBank Accession Number
            AC098816 clone RP86-615J23 (center project name coy)"
            1. .25568
                /note="assembly_fragment"
                clone_end:sp6
                vector_side:left"
                25669..36116
                /note="assembly_fragment"
                36217..104093
                /note="assembly_fragment"
                104194..142495
                /note="assembly_fragment"

```

```

misc_feature      112235..150967
                  /note="clone overlaps with GenBank Accession Number
                  AC105458 clone RP86-283114 (center project name coz)"
misc_feature      142596..150967
                  /note="assembly_fragment
                  clone_end:77
                  vector_side:right"
ORIGIN
Query Match      72.2%; Score 13; DB 2; Length 150967;
Best Local Similarity 92.3%; Pred. No. 4.5e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy               6 CCUGAGGNNNNNN 18
Db               104200 CCTGGAGNNNNNN 104188

RESULT 198
AC150970/c
LOCUS
DEFINITION
AC150970          152179 bp    DNA          linear   HTG 04-SEP-2004
Bos taurus clone CH240-312P22, WORKING DRAFT SEQUENCE, 16 unordered
pieces.
AC150970
VERSION
AC150970.2 GI:51491793
KEYWORDS
HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE
Bos taurus (cow)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 152179)
Muzny,D., Metzker,M., Adams,C., Agbai II,O., Allen,C.,
Alabrook,S., Archer,P., Arredondo,H., Bandaranaike,D., Bangura,L.,
Beltran,B., Beltran,R., Beraducci,A., Biswal,K., Blyth,P.,
Bonham,H., Buhay,C., Burch,P., Cadore,I., Canada,A., Cardenas,V.,
Carter,K., Cavazos,I., Chacko,J., Chahrouh,M., Chavez,D., Chen,A.,
Chen,G., Chen,R., Cheng,M.-T., Chu,J., Clerc,K., Cockrell,R.,
Coyle,M., Cree,A., Curry,S., Dai,W., Davila,M.L., Davis,C.,
Davy-Carroll,L., De Anda,C., Delgado,O., Denon,S., Detamo,C.,
Ding,Y., Dinh,H., Donlin,J., McCauley,S., Dugan-Rocha,S., Dunn,A.,
Durbin,K., Dziuda,D., Egan,A., Escotte,M., Espinosa,V., Eugene,C.,
Pa,M., Fernandez,S., Fernando,P., Flagg,N., Forbes,L., Foster,P.,
Fowler,G., Fu,Q., Fuh,E., Garcia,A., Garcia,R., Garner,T.,
Gaskin,C., Gench,S., Ghose,S., Gill,R., Gonzalez,D.,
Gonzalez-Garay,M., Guevara,W., Holder,M., Haaland,W., Haeblerlein,K.,
Hall,B., Hamid,H., Hamilton,K., Harbee,B., Harris,R., Havlak,P.,
Hawes,A., Hawkins,E., Hayes,S., Hemphill,L., Hernandez,J.,
Hines,S., Hitchens,M., Hodgson,A., Hogue,M., Hollins,B.,
Howell,L.T., Hulik,S., Hume,J., Imo,K., Jackson,A., Jackson,L.,
Jacob,L., Jiang,H., Johnson,B., Johnson,R., Kalafus,K., Kelly,S.,
Keys,T., Khan,Z., King,L., Kovar,C., Kowis,A., Kowis,C., Lara,F.,
Leal,S., Lee,K., Lee,S., Legall,F.I., Lemon,S., Lewis,L., Li,B.,
Li,Y., Li,Z., Linell,M., Liu,W., Liu,Y.-S., Liu,Y., Lyanage,D.,
London,P., Lopez,J., Lorensunewa,L., Lozada,R., Luk,T., Madu,R.,
Maheshwari,M., Mahoney,C., Malloy,K., Mansouri,D., Martinez,E.,
McClelland,H., McPherson,J., Mercadao,C., Milosavljevic,A.,
Minja,E., Morgan,M., Morris,S., Murdasa,M., Murray,D.,
Nazareth,L., Ngo,D., Nguyen,N., Norwig-Bastaguh,E., Nott,A.,
Nwackeleme,O., Obregon,M., Ochi-Okorie,C., Odeh,E., Okumou,G.,
Okumou,K., Parker,D., Pasternak,S., Patel,B., Patel,V., Paul,H.,
Perez,A., Perez,L., Petrosino,D., Pham,T., Primus,E., Pu,L.-L.,
Punzo,M., Qin,X., Quinn,A., Quiroz,J., Rabata,D., Rachlin,E.,
Reigh,R., Ren,Y., Reuter,M., Richards,S., Rives,C., Rodriguez,F.,
Rojas,A., Ruiz,S.J., Sana,M., Sanders,W., Santibanez,J., Santos,R.,
Savery,G., Scherer,S., Shen,H., Shen,Y., Sisson,I., Speed,A.,
Sodergren,E., Song,X.-Z., Sorelle,R., Svatek,A., Taylor,E.,
Taylor,T., Thomas,N., Thorm,R., Thormon,R., Trejos,Z., Usmami,K.,
Varzo,C., Verduzco,D., Villaseca,D., Virk,D., Volkov,A.,
Walton,L., Walker,B., Wang,Q., Wang,S., Warren,J., Wei,X.,
Wheeler,D., Williams,G., Williams,R., Worley,K., Wright,R., Wu,J.,
Yakub,S., Yan,K., Yaun,Y., Yu,F., Zhang,J., Zhang,L., Zhang,Z.,
Zhou,J., Weinstein,G. and Gibbs,R.

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Direct Submission
Unpublished
2 (bases 1 to 152179)
Worley,K.C.
Direct Submission
Submitted (17-AUG-2004) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 152179)
Worley,K.C.
Direct Submission
Submitted (04-SEP-2004) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Aug 22, 2004 this sequence version replaced gi:51315474.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help.tmc.edu
Project Information
Center project name: FBGY
Center clone name: CH240-312P22
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 152191 bases at least Q40
Consensus quality: 155092 bases at least Q30
Consensus quality: 158513 bases at least Q20
Estimated insert size: 162494, sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; agarose-fp estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
3933: contig of 3933 bp in length
3934
4033: gap of unknown length
4034
6212: contig of 2179 bp in length
6213
10782: contig of 4470 bp in length
10783
10882: gap of unknown length
10883
34456: contig of 23574 bp in length
34457
34556: gap of unknown length
34557
43491: contig of 8935 bp in length
43492
43591: gap of unknown length
43592
54663: contig of 11072 bp in length
54664
54763: gap of unknown length
54764
57816: contig of 3053 bp in length
57817
57916: gap of unknown length
57917
65126: contig of 7210 bp in length
65127
65226: gap of unknown length
65227
76143: contig of 10917 bp in length
76144
76244: gap of unknown length
76245
78896: contig of 2653 bp in length
78897
78997: gap of unknown length
78998
91136: contig of 12140 bp in length
91137
91236: gap of unknown length
91237
94157: contig of 2921 bp in length
94158
94258: gap of unknown length
94259
112511: contig of 18254 bp in length
112512
112611: gap of unknown length
112612
116634: contig of 4023 bp in length
116635
116734: gap of unknown length

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\* 116735 132245: contig of 15511 bp in length  
\* 132246 132345: gap of unknown length  
\* 132346 152179: contig of 19634 bp in length.  
Location/Qualifiers  
1. 152179  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9913"  
/clone="CH240-312P22"

ORIGIN  
Query Match 72.2% Score 13; DB 2; length 152179;  
Best Local Similarity 92.3%; Pred. No. 4.5e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGAGNNNNN 18  
|||:|||||  
Db 6319 CCTGGAGNNNNN 6307

RESULT 199  
AC016082 152679 bp DNA linear HTG 13-JUL-2000  
LOCUS Homo sapiens clone RP11-24B21, LOW-PASS SEQUENCE SAMPLING.  
AC016082  
AC016082.2 GI:9129716  
KEYWORDS HTG; HTGS\_PHASE0.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 152679)  
Britten, B., Linton, L., Nusbaum, C. and Lander, E.  
Homo sapiens, clone RP11-24B21  
Unpublished  
2 (bases 1 to 152679)  
Britten, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,  
Baldwin, J., Barna, N., Beckert, R., Boguslavsky, L., Bouckgalter, B.,  
Brown, A., Casale, A., Colangelo, M., Collins, S., Collymore, A.,  
Cooke, P., DeRellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,  
Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,  
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
Hewland, J. C., Johnson, R., Jones, C., Kan, L., Karas, A., Klein, J.,  
Lohocky, J., Liu, C., Locke, K., MacDonald, P., Marguis, N.,  
McMan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,  
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,  
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,  
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
Teefaye, S., Titrrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,  
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (20-NOV-1999) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced gi:6456232.  
All repeats were identified using RepeatMasker:  
Smit, A.P.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIPR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L4422  
Center clone name: 24\_B\_21

\*\*\*\*\* NOTE: This record contains 167 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.

\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
1  
755 754: contig of 754 bp in length  
855 854: gap of 100 bp  
1624 1623: contig of 769 bp in length  
1724 1723: gap of 100 bp  
2490 2489: contig of 766 bp in length  
2590 2589: gap of 100 bp  
3333 3332: contig of 743 bp in length  
3433 3432: gap of 100 bp  
4181 4180: contig of 748 bp in length  
4281 4280: gap of 100 bp  
5055 5054: contig of 774 bp in length  
5155 5154: gap of 100 bp  
5952 5951: contig of 797 bp in length  
6052 6051: gap of 100 bp  
6832 6831: contig of 780 bp in length  
6932 6931: gap of 100 bp  
7713 7712: contig of 781 bp in length  
7813 7812: gap of 100 bp  
8599 8598: contig of 787 bp in length  
8600 8599: gap of 100 bp  
8700 8699: gap of 100 bp  
9381 9380: contig of 681 bp in length  
9481 9480: gap of 100 bp  
10257 10256: contig of 776 bp in length  
10357 10356: gap of 100 bp  
11134 11133: contig of 777 bp in length  
11234 11233: gap of 100 bp  
12024 12023: contig of 791 bp in length  
12124 12123: gap of 100 bp  
12915 12914: contig of 791 bp in length  
13015 13014: gap of 100 bp  
13779 13778: contig of 764 bp in length  
13879 13878: gap of 100 bp  
13780 13779: gap of 100 bp  
13880 13879: contig of 760 bp in length  
14640 14639: gap of 100 bp  
14740 14739: gap of 100 bp  
15520 15519: contig of 781 bp in length  
15521 15520: gap of 100 bp  
15620 15619: gap of 100 bp  
16395 16394: contig of 775 bp in length  
16396 16395: gap of 100 bp  
16496 16495: gap of 100 bp  
17257 17256: contig of 762 bp in length  
17357 17356: gap of 100 bp  
17358 17357: gap of 100 bp  
17359 17358: contig of 764 bp in length  
18122 18121: gap of 100 bp  
18222 18221: gap of 100 bp  
19003 19002: contig of 782 bp in length  
19004 19003: gap of 100 bp  
19104 19103: gap of 100 bp  
19888 19887: contig of 785 bp in length  
19889 19888: gap of 100 bp  
19989 19988: gap of 100 bp  
20749 20748: contig of 761 bp in length  
20750 20749: gap of 100 bp  
20850 20849: gap of 100 bp  
21623 21622: contig of 774 bp in length  
21624 21623: gap of 100 bp  
21724 21723: gap of 100 bp  
22515 22514: contig of 793 bp in length  
22516 22515: gap of 100 bp  
22616 22615: gap of 100 bp  
23396 23395: contig of 782 bp in length  
23499 23498: gap of 100 bp  
24280 24279: contig of 782 bp in length  
24380 24379: gap of 100 bp  
25163 25162: contig of 783 bp in length  
25263 25262: gap of 100 bp  
25264 25263: gap of 100 bp  
26052 26051: contig of 789 bp in length  
26152 26151: gap of 100 bp  
26924 26923: contig of 772 bp in length  
27024 27023: gap of 100 bp  
27812 27811: contig of 788 bp in length  
27912 27911: gap of 100 bp  
27913 27912: gap of 100 bp  
27914 27913: gap of 100 bp  
28710 28709: contig of 798 bp in length  
28810 28809: gap of 100 bp  
29579 29578: contig of 769 bp in length  
29679 29678: gap of 100 bp  
29680 29679: gap of 100 bp  
30459 30458: contig of 780 bp in length

```

* 30460 30559: gap of 100 bp
* 30560 31344: contig of 785 bp in length
* 31345 31444: gap of 100 bp
* 31445 32236: contig of 792 bp in length
* 32237 32336: gap of 100 bp
* 32337 33086: contig of 750 bp in length
* 33087 33186: gap of 100 bp
* 33187 33981: contig of 795 bp in length
* 33982 34081: gap of 100 bp
* 34082 34857: contig of 776 bp in length
* 34858 34957: gap of 100 bp
* 34958 35739: contig of 782 bp in length
* 35740 35839: gap of 100 bp
* 35840 36617: contig of 778 bp in length
* 36618 36717: gap of 100 bp
* 36718 37494: contig of 777 bp in length
* 37495 37594: gap of 100 bp
* 37595 38331: contig of 737 bp in length
* 38332 38431: gap of 100 bp
* 38432 39189: contig of 758 bp in length
* 39190 39289: gap of 100 bp
* 39290 40053: contig of 764 bp in length
* 40054 40153: gap of 100 bp
* 40154 40939: contig of 786 bp in length
* 40940 41813: contig of 774 bp in length
* 41814 42698: contig of 785 bp in length
* 42699 42798: gap of 100 bp
* 42799 43669: contig of 771 bp in length
* 43670 44455: contig of 786 bp in length
* 44456 44555: gap of 100 bp
* 44556 45340: contig of 785 bp in length
* 45341 45440: gap of 100 bp
* 45441 46232: contig of 792 bp in length
* 46233 46332: gap of 100 bp
* 46333 47100: contig of 768 bp in length
* 47101 47200: gap of 100 bp
* 47201 47948: contig of 748 bp in length
* 47949 48048: gap of 100 bp
* 48049 48810: contig of 762 bp in length
* 48811 48910: gap of 100 bp
* 48910 49672: contig of 762 bp in length
* 49673 49772: gap of 100 bp
* 49773 50558: contig of 786 bp in length
* 50559 50658: gap of 100 bp
* 50659 51424: contig of 766 bp in length
* 51425 51524: gap of 100 bp
* 51525 52300: contig of 776 bp in length
* 52301 52400: gap of 100 bp
* 52401 53170: contig of 770 bp in length
* 53171 53270: gap of 100 bp
* 53271 54055: contig of 785 bp in length
* 54056 54155: gap of 100 bp
* 54156 54937: contig of 782 bp in length
* 54938 55037: gap of 100 bp
* 55038 55802: contig of 765 bp in length
* 55803 55902: gap of 100 bp
* 55903 56764: contig of 762 bp in length
* 56765 57537: gap of 100 bp
* 57538 57637: gap of 100 bp
* 57637 58396: contig of 759 bp in length
* 58397 58496: gap of 100 bp
* 58497 59279: contig of 783 bp in length
* 59280 59379: gap of 100 bp
* 59380 60177: contig of 798 bp in length
* 60178 60277: gap of 100 bp
* 60278 61065: contig of 788 bp in length
* 61066 61165: gap of 100 bp
* 61166 61948: contig of 783 bp in length
* 61949 62048: gap of 100 bp

```

```

Query Match      72.2%; Score 13; DB 2; Length 152679;
Best Local Similarity 92.3%; Pred. No. 4.5e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CCUGGAGNNNNNN 18
Db      79853 CCTGGAGNNNNNN 79865

RESULT 200
AC150792
LOCUS
DEFINITION
AC150792
VERSION
AC150792.3 GI:52000546
KEYWORDS
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE
Bos taurus
ORGANISM
Bos taurus

REFERENCE
1 (bases 1 to 153541)
AUTHORS
Muzny,D., Adams,C., Agbai II,O., Allen,C., Alsbrooks,S., Archer,P.,
Arredondo,H., Bandaranaike,D., Bangura,L., Beltran,B., Beltran,R.,
Beraducci,A., Biswal,K., Blyth,P., Bonham,H., Buhay,C., Burch,P.,
Cadoree,I., Canada,A., Cardenas,V., Carter,K., Cavazos,I.,
Chacko,J., Chahrouh,M., Chavez,D., Chen,A., Chen,G., Chen,R.,
Cheng,M.-T., Chu,J., Clerc,K., Cockrell,R., Coyle,M., Crean,A.,
Curry,S., Dai,W., Davila,M.L., Davis,C., Davy-Carroli,L., De
Anda,C., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H.,
Donlin,J., McCauley,S., Dugan-Rocha,S., Dunn,A., Durbin,K.,
Dzinda,D., Egan,A., Escotto,M., Espinosa,V., Eugene,C., Fa,M.,
Fernandez,S., Fernando,P., Flagg,N., Forbes,L., Foster,P.,
Fowler,G., Fu,Q., Fun,E., Garcia,A., Garcia,R., Garner,T.,
Gaskin,C., Gench,S., Ghose,S., Gill,R., Gonzalez,D.,
Gonzalez-Garay,M., Guevara,W., Holder,M., Haland,W., Haebleren,K.,
Hall,B., Hamid,H., Hamilton,K., Harbes,B., Harris,R., Havlak,P.,
Hawes,A., Hawkins,E., Hayes,S., Hemphill,L., Hernandez,J.,
Hines,S., Hitchens,M., Hodgeson,A., Hogue,M., Hollins,B.,
Howell,L.T., Huylk,S., Hume,U., Iino,K., Jackson,A., Jackson,L.,
Jacob,D., Jiang,H., Johnson,B., Johnson,R., Kalatus,K., Kelly,S.,
Keys,T., Khan,Z., King,L., Kovar,C., Kowis,A., Kowis,C., Lara,F.,
Leal,S., Lee,K., Lee,S., Legall,F.I., Lemon,S., Lewis,L., Li,B.,
Li,Y., Li,Z., Linnell,M., Liu,W., Liu,Y.-S., Liu,Y., Liyanage,D.,
London,P., Lopez,J., Lorenshewa,L., Lozada,R., Luk,T., Madu,R.,
Maheshwari,M., Mahoney,C., Malloy,K., Mansouri,D., Martinez,E.,
McClelland,H., McPherson,J., Mercadao,C., Metzger,M.,
Mitsavlievic,A., Minja,E., Morgan,M., Morris,S., Muidasa,M.,
Murray,D., Nazareth,L., Ngo,D., Nguyen,N., Norwig-Eastachn,E.,
Nott,A., Nwaokemelehu,O., Obregon,M., Ochi-Okorie,C., Odeh,E.,
Okwomu,K., Okwomu,K., Parker,D., Pasternak,S., Patel,B.,
Patel,V., Paul,H., Perez,A., Perez,L., Petrosino,J., Pham,T.,
Primus,E., Pu,L.-L., Puzos,M., Qin,X., Quim,A., Quintoz,J.,
Rabata,D., Rachlin,E., Reigh,R., Ren,Y., Reuter,M., Richards,S.,
Rives,C., Rodriguez,F., Rojase,A., Ruiz,S.J., Sana,M., Sanders,S.,
Santibanez,J., Santos,R., Savery,G., Scherer,S., Shen,H., Shen,Y.,
Sison,I., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R.,
Svatek,A., Taylor,E., Taylor,T., Thomas,N., Thorn,R., Thornton,R.,
Trijos,Z., Umanit,K., Vargo,C., Verduzco,D., Villasana,D., Virk,D.,
Volkov,A., Waldron,L., Walker,B., Wang,Q., Wang,S., Warren,J.,
Wel,X., Wheeler,D., Williams,G., Williams,R., Worley,K., Wright,R.,
Wu,J., Yakub,S., Yan,K., Yau,Y., Yu,F., Zhang,J., Zhang,L.,
Zhang,Z., Zhou,J., Weinstein,G. and Gibbs,R.

Direct Submission
TITLE
JOURNAL
REFERENCE
2 (bases 1 to 153541)
AUTHORS
Worley,K.C.
TITLE
Direct Submission

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## JOURNAL

Submitted (10-AUG-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 153541)  
Worley, K.C.

## REFERENCE

Submitted (14-SEP-2004) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Sep 14, 2004 this sequence version replaced gi:51172638.

## COMMENT

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help.tmc.edu

Project Information

Center project name: FBXK

Center clone name: CH240-397L15

Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 163292 bases at least Q40

Consensus quality: 163699 bases at least Q30

Estimated insert size: 163519; sum-of-contigs estimation

Quality coverage: 15x in Q20 bases; sum-of-contigs estimation

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\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbankdraft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbankdraft_data.html))  
\* The sequence data in this record represents an 'enhanced' version  
\* of a Phase 2 submission. The indicated order and orientation of  
\* each sequence has been established using one or more of the  
\* following: read-pair data from individual subclones, overlaps  
\* with neighboring clones, alignment with available reference  
\* sequence (e.g., human), and/or confirmation by PCR testing.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 3 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* been provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 81569: contig of 81569 bp in length  
\* 81570 81619: gap of 50 bp  
\* 81620 132377: contig of 50758 bp in length  
\* 132378 132577: gap of 200 bp  
\* 132578 153541: contig of 20964 bp in length.  
Location/Qualifiers  
1. 153541

## FEATURES

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/db\_xref="taxon:9913"  
/clone="CH240-397L15"

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132378..132577

## misc\_feature

/note="assembly\_name:gap"  
132578..153541  
/note="assembly\_name:Contig26"

## ORIGIN

Query Match 72.2%; Score 13; DB 2; Length 153541;  
Best Local Similarity 92.3%; Pred. No. 4.5e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18

DB 132371 CCTGAGNNNNNN 132383

Search completed: April 25, 2005, 13:38:08  
Job time : 824.211 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 25, 2005, 13:09:42 ; Search time 206.053 Seconds  
(without alignments)  
517.127 Million cell updates/sec

Title: US-08-887-505B-38

Perfect score: 18

Sequence: 1 GCGGUCGCGAGNNNNNN 18

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size: 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database:

N\_Geneseq\_16Dec04:\*  
1: geneeqn1980s:\*  
2: geneeqn1990s:\*  
3: geneeqn2000s:\*  
4: geneeqn2001as:\*  
5: geneeqn2001bs:\*  
6: geneeqn2002as:\*  
7: geneeqn2002bs:\*  
8: geneeqn2003as:\*  
9: geneeqn2003bs:\*  
10: geneeqn2003cs:\*  
11: geneeqn2003ds:\*  
12: geneeqn2004as:\*  
13: geneeqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	AAT80248	Aat80248 Oligo HCV
2	18	100.0	18	ABSE5832	ABSE5832 Inhibitor
3	18	100.0	24	AAT80277	Aat80277 Oligo HCV
4	18	100.0	24	ABSE5861	ABSE5861 Inhibitor
5	15	83.3	29	AD43827	Ad43827 Adapter o
6	15	83.3	2400	ABK50461	ABK50461 Human cas
7	14	77.8	503	ADQ55353	ADQ55353 Novel can
8	14	72.2	418	AA576001	AA576001 DNA encod
9	13	72.2	784	AA197596	AA197596 Human neu
10	13	72.2	3286	ADQ22970	Adq22970 Human soc
11	13	72.2	5132	ADQ22880	Adq22880 Human soc
12	13	72.2	92726	ADA02927	Ada02927 Mouse pik
13	13	72.2	92726	AD872665	Ad872665 Mouse pik
14	13	72.2	92726	AD85407	Ad85407 Mouse pik
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47	12	66.7	12	18	AAT80256	Aat80256 Oligo HCV
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C 109	12	66.7	19	13	ADRS1223	Adrs1223 Hepatitis	181	12	66.7	24	2	AAQ64938	AAQ64938 Antisense
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C 127	12	66.7	20	2	AAQ6516776	AAq6516776 Hepatitis	199	12	66.7	24	2	AAQ650365	AAQ650365 HCV
C 128	12	66.7	20	3	AAQ652565	AAa52565 Oligonuc	200	12	66.7	24	2	AAQ650258	AAQ650258 HCV
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C 132	12	66.7	20	6	ABD3151	ABd3151 Gnu enzy	204	12	66.7	24	2	AAQ650362	AAQ650362 HCV
C 133	12	66.7	20	6	ABO78212	ABq78212 Probe com	205	12	66.7	24	2	AAQ650364	AAQ650364 HCV
C 134	12	66.7	20	6	ABK55813	ABs65813 Inhibitor	206	12	66.7	24	2	AAQ650268	AAQ650268 HCV
C 135	12	66.7	21	2	AAQ655814	AAq655814 Antisense	207	12	66.7	24	2	AAQ650273	AAQ650273 HCV
C 136	12	66.7	21	2	AAQ65101	AAq65101 Antisense	208	12	66.7	24	2	AAQ650197	AAQ650197 HCV
C 137	12	66.7	21	2	AAQ654923	AAq654923 Antisense	209	12	66.7	24	6	ABK65842	ABK65842 Inhibitor
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C 139	12	66.7	21	2	AAQ65130	AAq65130 Antisense	211	12	66.7	24	6	ABK65853	ABK65853 Inhibitor
C 140	12	66.7	21	2	AAQ65115	AAq65115 Antisense	212	12	66.7	24	6	ABK65859	ABK65859 Inhibitor
C 141	12	66.7	21	2	AAQ65076	AAq65076 Antisense	213	12	66.7	24	6	ABK65859	ABK65859 Inhibitor
C 142	12	66.7	21	2	AAQ65146	AAq65146 Antisense	214	12	66.7	24	6	ABK65852	ABK65852 Inhibitor
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C 144	12	66.7	21	3	AAQ652991	AAa72991 Hepatitis	216	12	66.7	24	6	ABK65856	ABK65856 Inhibitor
C 145	12	66.7	21	10	ADD67935	ADD67935 Hepatitis	217	12	66.7	24	6	ABK65849	ABK65849 Inhibitor
C 146	12	66.7	21	10	ABX10607	ABx10607 Light Cyc	218	12	66.7	24	6	ABK65854	ABK65854 Inhibitor
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C 149	12	66.7	22	2	AAQ65131	AAq65131 Antisense	221	12	66.7	24	6	ABK65844	ABK65844 Inhibitor
C 150	12	66.7	22	2	AAQ65086	AAq65086 Antisense	222	12	66.7	24	6	ABK65845	ABK65845 Inhibitor
C 151	12	66.7	22	2	AAQ65056	AAq65056 Antisense	223	12	66.7	24	6	ABK65847	ABK65847 Inhibitor
C 152	12	66.7	22	2	AAQ65056	AAq65056 Antisense	224	12	66.7	24	6	ABK65846	ABK65846 Inhibitor
C 153	12	66.7	22	2	AAQ65077	AAq65077 Antisense	225	12	66.7	24	6	ABK65849	ABK65849 Inhibitor
C 154	12	66.7	22	2	AAQ65089	AAq65089 Antisense	226	12	66.7	24	6	ABK65855	ABK65855 Inhibitor
C 155	12	66.7	22	2	AAQ65147	AAq65147 Antisense	227	12	66.7	24	6	ABK65860	ABK65860 Inhibitor
C 156	12	66.7	22	2	AAQ64928	AAq64928 Antisense	228	12	66.7	24	6	ABK65851	ABK65851 Inhibitor
C 157	12	66.7	22	6	ADP33107	Adp33107 Gnu enzy	229	12	66.7	24	6	ABK65848	ABK65848 Inhibitor
C 158	12	66.7	22	8	ADP45772	Adp45772 Single st	230	12	66.7	24	6	ABK65850	ABK65850 Inhibitor
C 159	12	66.7	22	10	ABP15975	ABp15975 HCV varia	231	12	66.7	24	6	ABK65850	ABK65850 Inhibitor
C 160	12	66.7	22	10	AAQ63097	AAq63097 Human tan	232	12	66.7	24	6	ABK65857	ABK65857 Inhibitor
C 161	12	66.7	22	12	ABZ37284	ABz37284 Type II r	233	12	66.7	25	2	AAQ65134	AAQ65134 Inhibitor
C 162	12	66.7	23	2	AAQ629087	AAq629087 Hepatitis	234	12	66.7	25	2	AAQ65119	AAQ65119 Antisense
C 163	12	66.7	23	2	AAQ65090	AAq65090 Antisense	235	12	66.7	25	2	AAQ65119	AAQ65119 Antisense
C 164	12	66.7	23	2	AAQ65078	AAq65078 Antisense	236	12	66.7	25	2	AAQ65050	AAQ65050 Antisense
C 165	12	66.7	23	2	AAQ65148	AAq65148 Antisense	237	12	66.7	25	2	AAQ65105	AAQ65105 Antisense
C 166	12	66.7	23	2	AAQ65103	AAq65103 Antisense	238	12	66.7	25	2	AAQ65035	AAQ65035 Antisense
C 166	12	66.7	23	2	AAQ65067	AAq65067 Antisense	239	12	66.7	25	2	AAQ65042	AAQ65042 Antisense



240	12	66.7	25	2	AA065069	AA065069	Antisense	313	12	66.7	30	2	AA065097	AA065097	Antisense
241	12	66.7	25	2	AA065080	AA065080	Antisense	314	12	66.7	30	2	AA065085	AA065085	Antisense
242	12	66.7	25	2	AA065059	AA065059	Antisense	315	12	66.7	30	2	AA064889	AA064889	Hepatitis
243	12	66.7	25	2	AA065092	AA065092	Antisense	316	12	66.7	30	6	ABN80437	ABN80437	Oligonuci
244	12	66.7	25	9	AA065043	AA065043	Human mic	317	12	66.7	32	6	AAK99674	AAK99674	Synthetic
245	12	66.7	26	2	AA065070	AA065070	Antisense	318	12	66.7	39	2	AAV00354	AAV00354	Bacillus
246	12	66.7	26	2	AA065093	AA065093	Antisense	319	12	66.7	39	5	AAF73272	AAF73272	Oligonuci
247	12	66.7	26	2	AA065036	AA065036	Antisense	320	12	66.7	39	10	ADD41449	ADD41449	Hepatitis
248	12	66.7	26	2	AA065151	AA065151	Antisense	321	12	66.7	42	2	AAT92127	AAT92127	Template
249	12	66.7	26	2	AA065051	AA065051	Antisense	322	12	66.7	45	12	AAT92132	AAT92132	Product o
250	12	66.7	26	2	AA065060	AA065060	Antisense	323	12	66.7	47	3	AAZ68250	AAZ68250	Human map
251	12	66.7	26	2	AA065081	AA065081	Antisense	324	12	66.7	48	2	AAZ23541	AAZ23541	HCV DNA f
252	12	66.7	26	2	AA065106	AA065106	Antisense	325	12	66.7	48	2	AAZ23542	AAZ23542	Human DNA
253	12	66.7	26	2	AA065120	AA065120	Antisense	326	12	66.7	48	11	ADU54923	ADU54923	Human iXK
254	12	66.7	26	2	AA065030	AA065030	Antisense	327	12	66.7	50	4	AA092382	AA092382	Oligonuci
255	12	66.7	26	2	AA065135	AA065135	Antisense	328	12	66.7	51	4	AA032522	AA032522	Human SNP
256	12	66.7	26	2	AA070178	AA070178	Hepatitis	329	12	66.7	51	4	AA032875	AA032875	Human SNP
257	12	66.7	26	6	AAK99673	AAK99673	Synthetic	330	12	66.7	52	2	AAT92125	AAT92125	Template
258	12	66.7	27	2	AA065071	AA065071	Antisense	331	12	66.7	52	2	AAT92128	AAT92128	Product o
259	12	66.7	27	2	AA065044	AA065044	Antisense	332	12	66.7	57	6	ACN25672	ACN25672	MYV Amber
260	12	66.7	27	2	AA065052	AA065052	Antisense	333	12	66.7	70	2	AAT11268	AAT11268	Hepatitis
261	12	66.7	27	2	AA065037	AA065037	Antisense	334	12	66.7	86	12	ADU53747	ADU53747	HBV spect
262	12	66.7	27	2	AA065061	AA065061	Antisense	335	12	66.7	97	12	ACH81857	ACH81857	Human gen
263	12	66.7	27	2	AA065082	AA065082	Antisense	336	12	66.7	124	12	ACH80864	ACH80864	Human gen
264	12	66.7	27	2	AA065121	AA065121	Antisense	337	12	66.7	127	6	ABX03545	ABX03545	Hepatitis
265	12	66.7	27	2	AA065152	AA065152	Antisense	338	12	66.7	138	2	AAT11267	AAT11267	Hepatitis
266	12	66.7	27	2	AA065107	AA065107	Antisense	339	12	66.7	138	12	ACH82399	ACH82399	Human gen
267	12	66.7	27	2	AA065026	AA065026	Antisense	340	12	66.7	140	2	AAT11269	AAT11269	Hepatitis
268	12	66.7	27	2	AA065031	AA065031	Antisense	341	12	66.7	155	3	AAZ57775	AAZ57775	Hepatitis
269	12	66.7	27	2	AA065136	AA065136	Antisense	342	12	66.7	159	2	AA043069	AA043069	-255 to -
270	12	66.7	27	2	AA065094	AA065094	Antisense	343	12	66.7	159	2	AA043071	AA043071	-255 to -
271	12	66.7	27	6	ABX03516	ABX03516	Hepatitis	344	12	66.7	177	2	AA079456	AA079456	HCV isola
272	12	66.7	27	6	AA043828	AA043828	Adapter o	345	12	66.7	177	2	AA079457	AA079457	HCV isola
273	12	66.7	28	2	AA065045	AA065045	Antisense	346	12	66.7	177	2	AA079459	AA079459	HCV isola
274	12	66.7	28	2	AA065053	AA065053	Antisense	347	12	66.7	177	2	AA068063	AA068063	HCV isola
275	12	66.7	28	2	AA065032	AA065032	Antisense	348	12	66.7	177	2	AA068068	AA068068	HCV isola
276	12	66.7	28	2	AA065095	AA065095	Antisense	349	12	66.7	177	2	AA079454	AA079454	HCV isola
277	12	66.7	28	2	AA065095	AA065095	Antisense	350	12	66.7	177	2	AA068069	AA068069	HCV isola
278	12	66.7	28	2	AA065122	AA065122	Antisense	351	12	66.7	177	2	AA068070	AA068070	HCV isola
279	12	66.7	28	2	AA065137	AA065137	Antisense	352	12	66.7	177	2	AA079457	AA079457	HCV isola
280	12	66.7	28	2	AA065108	AA065108	Antisense	353	12	66.7	177	2	AA068063	AA068063	HCV isola
281	12	66.7	28	2	AA065153	AA065153	Antisense	354	12	66.7	177	2	AA079460	AA079460	HCV isola
282	12	66.7	28	2	AA065072	AA065072	Antisense	355	12	66.7	177	2	AA079455	AA079455	HCV isola
283	12	66.7	28	2	AA065027	AA065027	Antisense	356	12	66.7	177	2	AA068066	AA068066	HCV isola
284	12	66.7	28	2	AA065038	AA065038	Antisense	357	12	66.7	177	2	AA079448	AA079448	HCV isola
285	12	66.7	28	2	AA065083	AA065083	Antisense	358	12	66.7	177	2	AA079458	AA079458	HCV isola
286	12	66.7	28	6	AAK99672	AAK99672	Synthetic	359	12	66.7	180	2	AA068064	AA068064	HCV isola
287	12	66.7	29	2	AA065109	AA065109	Antisense	360	12	66.7	180	2	AA031083	AA031083	HCV-1 gen
288	12	66.7	29	2	AA065046	AA065046	Antisense	361	12	66.7	180	2	AA031082	AA031082	HCV-1 gen
289	12	66.7	29	2	AA065096	AA065096	Antisense	362	12	66.7	184	2	AA043061	AA043061	-255 to -
290	12	66.7	29	2	AA065033	AA065033	Antisense	363	12	66.7	184	2	AA043068	AA043068	-255 to -
291	12	66.7	29	2	AA065138	AA065138	Antisense	364	12	66.7	184	2	AA043067	AA043067	-255 to -
292	12	66.7	29	2	AA065123	AA065123	Antisense	365	12	66.7	187	2	AA043059	AA043059	-255 to -
293	12	66.7	29	2	AA065073	AA065073	Antisense	366	12	66.7	190	12	ACH89341	ACH89341	Human gen
294	12	66.7	29	2	AA065054	AA065054	Antisense	367	12	66.7	194	2	AA043073	AA043073	-255 to -
295	12	66.7	29	2	AA065154	AA065154	Antisense	368	12	66.7	194	2	AA043074	AA043074	-255 to -
296	12	66.7	29	2	AA065063	AA065063	Antisense	369	12	66.7	194	2	AA043072	AA043072	-255 to -
297	12	66.7	29	2	AA065028	AA065028	Antisense	370	12	66.7	194	2	AA043070	AA043070	-255 to -
298	12	66.7	29	2	AA065084	AA065084	Antisense	371	12	66.7	201	13	AD840150	AD840150	Human aut
299	12	66.7	29	2	AA065039	AA065039	Antisense	372	12	66.7	202	1	AA014084	AA014084	HCV-I (1-
300	12	66.7	30	2	AA037575	AA037575	HCV conse	373	12	66.7	202	2	AA014083	AA014083	HCV-T (1-
301	12	66.7	30	2	AA065047	AA065047	Antisense	374	12	66.7	209	8	ADA93664	ADA93664	Competito
302	12	66.7	30	2	AA065124	AA065124	Antisense	375	12	66.7	217	12	ACH83248	ACH83248	Human gen
303	12	66.7	30	2	AA065040	AA065040	Antisense	376	12	66.7	221	3	AA025474	AA025474	Human sec
304	12	66.7	30	2	AA065155	AA065155	Antisense	377	12	66.7	226	2	AAT24352	AAT24352	Human gen
305	12	66.7	30	2	AA065034	AA065034	Antisense	378	12	66.7	226	12	AD005658	AD005658	HCV templ
306	12	66.7	30	2	AA065110	AA065110	Antisense	379	12	66.7	230	12	AD005662	AD005662	PCR ampli
307	12	66.7	30	2	AA065139	AA065139	Antisense	380	12	66.7	230	12	AD005661	AD005661	PCR ampli
308	12	66.7	30	2	AA065029	AA065029	Antisense	381	12	66.7	230	12	ACH88756	ACH88756	Human gen
309	12	66.7	30	2	AA065064	AA065064	Antisense	382	12	66.7	232	12	AAV70460	AAV70460	Partial s
310	12	66.7	30	2	AA065074	AA065074	Antisense	383	12	66.7	232	6	ABL46070	ABL46070	Hepatitis
311	12	66.7	30	2	AA065055	AA065055	Antisense	384	12	66.7	232	12	ADK82260	ADK82260	Hepatitis
312	12	66.7	30	2	AA065055	AA065055	Antisense	385	12	66.7	232	12	ADK82260	ADK82260	Hepatitis

C 386	12	66.7	239	2	AAV70459	AAV70459	Partial s	459	12	66.7	297	4	ABA68279	AbA68279	Human fce
C 387	12	66.7	239	2	AAV70455	AAV70455	Partial s	460	12	66.7	297	4	AAI48494	AAI48494	Probe #17
C 388	12	66.7	239	6	ABL46065	ABL46065	Hepatit	461	12	66.7	297	4	AAK42417	AAK42417	Human bon
C 389	12	66.7	239	6	ABL46069	ABL46069	Hepatit	462	12	66.7	297	4	AAK16653	AAK16653	Human bra
C 390	12	66.7	239	12	ADK82255	ADK82255	Hepatit	463	12	66.7	297	4	ABE442074	ABE442074	Human ltv
C 391	12	66.7	239	12	ADK82259	ADK82259	Hepatit	464	12	66.7	297	6	ABE16471	ABE16471	Human gen
C 392	12	66.7	240	2	AAV70456	AAV70456	Partial s	465	12	66.7	299	8	ABX55952	ABX55952	Bovine ES
C 393	12	66.7	240	2	AAV70461	AAV70461	Partial s	466	12	66.7	299	10	AAD55565	AAD55565	IG57272 H
C 394	12	66.7	240	6	ABL46066	ABL46066	Hepatit	467	12	66.7	299	10	AAZ14348	AAZ14348	Human gen
C 395	12	66.7	240	6	ABL46071	ABL46071	Hepatit	468	12	66.7	300	2	AAZ49261	AAZ49261	Human hyd
C 396	12	66.7	240	12	ADK82261	ADK82261	Hepatit	469	12	66.7	305	3	AAZ87088	AAZ87088	HCV ampli
C 397	12	66.7	240	12	ADK82256	ADK82256	Hepatit	470	12	66.7	305	6	ABN79969	ABN79969	Hepatit
C 398	12	66.7	241	6	ADD43290	ADD43290	HCV targe	471	12	66.7	305	6	ABN79970	ABN79970	Hepatit
C 399	12	66.7	242	2	AAO37742	AAO37742	HCV ampli	472	12	66.7	306	2	AAQ67079	AAQ67079	Hepatit
C 400	12	66.7	242	2	AAO37774	AAO37774	Cloned HC	473	12	66.7	306	6	ABE53053	ABE53053	Hepatit
C 401	12	66.7	244	2	AAV70454	AAV70454	Partial s	474	12	66.7	308	3	AAA75294	AAA75294	Novel hep
C 402	12	66.7	244	2	AAV70449	AAV70449	HCV subty	475	12	66.7	308	12	ADN35973	ADN35973	HCV cDNA
C 403	12	66.7	244	6	ABL46052	ABL46052	Hepatit	476	12	66.7	309	3	AAZ36198	AAZ36198	Adapted H
C 404	12	66.7	244	6	ABL46059	ABL46059	Hepatit	477	12	66.7	312	3	AAZ36197	AAZ36197	Adapted H
C 405	12	66.7	244	6	ABL46064	ABL46064	Hepatit	478	12	66.7	314	3	AAZ36197	AAZ36197	Adapted H
C 406	12	66.7	244	12	ADK82254	ADK82254	Hepatit	479	12	66.7	319	2	AAZ40689	AAZ40689	Human sec
C 407	12	66.7	244	12	ADK82351	ADK82351	Hepatit	480	12	66.7	321	4	ABL13141	ABL13141	Drosophi
C 408	12	66.7	244	12	ADK82347	ADK82347	Hepatit	481	12	66.7	326	6	ABK70880	ABK70880	HCV genom
C 409	12	66.7	244	12	ADK82252	ADK82252	Hepatit	482	12	66.7	326	12	ADP20410	ADP20410	Hepatit
C 410	12	66.7	244	12	ADK82350	ADK82350	Hepatit	483	12	66.7	327	3	AAZ36199	AAZ36199	Adapted H
C 411	12	66.7	244	12	ADK82349	ADK82349	Hepatit	484	12	66.7	327	6	ABK70884	ABK70884	HCV genom
C 412	12	66.7	244	12	ADK82350	ADK82350	Hepatit	485	12	66.7	328	2	ABL46275	ABL46275	Hepatit
C 413	12	66.7	244	12	ADK82349	ADK82349	Hepatit	486	12	66.7	328	6	ABL46275	ABL46275	Hepatit
C 414	12	66.7	252	2	AAQ31071	AAQ31071	HCV-1 gen	487	12	66.7	328	6	AAZ36197	AAZ36197	Adapted H
C 415	12	66.7	252	2	AAQ31069	AAQ31069	HCV-1 gen	488	12	66.7	328	8	AAZ36197	AAZ36197	Adapted H
C 416	12	66.7	252	2	AAQ31070	AAQ31070	HCV-1 gen	489	12	66.7	328	8	AAZ36197	AAZ36197	Adapted H
C 417	12	66.7	252	2	AAQ31068	AAQ31068	HCV-1 gen	490	12	66.7	328	8	AAZ36197	AAZ36197	Adapted H
C 418	12	66.7	252	2	AAQ31081	AAQ31081	HCV-1 gen	491	12	66.7	333	6	ABK70872	ABK70872	HCV genom
C 419	12	66.7	252	2	AAQ31067	AAQ31067	HCV-1 gen	492	12	66.7	333	2	AAZ36197	AAZ36197	Hepatit
C 420	12	66.7	252	2	AAQ31066	AAQ31066	HCV-1 gen	493	12	66.7	337	2	AAZ36197	AAZ36197	Hepatit
C 421	12	66.7	252	2	AAQ31072	AAQ31072	Human ORF	494	12	66.7	337	6	AAZ36197	AAZ36197	Hepatit
C 422	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	495	12	66.7	338	3	AAZ36197	AAZ36197	Hepatit
C 423	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	496	12	66.7	339	3	AAZ36197	AAZ36197	Hepatit
C 424	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	497	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 425	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	498	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 426	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	499	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 427	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	500	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 428	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	501	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 429	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	502	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 430	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	503	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 431	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	504	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 432	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	505	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 433	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	506	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 434	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	507	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 435	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	508	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 436	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	509	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 437	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	510	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 438	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	511	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 439	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	512	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 440	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	513	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 441	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	514	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 442	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	515	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 443	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	516	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 444	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	517	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 445	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	518	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 446	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	519	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 447	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	520	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 448	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	521	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 449	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	522	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 450	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	523	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 451	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	524	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 452	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	525	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 453	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	526	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 454	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	527	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 455	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	528	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 456	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	529	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 457	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	530	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit
C 458	12	66.7	256	2	AAQ32981	AAQ32981	HCV BI 5'	531	12	66.7	341	2	AAZ36197	AAZ36197	Hepatit

C 532	12	66.7	373	13	ADQ52891	Adq52891 Novel can	605	12	66.7	480	10	AD587360	Ad587360 Toxicity-
C 533	12	66.7	374	12	ADK11630	Adk11630 Breast ca	606	12	66.7	480	10	AD104970	Ad104970 Rat odora
C 534	12	66.7	375	10	ADQ04032	Adq04032 Hepatitis	C 607	12	66.7	480	2	AAQ32446	Aaq32446 HCV core-
C 535	12	66.7	378	10	ADK66080	Adk66080 Standard1	C 608	12	66.7	483	2	AAQ32445	Aaq32445 HCV core-
C 536	12	66.7	381	4	AAH71906	Aah71906 Human cer	C 609	12	66.7	483	2	AAQ32453	Aaq32453 HCV core-
C 537	12	66.7	383	6	ABK15309	Abk15309 Hepatitis	C 610	12	66.7	483	2	AAQ32447	Aaq32447 HCV core-
C 538	12	66.7	384	4	AA504594	AA504594 Gene expr	C 611	12	66.7	483	2	AAQ32444	Aaq32444 HCV core-
C 539	12	66.7	384	6	ABK15314	Abk15314 Hepatitis	C 612	12	66.7	484	4	AAK73138	Aak73138 Human imm
C 540	12	66.7	386	2	AAAT2917	Aat2917 Hepatitis	C 613	12	66.7	484	4	AAK80321	Aak80321 Human imm
C 541	12	66.7	386	5	ABV11141	Abv11141 Human pro	C 614	12	66.7	485	6	AAK63937	Aak63937 CDNA enco
C 542	12	66.7	386	9	ADB116263	Adb116263 Cleavage	C 615	12	66.7	490	4	AA530914	AA530914 Human CDN
C 543	12	66.7	387	4	AAH69040	Aah69040 Human cer	C 616	12	66.7	492	6	ABL89981	AbL89981 Human pol
C 544	12	66.7	390	4	AA532240	Aa532240 Mouse uri	C 617	12	66.7	494	5	AA571629	Aa571629 DNA enco
C 545	12	66.7	391	5	AA566301	Aa566301 Novel hum	C 618	12	66.7	498	4	AA186991	AA186991 Human pol
C 546	12	66.7	391	6	ABQ72616	Abq72616 Human MD	C 619	12	66.7	500	13	AD534658	Ad534658 Hepatitis
C 547	12	66.7	393	6	ABA96260	AbA96260 Hepatitis	C 620	12	66.7	500	13	AD534660	Ad534660 Hepatitis
C 548	12	66.7	394	2	AAQ61266	Aaq61266 Human bra	C 621	12	66.7	500	13	AD534661	Ad534661 Hepatitis
C 549	12	66.7	394	5	ABV11103	Abv11103 Human pro	C 622	12	66.7	502	12	AD534659	Ad534659 Hepatitis
C 550	12	66.7	394	6	ABL83300	AbL83300 Human ova	C 623	12	66.7	502	12	ACH75615	Ach75615 Human gen
C 551	12	66.7	395	4	AA559135	AA559135 Human can	C 624	12	66.7	504	2	AAQ12239	AAQ12239 Clone 164
C 552	12	66.7	397	5	ABV01972	Abv01972 Human pro	C 625	12	66.7	506	12	ACH75056	Ach75056 Human gen
C 553	12	66.7	398	5	ABV01934	Abv01934 Human pro	C 626	12	66.7	508	4	AA117280	AA117280 Probe #72
C 554	12	66.7	401	3	AA565960	Aa565960 Human lun	C 627	12	66.7	508	4	ABA62087	AbA62087 Human foe
C 555	12	66.7	401	6	ABL49179	AbL49179 Human lun	C 628	12	66.7	508	4	AA142030	AA142030 Probe #10
C 556	12	66.7	401	6	ABO92365	AbO92365 Human lun	C 629	12	66.7	508	4	ABA29528	AbA29528 Probe #79
C 557	12	66.7	401	6	ABO92365	AbO92365 Human lun	C 630	12	66.7	508	4	AAK36307	Aak36307 Human bon
C 558	12	66.7	401	10	ADA28354	Ada28354 Human lun	C 631	12	66.7	508	4	AAK10404	Aak10404 Human bra
C 559	12	66.7	401	12	ADH36918	Adh36918 Human lun	C 632	12	66.7	508	4	AB535986	Ab535986 Human liv
C 560	12	66.7	403	5	AA565763	AA565763 DNA enco	C 633	12	66.7	508	6	AB510382	Ab510382 Human gen
C 561	12	66.7	404	5	ABL82185	AbL82185 Human ova	C 634	12	66.7	510	4	AAK84409	Aak84409 Human imm
C 562	12	66.7	408	10	ADC32161	AdC32161 Human nov	C 635	12	66.7	510	4	AAK84410	Aak84410 Human imm
C 563	12	66.7	408	4	AAH70703	Aah70703 Human cer	C 636	12	66.7	510	12	ACH73394	Ach73394 Human gen
C 564	12	66.7	409	3	AACT4799	Aac74799 Human ORF	C 637	12	66.7	513	12	ACH67159	Ach67159 Human gen
C 565	12	66.7	410	5	ADL40350	AdL40350 Human ova	C 638	12	66.7	519	12	ADL81839	AdL81839 Human lun
C 566	12	66.7	411	9	ACH29499	Ach29499 Human adu	C 639	12	66.7	530	12	ADP72173	AdP72173 Renal tox
C 567	12	66.7	412	6	ABA96259	AbA96259 Hepatitis	C 640	12	66.7	532	12	ACH69548	Ach69548 Human gen
C 568	12	66.7	416	5	AA580250	AA580250 DNA enco	C 641	12	66.7	533	13	ADQ51434	AdQ51434 Novel can
C 569	12	66.7	418	8	ABX35423	Abx35423 Bovine ES	C 642	12	66.7	535	5	ABV39222	Abv39222 Human pro
C 570	12	66.7	420	12	ADQ80848	AdQ80848 Hepatitis	C 643	12	66.7	544	13	ADQ78538	AdQ78538 Novel can
C 571	12	66.7	422	8	ACC79264	Acc79264 Hepatitis	C 644	12	66.7	546	2	AAQ79776	Aaq79776 Hepatitis
C 572	12	66.7	428	5	AA591871	AA591871 DNA enco	C 645	12	66.7	556	2	AA500458	Aa500458 Hepatitis
C 573	12	66.7	431	5	ABV32287	Abv32287 Human pro	C 646	12	66.7	556	2	AA526743	Aa526743 Sequence
C 574	12	66.7	433	5	ABV07225	Abv07225 Human pro	C 647	12	66.7	556	2	ADP66079	Adp66079 Hepatitis
C 575	12	66.7	434	7	AD572443	Ad572443 Human kid	C 648	12	66.7	556	4	AA532731	Aa532731 Human bec
C 576	12	66.7	440	5	ABV32249	Abv32249 Human pro	C 649	12	66.7	557	12	ACH73429	Ach73429 Human gen
C 577	12	66.7	440	5	ABV41180	Abv41180 Human pro	C 650	12	66.7	559	12	ACH68699	Ach68699 Human gen
C 578	12	66.7	440	5	ABV41218	Abv41218 Human pro	C 651	12	66.7	560	2	AA207662	Aa207662 HCV J1 co
C 579	12	66.7	446	9	ACH41449	Ach41449 Human foe	C 652	12	66.7	562	4	AAH11923	Aah11923 Human CDN
C 580	12	66.7	447	8	AB236902	Ab236902 Human GEN	C 653	12	66.7	562	12	ACH68155	Ach68155 Human gen
C 581	12	66.7	452	2	AAV86924	Aav86924 EST clone	C 654	12	66.7	566	13	ADQ53929	AdQ53929 Novel can
C 582	12	66.7	457	4	ACH41467	Ach41467 Human foe	C 655	12	66.7	569	6	AB511486	Ab511486 Human gen
C 583	12	66.7	458	5	ABV37165	Abv37165 Human pro	C 656	12	66.7	569	12	ACH67981	Ach67981 Human gen
C 584	12	66.7	459	6	ABQ77833	AbQ77833 Human PTO	C 657	12	66.7	571	12	ACH69618	Ach69618 Human gen
C 585	12	66.7	460	13	ADQ57171	AdQ57171 Novel can	C 658	12	66.7	572	13	AD534704	Ad534704 sRNA-1 P
C 586	12	66.7	461	2	AAT27988	Aat27988 Hepatitis	C 659	12	66.7	578	13	ADQ49838	AdQ49838 Novel can
C 587	12	66.7	462	2	AAV09665	Aav09665 Human cat	C 660	12	66.7	584	4	ABA11365	AbA11365 Probe #98
C 588	12	66.7	463	3	AAA80646	Aaa80646 Human sec	C 661	12	66.7	584	6	AB512474	Ab512474 Human gen
C 589	12	66.7	463	9	ADA27108	Ada27108 Human nov	C 662	12	66.7	587	3	AA257395	Aa257395 Hepatitis
C 590	12	66.7	469	12	AD586644	Ad586644 Novel hum	C 663	12	66.7	587	12	ADL87163	AdL87163 DNA up-re
C 591	12	66.7	470	9	ACD28233	Acd28233 Human BT2	C 664	12	66.7	590	13	ADQ55673	AdQ55673 Novel can
C 592	12	66.7	470	9	ACH28402	Ach28402 Human adu	C 665	12	66.7	591	6	ABQ56531	AbQ56531 Human col
C 593	12	66.7	475	4	AA113958	Aa113958 Probe #38	C 666	12	66.7	600	11	ACH92766	Ach92766 Breast ca
C 594	12	66.7	475	4	ABA55681	AbA55681 Human foe	C 667	12	66.7	602	12	ADQ51140	AdQ51140 Novel can
C 595	12	66.7	475	4	AA135338	Aa135338 Probe #40	C 668	12	66.7	610	5	ABV21206	Abv21206 Human pro
C 596	12	66.7	475	4	AAK29377	Aak29377 Human bon	C 669	12	66.7	610	5	ABV27027	Abv27027 Human pro
C 597	12	66.7	475	4	AAK03903	Aak03903 Human bra	C 670	12	66.7	610	5	ABV27059	Abv27059 Human pro
C 598	12	66.7	475	4	AB528997	Ab528997 Human liv	C 671	12	66.7	610	5	ABV21238	Abv21238 Human pro
C 599	12	66.7	475	6	AB503936	Ab503936 Human gen	C 672	12	66.7	617	5	AA575955	Aa575955 DNA enco
C 600	12	66.7	475	10	ADP28115	Adp28115 Human neu	C 673	12	66.7	621	3	AA535286	Aa535286 Human ade
C 601	12	66.7	477	9	ACH34902	Ach34902 Human end	C 674	12	66.7	621	3	AA521408	Aa521408 Human low
C 602	12	66.7	477	12	ACH87352	Ach87352 Human gen	C 675	12	66.7	621	10	AB297102	Ab297102 Human nuc
C 603	12	66.7	480	2	AAQ29877	Aaq29877 Pheromone	C 676	12	66.7	621	11	ABD20951	Abd20951 Human pul
C 604	12	66.7	480	6	ABK63172	Abk63172 Rat seque	C 677	12	66.7	625	4	ABA08653	AbA08653 Human Zn

C 678	12	66.7	631	4	AAS30882	Aae30882 Human cDN	C 751	12	66.7	842	6	ABK24021	Abk24021 B7-relate
C 679	12	66.7	631	12	ACH87610	Ach87610 Human gen	C 752	12	66.7	843	5	AA575956	AA575956 DNA encod
C 680	12	66.7	637	13	ADQ53698	Adq53698 Novel can	C 753	12	66.7	846	6	ABO89154	ABO89154 Human pro
C 681	12	66.7	646	10	ADE09608	Ad09608 Novel DNA	C 754	12	66.7	857	5	AA564511	AA564511 DNA encod
C 682	12	66.7	646	13	ADRO7612	Adro7612 Full leng	C 755	12	66.7	861	6	AB552108	AB552108 Human but
C 683	12	66.7	650	4	ABA09468	Ab09468 Human cat	C 756	12	66.7	866	4	AA194061	AA194061 Human neu
C 684	12	66.7	652	2	AAT27966	Aat27966 Hepatitis	C 757	12	66.7	888	4	AAH32577	AAH32577 Human sec
C 685	12	66.7	663	13	AAA75292	Aaa75292 Bacterial	C 758	12	66.7	904	13	ABD32563	ABD32563 Human can
C 686	12	66.7	665	3	AAH75292	Aah75292 Novel hep	C 759	12	66.7	923	5	AA568258	AA568258 DNA encod
C 687	12	66.7	665	12	ADN35969	Adn35969 HCV cDNA	C 760	12	66.7	950	8	AAT28348	Aat28348 Hepatitis
C 688	12	66.7	668	5	AAH26695	Aah26695 Human bre	C 761	12	66.7	950	8	ABX72221	Abx72222 Human NOV
C 689	12	66.7	669	5	AAH97948	Aah97948 Murine 7-	C 762	12	66.7	961	4	AA111631	AA111631 Probe #15
C 690	12	66.7	684	4	AAH72670	Aah72670 Human cer	C 763	12	66.7	961	4	ABAS3333	ABas3333 Human fce
C 691	12	66.7	685	2	AAZ17719	Aaz17719 Hepatitis	C 764	12	66.7	961	4	AA132930	AA132930 Probe #16
C 692	12	66.7	685	10	ADA49755	Ada49755 HCV 5'UTR	C 765	12	66.7	961	4	ABAA2903	ABaa2903 Human bre
C 693	12	66.7	685	12	ADN03472	Adn03472 Hepatitis	C 766	12	66.7	961	4	ABA23100	ABa23100 Human b're
C 694	12	66.7	686	2	AAQ44921	Aaq44921 Hepatitis	C 767	12	66.7	961	4	AAK27031	AAK27031 Human b're
C 695	12	66.7	688	10	ADE09592	Ade09592 Novel DNA	C 768	12	66.7	961	4	AAK01588	AAK01588 Human bon
C 696	12	66.7	700	4	AAH92795	Aah92795 Human inf	C 769	12	66.7	961	4	AB526617	AB526617 Human b'ta
C 697	12	66.7	703	3	AAZ57396	Aaz57396 Hepatitis	C 770	12	66.7	961	5	AA101558	AA101558 Probe #15
C 698	12	66.7	710	6	ABT09501	Abt09501 Phase-1 R	C 771	12	66.7	961	5	AB501611	AB501611 Human gen
C 699	12	66.7	710	10	ADG30929	Adg30929 Liver tox	C 772	12	66.7	963	4	AAAC89281	AAc89281 Human bra
C 700	12	66.7	710	12	ADG45517	Adg45517 Liver inf	C 773	12	66.7	977	12	ACH90998	ACH90998 Human gen
C 701	12	66.7	710	12	ADH22819	Adh22819 Partial D	C 774	12	66.7	994	10	ABR07354	ABr07354 Novel cod
C 702	12	66.7	713	3	AAA08097	Aaa08097 Partial D	C 775	12	66.7	1001	13	ADQ81128	ADq81128 Human phe
C 703	12	66.7	713	12	ADP20088	Adp20088 Hepatitis	C 776	12	66.7	1008	10	AD122503	AD122503 Rat liver
C 704	12	66.7	720	3	ABL52861	AbL52861 Human imm	C 777	12	66.7	1009	6	ABL89555	ABl89555 Human pol
C 705	12	66.7	721	6	ABK75107	Abk75107 Bacillus	C 778	12	66.7	1018	5	ABAA15978	ABa15978 Human ner
C 706	12	66.7	725	3	AAZ97434	Aaz97434 Human pro	C 779	12	66.7	1019	10	AD160268	AD160268 Secreted
C 707	12	66.7	725	10	ADK11634	Adk11634 Breast ca	C 780	12	66.7	1024	5	ABBA83180	ABb83182 HOSR-3 (c
C 708	12	66.7	732	5	AA564405	Aa564405 DNA encod	C 781	12	66.7	1024	6	AB576392	AB576392 cDNA encod
C 709	12	66.7	736	3	AAZ97433	Aaz97433 Human pro	C 782	12	66.7	1024	10	ABX74465	ABx74465 Human cDN
C 710	12	66.7	736	10	ADK11633	Adk11633 Breast ca	C 783	12	66.7	1024	10	ABZ83502	ABz83502 ToxColoG
C 711	12	66.7	752	4	AAH04810	Aah04810 Human cDN	C 784	12	66.7	1024	10	ABZ83381	ABz83381 ToxColoG
C 712	12	66.7	770	10	ADC26809	Adc26809 Human l'ip	C 785	12	66.7	1024	11	ADMI0943	ADm10943 Human O64
C 713	12	66.7	780	3	AAZ57789	Aaz57789 Hepatitis	C 786	12	66.7	1024	11	ADMI0943	ADm10944 Human O64
C 714	12	66.7	786	4	AAAD05242	Aaad05242 Human sec	C 787	12	66.7	1024	12	ADJ11274	ADj11274 Human ova
C 715	12	66.7	786	6	AAAD35258	Aad35258 Human B7-	C 788	12	66.7	1024	12	ADJ11273	ADj11273 Human ova
C 716	12	66.7	786	10	ADA56468	Ada56468 Gene enco	C 789	12	66.7	1024	12	ADMA4534	ADm4534 Human ova
C 717	12	66.7	789	3	AAZ46029	Aaz46029 Partial c	C 790	12	66.7	1026	2	AAV73480	AAv73480 Human mve
C 718	12	66.7	793	4	AAH07485	Aah07485 Human cDN	C 791	12	66.7	1031	3	AACT7987	AAc77987 Human can
C 719	12	66.7	794	10	ADE08933	Ade08933 Novel DNA	C 792	12	66.7	1057	2	AAV84604	AAv84604 Human sec
C 720	12	66.7	799	5	AA571896	Aa571896 DNA encod	C 793	12	66.7	1057	4	ABBA83387	ABb83387 Human sec
C 721	12	66.7	803	2	AAO70437	Aao70437 Recombina	C 794	12	66.7	1057	9	ACH04688	ACH04688 Novel hum
C 722	12	66.7	803	2	AAO70438	Aao70438 Recombina	C 795	12	66.7	1057	4	ACD44698	ACd44698 Human cDN
C 723	12	66.7	803	2	AAO70439	Aao70439 Recombina	C 796	12	66.7	1057	5	AA583425	AA583425 DNA encod
C 724	12	66.7	803	2	AAQ70100	Aaq70100 Recombina	C 797	12	66.7	1057	12	ADQ29788	ADq29788 Human nov
C 725	12	66.7	806	4	AAI22065	Aai22065 Probe #11	C 798	12	66.7	1089	12	ADK71921	ADK71921 Human kin
C 726	12	66.7	806	4	ABA67141	AbA67141 Human fce	C 799	12	66.7	1092	6	ABL39804	ABl39804 Human NS
C 727	12	66.7	806	4	AAI47357	Aai47357 Probe #16	C 800	12	66.7	1104	12	ADK71921	ADK71921 Human kin
C 728	12	66.7	806	4	ABA49226	AbA49226 Human bre	C 801	12	66.7	1105	2	AACT09552	AAcT09552 H'ign-af'fl
C 729	12	66.7	806	4	ABA49226	AbA49226 Human bre	C 802	12	66.7	1105	10	ADCT7760	ADcT7760 Human 314
C 730	12	66.7	806	4	AAK14315	Aak14315 Human bon	C 803	12	66.7	1105	10	ACAS6883	ACa56883 Human sig
C 731	12	66.7	806	4	AAK15582	Aak15582 Human b'ta	C 804	12	66.7	1105	12	AD156679	AD156679 Human pol
C 732	12	66.7	806	5	ABS40915	AbS40915 Human l'iv	C 805	12	66.7	1120	12	ADQ84424	ADq84424 Human tum
C 733	12	66.7	806	5	AAI07759	Aai07759 Probe #77	C 806	12	66.7	1131	2	AAZ40843	AAz40843 Secreted
C 734	12	66.7	808	6	ABS15324	AbS15324 Human gen	C 807	12	66.7	1131	11	ADM77865	ADm77865 Human cDN
C 735	12	66.7	808	4	AAH07625	Aah07625 Human cDN	C 808	12	66.7	1131	11	ADP19141	ADp19141 Human sec
C 736	12	66.7	817	13	AD534705	Ad534705 siRNA-2 P	C 809	12	66.7	1132	5	AAH64784	AAh64784 Human sec
C 737	12	66.7	819	6	AAH50556	Aah50556 Human B7-	C 810	12	66.7	1147	13	ACN39111	ACn39111 Tumour-as
C 738	12	66.7	819	6	ABK88228	Abk88228 DNA encod	C 811	12	66.7	1147	4	AAAD09567	AAaD09567 Human t'ra
C 739	12	66.7	819	6	AAI70887	Aai70887 Human co-	C 812	12	66.7	1157	10	ADQ66640	ADQ66640 Hepatitis
C 740	12	66.7	819	12	ADQ76312	Adq76312 Human B7-	C 813	12	66.7	1171	12	ADQ26862	ADQ26862 cDNA enco
C 741	12	66.7	821	6	ABL51013	AbL51013 Human ED4	C 814	12	66.7	1176	6	ABL51020	ABL51020 Human ED4
C 742	12	66.7	821	8	AAAD8335	Aad8335 Human B7-	C 815	12	66.7	1176	9	ACD07906	ACd07906 DNA encod
C 743	12	66.7	822	8	AAAD8335	Aad8335 Human B7-	C 816	12	66.7	1183	12	ADL14952	ADl14952 Human gl'a
C 744	12	66.7	822	8	AAAD8335	Aad8335 Human B7-	C 817	12	66.7	1185	5	AA580276	AA580276 DNA encod
C 745	12	66.7	822	9	ADA63076	Ada63076 Human hCG	C 818	12	66.7	1192	11	AD131274	AD131274 Human cDN
C 746	12	66.7	822	9	ADA63076	Ada63076 Human hCG	C 819	12	66.7	1193	5	AD145984	AD145984 Human ova
C 747	12	66.7	822	10	ADL27814	AdL27814 Human hCG	C 820	12	66.7	1202	8	ABZ18474	ABz18474 Group I'I'I
C 748	12	66.7	822	11	ADL27154	AdL27154 Human cod	C 821	12	66.7	1207	4	AAH99734	AAh99734 Human pro
C 749	12	66.7	824	9	AAH34088	Aah34088 Human col	C 822	12	66.7	1209	6	AAAD36968	AAAD36968 Human B7-
C 750	12	66.7	828	9	ADBB2098	Adbb2098 Human cDN	C 823	12	66.7	1210	4	AA163821	AA163821 Human pol

824	12	66.7	1210	12	ADM24372	Adm24372 Human PRO	897	12	66.7	1614	8	AB224646	AB224646 Novel hum
825	12	66.7	1212	3	AAA75127	Aa75127 CDNA enco	898	12	66.7	1632	10	ADD26578	Ad26578 Human par
826	12	66.7	1223	6	AA27371	Aa27371 Human PD-	899	12	66.7	1635	5	AA18558	Aa18558 Human pol
827	12	66.7	1223	6	AA141871	Aa141871 Human PD-	900	12	66.7	1635	5	ADQ98775	Ad98775 DNA enco
828	12	66.7	1223	8	ABX13050	Abx13050 Human PD-	901	12	66.7	1635	9	AD848535	Ad848535 Novel hum
829	12	66.7	1223	8	ADA03075	Ada03075 Human hCG	902	12	66.7	1638	4	AA159268	Aa159268 Human pol
830	12	66.7	1223	9	ADA66359	Ada66359 Human hCG	903	12	66.7	1644	2	AA60775	Aa60775 Soybean c
831	12	66.7	1223	10	ADB72813	Ad72813 Human hCG	904	12	66.7	1644	10	ADD19238	Ad19238 Human CDN
832	12	66.7	1223	10	ABT14005	Abt14005 Human PD-	905	12	66.7	1650	5	AA591844	Aa591844 DNA enco
833	12	66.7	1223	11	ADL27153	Adl27153 Human CDN	906	12	66.7	1662	8	AB242687	Ab242687 Human mel
834	12	66.7	1237	3	AAFI6043	Aafi6043 Human pro	907	12	66.7	1665	6	ABK43363	Abk43363 DNA enco
835	12	66.7	1247	3	AAA64172	Aaa64172 DNA enco	908	12	66.7	1669	4	AAH17479	Aah17479 Human CDN
836	12	66.7	1248	6	AB211962	Ab211962 Human pol	909	12	66.7	1670	4	AA526675	Aa526675 Human gen
837	12	66.7	1248	12	ADM44480	Adm44480 Novel hum	910	12	66.7	1670	8	ABX74024	Abx74024 Human nov
838	12	66.7	1251	6	ABK63916	Abk63916 CDNA enco	911	12	66.7	1678	3	AAF15718	Aaf15718 Human pro
839	12	66.7	1270	6	AAV60668	Aav60668 Fragment	912	12	66.7	1707	3	AA55834	Aa55834 S. lavend
840	12	66.7	1272	11	ABD00501	Abd00501 Klebsiell	913	12	66.7	1711	10	AD810253	Ad810253 S. lavend
841	12	66.7	1285	3	AA59828	Aa59828 Human sec	914	12	66.7	1717	10	ADD48175	Ad48175 Human gen
842	12	66.7	1294	4	AA527163	Aa527163 CDNA enco	915	12	66.7	1714	6	ABL34972	Ab134972 Rat CDNA
843	12	66.7	1294	4	ABK43862	Abk43862 DNA enco	916	12	66.7	1733	12	ADH13735	Adh13735 Human ENZ
844	12	66.7	1294	10	ADB93341	Adb93341 Human CDN	917	12	66.7	1741	2	AAV73481	Aav73481 Human mye
845	12	66.7	1294	12	AD154249	Ad154249 CDNA enco	918	12	66.7	1747	5	ABV24646	Abv24646 Human pro
846	12	66.7	1295	5	ADL63657	Adl63657 Human ova	919	12	66.7	1752	4	AA513672	Aa513672 DNA enco
847	12	66.7	1297	10	ADE28248	Ade28248 Human MDP	920	12	66.7	1752	6	ABO78589	Ab78589 Nucleotid
848	12	66.7	1314	3	AA598802	Aa598802 Human pan	921	12	66.7	1752	6	AA138753	Aa138753 Rat lambd
849	12	66.7	1314	6	ABO54135	Ab54135 Human ova	922	12	66.7	1752	10	ADP76244	Adp76244 Rat Pec-1
850	12	66.7	1323	11	ACN89216	Acn89216 Breast ca	923	12	66.7	1765	2	AAQ79141	Aaq79141 Hepatitis
851	12	66.7	1326	2	AAV73478	Aav73478 Human mye	924	12	66.7	1765	2	AAQ79143	Aaq79143 Hepatitis
852	12	66.7	1340	2	AA242034	Aa242034 Human end	925	12	66.7	1773	4	ABA54566	Ab54566 Therrus c
853	12	66.7	1344	3	AAA80619	Aaa80619 Human sec	926	12	66.7	1777	6	ABK99666	Abk99666 DNA enco
854	12	66.7	1344	10	ADA27043	Ada27043 Human nov	927	12	66.7	1798	12	ADM45315	Adm45315 Human enz
855	12	66.7	1344	12	ADD19201	Add19201 Human CDN	928	12	66.7	1801	12	ADM87048	Adm87048 Human pro
856	12	66.7	1344	12	ADB6573	Adb6573 Novel hum	929	12	66.7	1814	6	AAD36972	Aad36972 Human B7-
857	12	66.7	1356	6	ABK24018	Abk24018 DNA enco	930	12	66.7	1816	5	AA584220	Aa584220 DNA enco
858	12	66.7	1372	4	AAF59618	Aaf59618 Human cel	931	12	66.7	1819	4	AAH14818	Aah14818 Human CDN
859	12	66.7	1407	4	AA104515	Aa104515 Human rep	932	12	66.7	1824	13	ADR24373	Adr24373 Breast ca
860	12	66.7	1410	13	AD558688	Ad558688 Bacterial	933	12	66.7	1824	12	ADN98871	Adn98871 Novel hum
861	12	66.7	1427	2	AAV20959	Aav20959 Human rec	934	12	66.7	1824	12	ADO00440	Ado00440 Novel hum
862	12	66.7	1467	6	ABV78216	Abv78216 Human MMP	935	12	66.7	1837	4	AA160238	Aa160238 Human pol
863	12	66.7	1467	6	AB235792	Ab235792 Human MMP	936	12	66.7	1842	2	AA277570	Aa277570 Human ova
864	12	66.7	1467	6	ABX10035	Abx10035 Human MMP	937	12	66.7	1851	3	AA256729	Aa256729 Human tra
865	12	66.7	1467	6	AB191757	Ab191757 Human pol	938	12	66.7	1851	13	AA510426	Aa510426 Human the
866	12	66.7	1477	6	ABL61107	Ab161107 Deoxycti	939	12	66.7	1854	12	ADQ87127	Adq87127 Human tum
867	12	66.7	1493	5	AA576103	Aa576103 DNA enco	940	12	66.7	1856	8	ACC69466	Acc69466 Human mal
868	12	66.7	1494	3	AAAC4617	Aaac4617 Arabidops	941	12	66.7	1861	13	AD510078	Ad510078 Human the
869	12	66.7	1500	2	AAV20961	Aav20961 Human TFE	942	12	66.7	1863	2	AAQ15363	Aaq15363 Fragment
870	12	66.7	1511	9	AA161122	Aa161122 Human CID	943	12	66.7	1863	2	AAQ15362	Aaq15362 Fragment
871	12	66.7	1511	12	ADM98087	Adm98087 Human CID	944	12	66.7	1864	12	ADQ24314	Adq24314 Human sof
872	12	66.7	1536	3	AAA37847	Aaa37847 Human obe	945	12	66.7	1875	10	ADT60591	Adt60591 Secreted
873	12	66.7	1547	4	AAK91014	Aak91014 Human dig	946	12	66.7	1880	2	AAQ24466	Aaq24466 NAMB hepa
874	12	66.7	1547	5	AA532049	Aa532049 Human liv	947	12	66.7	1884	2	AAQ24467	Aaq24467 NAMB hepa
875	12	66.7	1547	6	ABN90404	Abn90404 Human liv	948	12	66.7	1890	4	ABL13343	Ab113343 Drosophi
876	12	66.7	1549	11	ADJ15317	Adj15317 Human liv	949	12	66.7	1899	3	AA599049	Aa599049 Human pan
877	12	66.7	1549	6	ABO70339	Ab70339 Listeria	950	12	66.7	1897	4	AAH34645	Aah34645 Human col
878	12	66.7	1551	6	ABO91947	Ab91947 Human NF-	951	12	66.7	1897	4	ABL03791	Ab103791 Drosophi
879	12	66.7	1551	8	AB24644	Ab24644 Novel hum	952	12	66.7	1901	12	ADQ19836	Adq19836 Human sof
880	12	66.7	1551	8	ACC42290	Acc42290 Human MAP	953	12	66.7	1908	13	ADT42221	Adt42221 Bacterial
881	12	66.7	1554	2	AAV63451	Aav63451 HCV core-	954	12	66.7	1913	8	ACC69467	Acc69467 Human mal
882	12	66.7	1562	2	AAV60672	Aav60672 Fragment	955	12	66.7	1915	8	AB224647	Ab224647 Novel hum
883	12	66.7	1566	11	ADN38899	Adn38899 Cancer/an	956	12	66.7	1917	3	AAA37848	Aaa37848 Human obe
884	12	66.7	1574	6	ABL51009	Ab151009 Human EDA	957	12	66.7	1918	4	AAH74769	Aah74769 Nucleotid
885	12	66.7	1574	9	ACD07895	Ac07895 CDNA enco	958	12	66.7	1918	8	ABT17361	Abt17361 Human SLC
886	12	66.7	1577	10	ADD48173	Ad48173 Rat gene	959	12	66.7	1925	8	AA54485	Aa54485 Human CIP
887	12	66.7	1578	5	AA580253	Aa580253 DNA enco	960	12	66.7	1927	13	ADR21620	Adr21620 Human enz
888	12	66.7	1587	4	AA161054	Aa161054 Human pol	961	12	66.7	1962	8	ABT17363	Abt17363 Human SLC
889	12	66.7	1595	13	AD511418	Ad511418 Human the	962	12	66.7	1967	11	ACN88620	Acn88620 Breast ca
890	12	66.7	1595	8	ABT17362	Abt17362 Human SLC	963	12	66.7	1969	4	AA114105	Aa114105 Probe #40
891	12	66.7	1599	5	AA578921	Aa578921 DNA enco	964	12	66.7	1969	4	ABA55830	Ab55830 Human f0e
892	12	66.7	1599	8	AB224645	Ab224645 Novel hum	965	12	66.7	1969	4	AA135486	Aa135486 Probe #41
893	12	66.7	1601	12	ADL15479	Adl15479 Human nep	966	12	66.7	1969	4	ABA45341	Ab45341 Human bre
894	12	66.7	1602	10	AD807108	Ad807108 Novel cod	967	12	66.7	1969	4	ABA25506	Ab25506 Probe #39
895	12	66.7	1608	2	AAQ71977	Aaq71977 Murine IL	968	12	66.7	1969	4	AAK29533	Aak29533 Human bon
896	12	66.7	1610	10	AD160463	Ad160463 Secreted	969	12	66.7	1969	4	AAK04048	Aak04048 Human bra

```
C 970 12 66.7 1969 4 ABS29157
C 971 12 66.7 1969 5 AAI03958
C 972 12 66.7 1969 6 ABS04084
C 973 12 66.7 1970 4 AAF32686
C 974 12 66.7 1974 5 AAS80252
C 975 12 66.7 1983 13 ADH85425
C 976 12 66.7 1985 10 ADH26576
C 977 12 66.7 1989 12 ADH13748
C 978 12 66.7 1992 4 AAL46384
C 979 12 66.7 1998 10 ADE07178
C 980 12 66.7 1998 10 ADE07178
C 981 12 66.7 2004 6 ABO86145
C 982 12 66.7 2002 3 AAF21635
C 983 12 66.7 2025 13 ADQ85640
C 984 12 66.7 2025 13 ADQ86738
C 985 12 66.7 2033 2 AAQ64913
C 986 12 66.7 2033 2 AAQ86788
C 987 12 66.7 2043 5 ABV30333
C 988 12 66.7 2050 12 ADQ87055
C 989 12 66.7 2052 6 ABK43375
C 990 12 66.7 2058 8 AAD53168
C 991 12 66.7 2061 6 ABQ86144
C 992 12 66.7 2076 5 AAS74039
C 993 12 66.7 2076 5 AAS74039
C 994 12 66.7 2094 6 ABS51497
C 995 12 66.7 2098 10 ADH31325
C 996 12 66.7 2106 2 AAQ43905
C 997 12 66.7 2106 2 AAQ86773
C 998 12 66.7 2106 2 AAT18792
C 999 12 66.7 2110 10 ADB63624
C1000 12 66.7 2116 2 AAQ12242
```

## ALIGNMENTS

```
RESULT 1
ID AAT80248 standard; DNA; 18 BP.
AC AAT80248;
XX
DT 15-OCT-1997 (first entry)
XX
DE Oligo HCV94 used in luciferase assay.
XX
KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW inhibition; replication; expression; detection; chronic hepatitis;
KW acute hepatitis; hepatocarcinoma; ss.
XX
OS Synthetic.
XX
PN WO9639500-A2.
XX
PD 12-DEC-1996.
XX
PF 04-JUN-1996; 96WO-EP002427.
XX
PR 06-JUN-1995; 95US-00471968.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PA (HYBR-) HYBRIDON INC.
XX
PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PI Roberts PC, Walther DM, Wolfe JL;
XX
DR WPI; 1997-043122/04.
XX
PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT carcinoma.
XX
PS Claim 19; Page 31; 100pp; English.
```

```
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC which are complementary to a portion of the 5' untranslated region (UTR)
CC of hepatitis C virus (HCV). These sequences may be used in a
CC pharmaceutical composition for the control or prevention of HCV
CC infection. They may be used to inhibit replication or expression of HCV
CC or for detecting the presence of HCV in a sample. They may be used to
CC inhibit HCV replication in a cell and are therefore useful in the
CC treatment of HCV infections such as chronic and acute hepatitis and
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine
CC whether it binds successfully to its target
XX
SQ Sequence 18 BP; 1 A; 2 C; 7 G; 0 T; 2 U; 6 Other;
Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCUCGAGNNNNNN 18
DB 1 GGGGUCUCGAGNNNNNN 18
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```
RESULT 2
ID ABS65832 standard; DNA; 18 BP.
AC ABS65832;
XX
DT 15-NOV-2002 (first entry)
XX
DE Inhibitory oligonucleotide specific for hepatitis C virus #38.
```

```
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
KW non-B hepatitis; acute hepatitis; chronic hepatitis;
KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;
KW gene therapy; ss; DNA-RNA hybrid.
```

OS Synthetic.

PN US2002081577-A1.

PD 27-JUN-2002.

PF 02-JUL-1997; 97US-00887505.

PR 06-JUN-1995; 95US-00471968.

PR 02-JUL-1996; 96US-0021104P.

PA (KILK/) KILKUSKIE R L.

PA (FRAN/) FRANK B L.

PA (GOOD/) GOODCHILD J.

PA (WOLF/) WOLFE J L.

PA (ROBE/) ROBERTS P C.

PA (HAML/) HAMLIN H A.

PA (ROBE/) ROBERTS N A.

PA (WALT/) WALTHER D M.

XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;

PI Hamlin HA, Roberts NA, Walther DM;

XX

DR WPI; 2002-537132/57.

XX Synthetic oligonucleotides complementary to a portion of the 5'

PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and

PT treating HCV infections and hepatocellular carcinoma.

XX

PS Claim 22; Page 10; 74pp; English.

CC The invention describes synthetic oligonucleotides complementary to a

CC portion of the 5' untranslated region of hepatitis C virus. The

CC oligonucleotides may be used in methods for controlling, preventing, and

CC treating hepatitis C virus infection, in antisense technology and gene

CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
 CC HCV replication and expression of HCV  
 CC  
 SQ Sequence 18 BP; 1 A; 2 C; 7 G; 0 T; 2 U; 6 Other;  
 Query Match 100.0%; Score 18; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTCGAGNNNNNN 18  
 1 GGGGUCCTCGAGNNNNNN 18  
 Db 1 GGGGUCCTCGAGNNNNNN 18  
 RESULT 3  
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 ID AAT80277 standard; DNA; 24 BP.  
 XX  
 AC AAT80277;  
 XX  
 DT 15-OCT-1997 (first entry)  
 XX  
 DE Oligo HCVJ34, used in luciferase assay.  
 XX  
 DE Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KW inhibition; replication; expression; detection; chronic hepatitis;  
 KW acute hepatitis; hepatocarcinoma; ss.  
 XX  
 OS Synthetic.  
 XX  
 FT Key Location/Qualifiers  
 FT modified\_base 1..24  
 FT /\*tag= a  
 FT /note= "Phosphorothioate linkages"  
 XX  
 PN W09639500-A2.  
 XX  
 XX 12-DEC-1996.  
 PD  
 XX  
 PF 04-JUN-1996; 96WO-EP002427.  
 PF  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR  
 XX  
 PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PA (HYBR-) HYBRIDON INC.  
 XX  
 PI Frank BL, Goodchild J, Hamlin HA, Kilbuckie RE, Roberts NA;  
 PI Roberts PC, Walther DM, Wolfe JL;  
 XX  
 DR WPI; 1997-043122/04.  
 XX  
 PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
 PT the treatment and detection of HCV infection, esp. hepatitis and hepa-  
 PT to carcinoma.  
 PT  
 PS Claim 19; Page 33; 100pp; English.  
 PS  
 CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
 CC which are complementary to a portion of the 5' untranslated region (UTR)  
 CC of hepatitis C virus (HCV). These sequences may be used in a  
 CC pharmaceutical composition for the control or prevention of HCV  
 CC infection. They may be used to inhibit replication or expression of HCV  
 CC or for detecting the presence of HCV in a sample. They may be used to  
 CC inhibit HCV replication in a cell and are therefore useful in the  
 CC treatment of HCV infections such as chronic and acute hepatitis and  
 CC hepatocarcinoma. This oligo was used in a luciferase assay to determine

CC whether it binds successfully to its target  
 XX  
 SQ Sequence 24 BP; 1 A; 2 C; 7 G; 0 T; 2 U; 12 Other;  
 Query Match 100.0%; Score 18; DB 2; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTCGAGNNNNNN 18  
 1 GGGGUCCTCGAGNNNNNN 18  
 Db 1 GGGGUCCTCGAGNNNNNN 18  
 RESULT 4  
 ABS65861  
 ID ABS65861 standard; DNA; 24 BP.  
 XX  
 AC ABS65861;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #67.  
 DE  
 DE Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
 KW non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KW gene therapy; ss; DNA-RNA hybrid.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002081577-A1.  
 PN  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 02-JUL-1997; 97US-00887505.  
 PF  
 XX  
 PR 06-JUN-1995; 95US-00471968.  
 PR 02-JUL-1996; 96US-0021104P.  
 PR  
 XX  
 PA (KILK/) KILBUCKIE R L.  
 PA (FRAN/) FRANK B L.  
 PA (GOOD/) GOODCHILD J.  
 PA (WOLF/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.  
 PA (HAML/) HAMLIN H A.  
 PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.  
 XX  
 PI Kilbuckie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
 PI Hamlin HA, Roberts NA, Walther DM;  
 XX  
 DR WPI; 2002-537132/57.  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.  
 PT  
 PS Claim 22; Page 11; 74pp; English.  
 PS  
 CC The invention describes synthetic oligonucleotides complementary to a  
 CC portion of the 5' untranslated region of hepatitis C virus. The  
 CC oligonucleotides may be used in methods for controlling, preventing, and  
 CC treating hepatitis C virus infection, in antisense technology and gene  
 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
 CC HCV replication and expression of HCV  
 CC

SO Sequence 24 BP; 1 A; 2 C; 7 G; 0 T; 2 U; 12 Other;

Query Match 100.0%; Score 18; DB 6; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGCGAGNNNNN 18  
 1 GGGGUCGCGAGNNNNN 18  
 DB 1 GGGGUCGCGAGNNNNN 18

RESULT 5  
 AAD43827  
 ID AAD43827 standard; DNA; 29 BP.  
 AC AAD43827;  
 DT 14-NOV-2002 (first entry)  
 DE Adapter oligo #5 used to illustrate the method of the invention.  
 KW Single stranded polynucleotide tag; cleavage agent; gene expression; ds.  
 XX Unidentified.  
 OS  
 FH Key Location/Qualifiers  
 FT misc\_feature 9..10  
 FT /\*tag= a  
 FT /note= "Nicking site"  
 FT misc\_feature 27..28  
 FT /\*tag= b  
 FT /note= "Nicking site"  
 XX  
 PN WO200259357-A2.  
 PD 01-AUG-2002.  
 PF 24-JAN-2002; 2002MO-DK000052.  
 PR 24-JAN-2001; 2001DK-00000126.  
 PR 12-FEB-2001; 2001US-0267704P.  
 PA (GENO-) GENOMIC EXPRESSION APS.  
 PI Pedersen ML;  
 XX  
 DR WPI; 2002-636542/68.  
 PT Obtaining single stranded polynucleotide tags from a biological sample,  
 PT for analyzing gene expression or diagnosing clinical conditions,  
 PT comprises employing nicking endonucleases that cleave complementary  
 PT strands.  
 XX  
 PS Disclosure; Page 284; 303pp; English.  
 XX  
 CC The invention relates to a method for obtaining a single stranded  
 CC polynucleotide tag from a double stranded sample by cleaving one of the  
 CC complementary strands of a double stranded polynucleotide with a cleavage  
 CC agent capable of recognizing a double stranded polynucleotide comprising  
 CC complementary strands and cleaving only one of the strands of the  
 CC polynucleotide in the process of generating a single stranded  
 CC polynucleotide tag. The method is useful for separating, analyzing,  
 CC quantifying or obtaining single stranded polynucleotides comprising tags  
 CC originating partly, and preferably wholly from a source of DNA and/or RNA  
 CC in a sample comprising biological cells. The method is particularly for  
 CC analyzing gene expression (expression profiling or differential gene  
 CC expression), or in diagnosing clinical conditions. The present sequence  
 CC is an adapter oligonucleotide used to illustrate the method of the  
 CC invention  
 CC  
 SO Sequence 29 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 18 Other;

Query Match 83.3%; Score 15; DB 6; Length 29;

Best Local Similarity 86.7%; Pred. No. 79;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 GUCCUGAGNNNNN 18  
 4 GUCCUGAGNNNNN 18  
 DB 3 GTCCTGAGNNNNN 17

RESULT 6  
 ABR50461  
 ID ABR50461 standard; DNA; 2400 BP.  
 AC ABR50461;  
 DT 13-AUG-2002 (first entry)  
 DE Human caspase 5, apoptosis-related cysteine protease modified DNA.  
 DE  
 KW Human; Caspase 5; apoptosis-related cysteine protease; CASP5; gene; ds;  
 KW haplotyping; haplotype pair; cancer; single nucleotide polymorphism;  
 KW hereditary nonpolyposis colorectal cancer; gastrointestinal tumour;  
 KW endometrial tumour; chromosome 11q22.2-q22.3.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200226769-A2.  
 PD 04-APR-2002.  
 PF 01-OCT-2001; 2001MO-US030878.  
 PR 29-SEP-2000; 2000US-0235668P.  
 PA (GENA-) GENAISSANCE PHARM INC.  
 PI Choi JY, Klien SE, Russo DP;  
 XX  
 DR WPI; 2002-435191/46.  
 PT Novel caspase 5 apoptosis-related cysteine protease, useful  
 PT therapeutically and in screening for drugs targeting protease  
 PT polypeptide.  
 XX  
 PS Example 2; Page 114-115; 115pp; English.  
 XX  
 CC The invention relates to single nucleotide polymorphisms in the gene  
 CC encoding the human caspase 5, apoptosis-related cysteine protease (CASP5)  
 CC polypeptide. A method for haplotyping the CASP5 gene in an individual  
 CC comprises identifying the nucleotide at one or more polymorphic sites and  
 CC determining whether one of the copies of the gene is defined by one of  
 CC the CASP5 haplotypes given in the specification or whether both copies  
 CC are defined by a haplotype pair. This method is useful in genotyping,  
 CC whereby all possible haplotype pairs can be assigned to specific  
 CC genotypes. An association between a trait and a haplotype or haplotype  
 CC pair of the CASP5 gene can be identified by comparing the frequency of  
 CC the haplotype or haplotype pair in a population exhibiting the trait with  
 CC the frequency of the haplotype or haplotype pair in a reference  
 CC population, where a higher haplotype frequency in the trait population  
 CC indicates the trait is associated with the haplotype or haplotype pair.  
 CC CASP5 and its corresponding DNA are used for studying the expression and  
 CC function of CASP5, for use in screening for candidate drugs to treat  
 CC diseases related to CASP5 activity, such as cancer (e.g. hereditary  
 CC nonpolyposis colorectal cancer, gastrointestinal tumours and endometrial  
 CC tumours). This sequence represents genomic DNA modified to facilitate  
 CC electronic searching of the CASP5 haplotypes  
 CC  
 SO Sequence 2400 BP; 366 A; 209 C; 272 G; 333 T; 0 U; 1220 Other;

Query Match 83.3%; Score 15; DB 6; Length 2400;  
 Best Local Similarity 86.7%; Pred. No. 57;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 GUCCUGAGNNNNN 18



Db 1732 GTCCCTGGAGNNNNNN 1746

## RESULT 7

ADQ55353/c  
ID ADQ55353 standard; DNA; 503 BP.

AC ADQ55353 ;

DT 21-OCT-2004 (first entry)

Novel canine microarray-related DNA sequence SeqID6655.

KM carcinomascroarray: drug screening; toxicity assay;  
KM environmental pollutant; cellular response; gene expression profile  
KM toxic response; liver necrosis; fatty liver disease;  
KM protein adduct formation; hepatitis; dog; ds.

OS *Canis familiaris*.

PN WO2004063324-A2.

PD 29-JUL-2004

PF 05-MAY-2003; 2003WO-US013853.

PR 03-MAY-2002; 2002US-0377240P.

PA	(GENE-)	GENE LOGIC INC.
PA	(PFIZ )	PFIZER PROD INC.

PI Diggans JC, Porter M, Wei T;

DR WPI; 2004-561890/54.

PT New isolated nucleic acid molecule, useful for drug screening and toxicity assays or for assessing the impact, including toxicity, of a compound, pharmaceutical agent or environmental pollutant on a cell or living organism.

PS Claim 1; SEQ ID NO 6655; 41pp; English

This invention is related to a novel isolated canine nucleic acid sequences and the construction of canine microarrays containing a significant portion of the canine genome. The isolated canine nucleic acid sequences of the invention may be useful for drug screening and toxicity assays. The invention is therefore useful for assessing the impact, including toxicity, of a compound, pharmaceutical agent or environmental pollutant on a cell or living organism. The methods are useful for detecting genes that are up- or down-regulated in canines in a disease state. The sequences are useful as diagnostic agents or markers to detect a cellular response in a sample individually or as part of a gene expression profile. It is also useful as a target for agents that modulate gene expression or activity. The database is useful for producing electronic Northern blots that allow the user to determine the cell type or tissue in which a given gene is expressed and to allow determination of the abundance or expression level of a given gene in a particular tissue or cell. The methods are useful for determining the similarity of a toxic response to one or more individual compounds. The methods are useful for predicting at least one toxic response or the likelihood that a compound or test agent will induce various specific pathologies such as those of the liver (liver necrosis, fatty liver disease, protein adduct formation or hepatitis), those of the kidney, heart, brain or testes, or other pathologies associated with at least one of the toxins. The methods are also useful for predicting or elucidating the potential cellular pathways influenced, induced or modulated by the compound or test agent due to the similarity of the expression profile compared to the profile induced by a known toxin. The present sequence is that of a canine DNA sequence which was claimed for use during the production of a canine microarray of the invention.

50 Sequence 503 BP; 86 A; 142 C; 86 G; 125 T; 0 U; 64 Other;

Query Match	77.8%;	Score 14;	DB 13;	Length 503;
Best Local Similarity	85.7%;	Pred. NO. 2.2e+02;		
Matches 12;	Conservative 2;	Mismatches 0;	Indels 0;	Gaps 0;

QY	4	GUCCTGGAGNNNNN	17
		: : : : : :	
Db	126	GTCCTGGAGNNNNN	113

## RESULT 8

ID	Accession	Source	Length (bp)
1	AAS76001	standard; cDNA	418

AC AAS76001;

DT 13-FEB-2002 (first entry)

**DE** DNA encoding novel human diagnostic protein #11805.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

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PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73

**XXIX**

PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

PS Claim 1; SEQ ID NO 11805; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. MS64197-MS64564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPAC at [http://wipac.int/pub/publibded\\_pct\\_sequences](http://wipac.int/pub/publibded_pct_sequences)

SQ Sequence 418 BP; 45 A; 71 C; 91 G; 51 T; 0 U; 160 Other;

Query Match      72.2%;    Score 13;    DB 5;    Length 418;

Best Local Similarity 92.3%; Pred. No. 7.9e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
||:|||||||  
Db 140 CCTGGAGNNNNNN 152

## RESULT 9

AA197596/c  
ID AA197596 standard; cDNA; 784 BP.

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XX AA197596;

DT 13-NOV-2001 (first entry)

XX Human neuroblastoma expressed polynucleotide SEQ ID NO 3671.

XX Human neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.

XX Homo sapiens.

XX WO200166719-A1.

XX 13-SEP-2001.

XX 02-MAR-2001; 2001WO-JP001629.

XX 07-MAR-2000; 2000JP-00159195.

XX (CHIB-) CHIBA PREFECTURE.

XX (HISM) HISAMITSU PHARM CO LTD.

XX Nakagawara A;

XX WPI; 2001-56584/63.

XX Nucleic acids originating in gene expressed in human neuroblastoma,  
PT useful as probe or primer in diagnosing prognosis of human neuroblastoma,  
PT malignancy and susceptibility indicator or tumor marker for anti-cancer  
PT agents.

XX Claim 1; Page 2664; 2979pp; Japanese.

XX The invention relates to novel genes (AA193926-AA197963) expressed in  
CC human neuroblastoma. The nucleic acids are applicable as a probe or  
CC primer in diagnosing the prognosis of human neuroblastoma, malignancy and  
CC susceptibility indicators or tumour markers for anti-cancer agents. The  
CC gene information for diagnosing prognosis is related to factors similar  
CC to that for N-myc and TrkA genes

XX Sequence 784 BP; 189 A; 223 C; 193 G; 153 T; 0 U; 26 Other;

XX Query Match 72.2%; Score 13; DB 4; Length 784;

XX Best Local Similarity 84.6%; Pred. No. 7.5e+02;

XX Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAGN 13  
|||:|||||

Db 570 GGGGTCCTGGAGN 558

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KW ds.

XX Homo sapiens.

XX WO2004048938-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US038193.

XX 26-NOV-2002; 2002US-0429739P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Aziz N, Ginsburg WM, Zlotnik A;

XX WPI; 2004-441208/41.

XX Early detection of soft tissue sarcoma comprises determining expression  
PT of a gene in a first soft tissue sample and a normal soft tissue sample  
PT and comparing the gene expression, also useful in treating soft tissue  
PT sarcoma.

XX Example 2; SEQ ID NO 5790; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma  
CC which comprises obtaining a first soft tissue sample from an individual  
CC and a normal soft tissue sample from the same or different individual,  
CC determining the expression of a gene in both samples and comparing the  
CC expression of the gene in both soft tissue samples, where a higher level  
CC of protein expression in the first soft tissue sample indicates the  
CC presence of soft tissue sarcoma. The method of the invention has  
CC cytostatic applications and may be useful for detecting soft tissue  
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
CC acid sequences may be useful in diagnostic and screening applications.  
CC The current sequence is that of a human soft tissue sarcoma-upregulated  
CC DNA of the invention. The current sequence is not shown within the  
CC specification per se but was submitted in CD format by the inventor.

XX Sequence 3286 BP; 648 A; 1104 C; 881 G; 629 T; 0 U; 24 Other;

XX Query Match 72.2%; Score 13; DB 12; Length 3286;

XX Best Local Similarity 92.3%; Pred. No. 6.8e+02;

XX Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
||:|||||||

Db 278 CCTGGAGNNNNNN 266

XX

XX

XX

XX

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XX

PA (PROT-) PROTEIN DESIGN LABS INC.  
 XX  
 PI Aziz N, Ginsburg WM, Zlotnick A;  
 XX WPI; 2004-441208/41.  
 DR  
 XX Early detection of soft tissue sarcoma comprises determining expression  
 PT of a gene in a first soft tissue sample and a normal soft tissue sample  
 PT and comparing the gene expression, also useful in treating soft tissue  
 PT sarcoma.  
 XX  
 XX Example 2; SEQ ID NO 5700; 210bp; English.  
 XX The invention relates to a novel method for detecting soft tissue sarcoma  
 CC which comprises obtaining a first soft tissue sample from an individual  
 CC and a normal soft tissue sample from the same or different individual,  
 CC determining the expression of a gene in both samples and comparing the  
 CC expression of the gene in both soft tissue samples, where a higher level  
 CC of protein expression in the first soft tissue sample indicates the  
 CC presence of soft tissue sarcoma. The method of the invention has  
 CC cytostatic applications and may be useful for detecting soft tissue  
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic  
 CC acid sequences may be useful in diagnostic and screening applications.  
 CC The current sequence is that of a human soft tissue sarcoma-upregulated  
 CC DNA of the invention. The current sequence is not shown within the  
 CC specification per se but was submitted in CD format by the inventor.  
 XX  
 XX Sequence 5132 BP; 1201 A; 1394 C; 1336 G; 1169 T; 0 U; 32 Other;  
 SQ  
 Query Match 72.2%; Score 13; DB 12; Length 5132;  
 Best Local Similarity 92.3%; Pred. No. 6.5e+02;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 6 CCUGGAGNNNNNN 18  
 Db 1012 CCTGGAGNNNNNN 1000  
 RESULT 12  
 ADA02927/c  
 ID ADA02927 standard; DNA; 92726 BP.  
 XX  
 AC ADA02927;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX  
 DE Mouse Plk3r1 carcinoma associated gene, SEQ ID NO:1445.  
 XX  
 KM Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;  
 KM prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;  
 KM gene; ds.  
 XX  
 OS Mus sp.  
 OS  
 XX WO2003057146-A2.  
 PN  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-US041414.  
 XX  
 PR 26-DEC-2001; 2001US-00035832.  
 XX  
 PA (SAGR-) SAGRES DISCOVERY.  
 XX  
 PI Morris DW;  
 PI  
 DR WPI; 2003-587068/55.  
 XX  
 PT New recombinant nucleic acid encoding carcinoma associated protein,  
 PT useful for preparing compositions for treating carcinomas.  
 XX  
 XX Claim 1; SEQ ID NO 1445; 245bp; English.  
 XX

CC The invention relates to recombinant carcinoma associated (CA) nucleic  
 CC acid sequences from mouse and human (ADA01482-ADA03094), and to  
 CC recombinant carcinoma associated proteins (CAP) encoded by them. The  
 CC invention also encompasses expression vectors and host cells comprising a  
 CC CA nucleic acid, a polypeptide (especially an antibody) that specifically  
 CC binds to the protein, and a biochip comprising CA nucleic acid or  
 CC fragments thereof. The sequences of the invention were identified using  
 CC oncogenic retroviruses, which insert into the genome of the host organism  
 CC at random. Many of these do not carry transduced host oncogenes or  
 CC pathogenic trans-acting viral genes, meaning that cancer incidence is a  
 CC direct consequence of the effects of proviral integration into host  
 CC protooncogenes. The CA nucleic acid sequences can be used to diagnose  
 CC carcinoma (especially breast cancer, prostate cancer, lymphoma or  
 CC leukaemia) or a propensity to carcinoma by determination of the sequence  
 CC of a CA gene, or by determination of CA gene expression in particular  
 CC tissues. CA nucleic acids, proteins and antibodies are also useful as  
 CC therapeutic agents and in screening and evaluating drug candidates. The  
 CC present sequence represents a specifically claimed murine CA nucleic acid  
 CC sequence of the invention. Note: The complete sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 92726 BP; 23819 A; 19174 C; 20109 G; 27030 T; 0 U; 2594 Other;  
 SQ  
 Query Match 72.2%; Score 13; DB 9; Length 92726;  
 Best Local Similarity 92.3%; Pred. No. 5.3e+02;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 6 CCUGGAGNNNNNN 18  
 Db 155 CCTGGAGNNNNNN 143  
 RESULT 13  
 ADB72665/c  
 ID ADB72665 standard; DNA; 92726 BP.  
 XX  
 AC ADB72665;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Mouse Plk3r1 gene.  
 XX  
 KM mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;  
 KM cancer; neoplasm; adenocarcinoma; sarcoma; gene.  
 XX  
 OS Mus sp.  
 OS  
 XX WO2003008583-A2.  
 PN  
 PD 30-JAN-2003.  
 XX  
 PF 26-DEC-2001; 2001WO-US051291.  
 XX  
 PR 02-MAR-2001; 2001US-00798586.  
 XX  
 PR 23-OCT-2001; 2001US-00004113.  
 XX  
 PR 08-NOV-2001; 2001US-00052482.  
 XX  
 PR 30-NOV-2001; 2001US-00997722.  
 XX  
 PR 20-DEC-2001; 2001US-00034650.  
 XX  
 PA (SAGR-) SAGRES DISCOVERY.  
 XX  
 PI Morris DW, Engelhard EK;  
 PI  
 DR WPI; 2003-239337/23.  
 XX  
 PT New recombinant nucleic acid, useful for treating carcinomas, lymphomas,  
 PT cancers, neoplasm, adenocarcinoma, or sarcomas.  
 XX  
 XX Claim 1; SEQ ID NO 493; 2304bp; English.  
 XX  
 CC The invention relates to a novel recombinant nucleic acid comprising a

CC nucleotide sequence selected from any of the 660 sequences fully defined  
CC in the specification. A polynucleotide of the invention has cytosstatic  
CC activity, and may have a use in gene therapy, or in a vaccine. The  
CC recombinant nucleic acids and polypeptides are useful for treating  
CC carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and  
CC sarcomas. The present sequence represents a mouse gene of the invention.  
XX

Sequence 92726 BP; 23819 A; 19174 C; 20109 G; 27030 T; 0 U; 2594 Other;

Query Match 72.2%; Score 13; DB 10; Length 92726;  
Best Local Similarity 92.3%; Pred. No. 5.3e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 6 CCUGAGAGNNNNNN 18  
||:|||||  
Db 155 CCTGAGAGNNNNNN 143

RESULT 14  
ADC85407/c  
ID ADC85407 standard; DNA; 92726 BP.

AC ADC85407;

DT 01-JAN-2004 (first entry)

DE Mouse Pk3r1 genomic sequence.

KM Cytostatic; gene therapy; vaccine; cancer; carcinoma-associated gene; CA;  
secreted; transmembrane; intracellular; ds.

OS Mus SP.

PN MO2003045230-A2.

PD 05-JUN-2003.

PF 02-DEC-2002; 2002MO-US038582.

PR 30-NOV-2001; 2001US-00997722.

XX (SAGR-) SAGRES DISCOVERY.

PI Morris DW, Engelhard EK;

XX WPI; 2003-513603/48.

PT New recombinant nucleic acid comprising a nucleotide sequence of any of  
the carcinoma-associated (CA) genes, useful for screening for drug  
PT candidates for diagnosing or treating carcinomas.

PS Claim 1; SEQ ID NO 193; 983pp; English.

CC The invention relates to a recombinant nucleic acid comprising a  
CC nucleotide sequence selected from any of the fully defined carcinoma-  
CC associated (CA) genes from the 50 tables given in the specification. The  
CC CA proteins are secreted, transmembrane or intracellular proteins. The  
CC recombinant nucleic acids are useful for screening for drug candidates  
CC for diagnosing or treating carcinomas. Sequences given in ADC85215-  
CC ADC85514 represent CA genes of the invention.  
XX

Sequence 92726 BP; 23819 A; 19173 C; 20110 G; 27030 T; 0 U; 2594 Other;

Query Match 72.2%; Score 13; DB 10; Length 92726;  
Best Local Similarity 92.3%; Pred. No. 5.3e+02;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 6 CCUGAGAGNNNNNN 18  
||:|||||  
Db 155 CCTGAGAGNNNNNN 143

RESULT 15

ADM74522/c  
ID ADM74522 standard; DNA; 92726 BP.

AC ADM74522;

DT 01-JUL-2004 (first entry)

DE Murine carcinoma associated (CA) nucleic acid #97.

KM Mouse; carcinoma associated nucleic acid; CA nucleic acid; gene; ds;  
KM carcinoma associated protein; CAP; carcinoma; leukemia; lymphoma;  
KM cytosstatic.

OS Mus musculus.

PN US2004072154-A1.

PD 15-APR-2004.

PF 30-NOV-2001; 2001US-00997722.

PR 22-DEC-2000; 2000US-00747377.

PR 02-MAR-2001; 2001US-00798586.

PA (MORR/) MORRIS D W.

PA (ENGEL/) ENGELHARD E K.

PI Morris DW, Engelhard EK;

XX WPI; 2004-328562/30.

PT New carcinoma associated gene or protein, useful for preparing a  
composition for diagnosing or treating carcinoma e.g., leukemia or  
PT lymphoma.

PS Claim 1; SEQ ID NO 193; 29pp; English.

CC The invention relates to new recombinant nucleic acids. The invention  
CC also relates to a host cell comprising a recombinant nucleic acid or  
CC expression vector, an expression vector comprising a recombinant nucleic  
CC acid, a recombinant protein, a method of screening for drug candidates, a  
CC method of screening for a bioactive agent capable of binding to a  
CC carcinoma associated protein (CAP) encoded by a nucleotide sequence, a  
CC method of screening for a bioactive agent capable of modulating the  
CC activity of a CAP, a method of evaluating the effect of a candidate  
CC carcinoma drug, a method of diagnosing carcinoma, a method for inhibiting  
CC the activity of a CAP, a method of treating carcinomas, a method of  
CC neutralising the effect of a CAP and a method of diagnosing carcinoma or  
CC propensity to carcinoma. A method of evaluating the effect of a candidate  
CC carcinoma drug comprises administering the drug to a patient, removing a  
CC cell sample from the patient and determining alterations in the  
CC expression or activation of a gene comprising the nucleotide sequence. A  
CC method of diagnosing carcinoma comprises determining the expression of  
CC one or more genes comprising the nucleic acid sequence in a first tissue  
CC type of a first individual and comparing the expression of the gene from  
CC a second normal tissue type from the first individual or a second  
CC unaffected individual, where a difference in the expression indicates  
CC that the first individual has carcinoma. A method of inhibiting the  
CC activity of a CAP comprises binding an inhibitor to the CAP. Treating  
CC carcinomas comprises administering to a patient an inhibitor of CAP.  
CC Neutralising the effect of a CAP comprises contacting an agent specific  
CC for the CAP. The polypeptide specifically binds to the protein encoded by  
CC the nucleic acid. It comprises an antibody that specifically binds to the  
CC protein encoded by the nucleic acid. The nucleic acids are useful for  
CC preparing a composition for diagnosing or treating carcinoma e.g.,  
CC leukemia or lymphoma. This sequence represents a murine carcinoma  
CC associated (CA) nucleic acid of the invention. Note: The sequence data  
CC for this patent did not form part of the printed specification but was  
CC obtained in electronic format directly from USPTO at  
CC segdata.uspto.gov/sequence.html.  
XX

Sequence 92726 BP; 23819 A; 19174 C; 20109 G; 27030 T; 0 U; 2594 Other;





CC and sensitive, reproducible and quantitative detection of one or more  
CC nucleic acids (single or double stranded). The design of primers and  
CC probes is sufficiently flexible to allow many nucleic acids to be  
CC detected in a standardized reaction format using partly the same primers  
CC and probes. Only small amplicons are produced (requiring short  
CC amplification cycles), there is no competition/displacement between the  
CC short counter-strand of the amplicon and the detection probe, and  
CC specificity is high because the relative proportion of the internal  
CC detection region is increased with respect to the total amplicon length,  
CC allowing better differentiation between (viral) subtypes. Also short  
CC amplicons are less likely to undergo non-specific hybridization, so  
CC background is low, and short RNA sequences are more stable, with reduced  
CC tendency to form secondary structures. AAX23968-69 and AAX24035-37 are  
CC PCR primers and probes used in the method of the invention

XX  
SQ Sequence 12 BP; 2 A; 7 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 12;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
12 GGGGTCCTGGAG 1

Db

RESULT 21  
ABS65841  
ID ABS65841 standard; RNA; 12 BP.  
XX  
AC ABS65841;  
XX  
DT 15-NOV-2002 (first entry)

XX  
DE Inhibitory oligonucleotide specific for hepatitis C virus #47.

XX  
KM Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
KM non-B hepatitis; acute hepatitis; chronic hepatitis;  
KM hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
KM gene therapy; ss.

XX  
OS Synthetic.

XX  
PN US2002081577-A1.

XX  
PD 27-JUN-2002.

XX  
PF 02-JUL-1997; 97US-00887505.

XX  
PR 06-JUN-1995; 95US-00471968.  
PR 02-JUL-1996; 96US-0021104P.

XX  
PA (KILK/) KILKUSKIE R L.  
PA (FRAN/) FRANK B L.  
PA (GOOD/) GOODCHILD J.  
PA (WOLF/) WOLFE J L.  
PA (ROBE/) ROBERTS P C.  
PA (HAML/) HAMLIN H A.  
PA (ROBE/) ROBERTS N A.  
PA (WALT/) WALTHER D M.

XX  
PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,  
PI Hamlin HA, Roberts NA, Walther DM;  
XX  
XX WPI; 2002-537132/57.

XX  
PT Synthetic oligonucleotides complementary to a portion of the 5'  
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
PT treating HCV infections and hepatocellular carcinoma.

XX  
PS Claim 1; Page 61; 74pp; English.

XX  
CC The invention describes synthetic oligonucleotides complementary to a

CC portion of the 5' untranslated region of hepatitis C virus. The  
CC oligonucleotides may be used in methods for controlling, preventing, and  
CC treating hepatitis C virus infection, in antisense technology and gene  
CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
CC -B, acute and chronic hepatitis, and has been associated with  
CC hepatocellular carcinoma. The invention describes methods and kits for  
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic oligonucleotide used for inhibiting HCV  
CC replication and expression of HCV

XX  
SQ Sequence 12 BP; 1 A; 2 C; 7 G; 0 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
1 GGGGUCCTGGAG 12

Db

RESULT 22  
AAQ70177/C  
ID AAQ70177 standard; RNA; 14 BP.  
XX  
AC AAQ70177;  
XX  
DT 16-OCT-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 04-OCT-1994 (first entry)

XX  
DE Hepatitis C virus 5'-UTR antisense oligonucleotide target (A).

XX  
KM Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBH;  
KM antisense oligonucleotide; translation inhibition; therapy;  
KM 5'-untranslated region; ss.

XX  
OS Hepatitis C virus; Virus.

XX  
PN WO9405813-A1.

XX  
PD 17-MAR-1994.

XX  
PF 10-SEP-1993; 93MO-JP001293.

XX  
PR 10-SEP-1992; 92US-00945289.  
PR 14-APR-1993; 93JP-00087195.

XX  
PA (MOCH) MOCHIDA PHARM CO LTD.  
PA (KAGA) CHEMO SERO THERAPEUTIC RES INST.  
PA (ISIS-) ISIS PHARM INC.

XX  
PI Anderson KP, Hanecak RC, Hoshiko K, Nozaki C, Nishihara T;  
PI Nakatake H, Hamada F, Eto T, Furukawa S;  
XX  
XX WPI; 1994-101217/12.

XX  
PT Anti-sense oligonucleotide(s) complementary to hepatitis C viral genome  
PT - useful for inhibiting HCV replication, to treat related diseases.

XX  
PS Claim 16; Page 71; 91pp; English.

XX  
CC Oligonucleotides which are complementary to part of the hepatitis C virus  
CC genomic or messenger RNA are claimed. AAQ70177 is a preferred target  
CC sequence which is present in the 5'-UTR of the HCV genome. (Updated on 25  
CC -MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise OS  
CC field)

XX  
SQ Sequence 14 BP; 2 A; 8 C; 3 G; 0 T; 1 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 14;  
 Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTCGAG 12  
 ||||:||||  
 Db 14 GGGGCTCTGAG 3

RESULT 23  
 AA065140  
 ID AA065140 standard; DNA; 15 BP.  
 XX  
 AC AA065140;  
 XX  
 DT 21-DEC-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 XX  
 KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KM inhibition; viral protein precursor; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN CA2104649-A.  
 XX  
 PD 26-FEB-1994.  
 XX  
 PF 23-AUG-1993; 93CA-02104649.  
 XX  
 PR 25-AUG-1992; 92JP-00248796.  
 PR 03-MAR-1993; 93JP-00042736.  
 XX  
 PA (SEKI/) SEKI M.  
 XX  
 PI Seki M, Honda Y, Yamada E;  
 XX  
 DR WPI; 1994-151836/19.  
 XX  
 PT Anti-sense oligo:nucleotide(s) complementary to the hepatitis C virus  
 PT genome - are useful as antiviral agents.  
 XX  
 PS Claim 5; Page 163; 262pp; English.  
 XX  
 CC This oligonucleotide is an example of a preferred antisense compound i.e.  
 CC it has a base sequence of 15-30 bases which is included within the 49  
 CC bases from G at position 127 to C at position 175 of AA064913 and which  
 CC contains at least 7 bases from C at position 147 to C at position 153.  
 CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 CC genes  
 XX  
 SQ Sequence 15 BP; 1 A; 2 C; 10 G; 2 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 12; DB 2; Length 15;  
 Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTCGAG 12  
 ||||:||||  
 Db 4 GGGGCTCTGAG 15

RESULT 24  
 ABX01805/c  
 ID ABX01805 standard; RNA; 15 BP.  
 XX  
 AC ABX01805;  
 XX  
 DT 23-DEC-2002 (first entry)  
 XX  
 DE Hepatitis C virus (HCV) ribozyme related RNA sequence #74.  
 XX  
 KM Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;  
 XX  
 OS

KM HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;  
 KM liver failure; hepatocellular carcinoma; HCV infection; drug therapy;  
 KM type I interferon; interferon alpha; interferon beta; cytostatic; ss;  
 KM interferon gamma; consensus interferon; hepatotropic; antiinflammatory.  
 XX  
 OS Unidentified.  
 XX  
 PN US2002082225-A1.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 23-MAR-1999; 99US-00274553.  
 XX  
 PR 23-MAR-1999; 99US-00274553.  
 XX  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J A.  
 PA (ROBE/) ROBERTS B.  
 PA (PAVC/) PAVCO P A.  
 PA (MACE/) MACEJACK D.  
 XX  
 PI Blatt L, Moswigen JA, Roberts B, Pavco PA, Macejack D;  
 XX  
 DR WPI; 2002-617759/66.  
 XX  
 PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral  
 PT replication and are useful to treat hepatitis C virus infections and  
 PT cirrhosis, liver failure or hepatocellular carcinoma.  
 XX  
 PS Disclosure; SEQ ID NO 1587; 80pp; English.  
 XX  
 CC The present invention relates to enzymatic nucleic acids which  
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The  
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin  
 CC (HP) motif where the binding arms comprise sequences complementary to one  
 CC of the substrate sequences defined in the specification. The HCV  
 CC ribozymes are useful for modulating the expression and/or replication of  
 CC HCV. They can be used to treat cirrhosis, liver failure and/or  
 CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating  
 CC a condition associated with HCV infection in conjunction with one or more  
 CC other drug therapies, particularly type I interferon, especially  
 CC interferon alpha, beta or gamma or consensus interferon. The present  
 CC sequence represents a RNA sequence of unknown function. Note: The present  
 CC sequence is given in the sequence data but is not mentioned elsewhere in  
 CC the specification. The complete sequence data for this patent was  
 CC obtained in electronic format directly from the USPTO web site at  
 CC seqdata.uspto.gov/psipdIDentry.html  
 XX  
 SQ Sequence 15 BP; 3 A; 8 C; 3 G; 0 T; 1 U; 0 Other;  
 Query Match 66.7%; Score 12; DB 6; Length 15;  
 Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTCGAG 12  
 ||||:||||  
 Db 15 GGGGCTCTGAG 4

RESULT 25  
 AA065141  
 ID AA065141 standard; DNA; 16 BP.  
 XX  
 AC AA065141;  
 XX  
 DT 21-DEC-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 XX  
 KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KM inhibition; viral protein precursor; ss.  
 XX  
 OS Synthetic.



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XX CA2104649-A.
XX
XX 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-02104649.
XX
XX 25-AUG-1992; 92JP-00248796.
XX
XX 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
XX
XX Seki M, Honda Y, Yamada E;
XX
XX WPI; 1994-151836/19.
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX
XX Claim 5; Page 163; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
XX it has a base sequence of 15-30 bases which is included within the 49
XX bases from G at position 127 to C at position 175 of AA064913 and which
XX contains at least 7 bases from C at position 147 to C at position 153.
XX The antisense oligonucleotide is useful for inhibiting translation of HCV
XX genes
XX
XX Sequence 16 BP; 2 A; 2 C; 10 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 16;
XX Best Local Similarity 83.3%; Pred. No. 3.5e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGGGUCUCUGAG 12
XX ||||:|||||
XX 5 GGGGTCTCTGGAG 16
XX
XX RESULT 26
XX AA065125
XX ID AA065125 standard; DNA; 16 BP.
XX
XX AC AA065125;
XX
XX 21-DEC-1994 (first entry)
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX inhibition; viral protein precursor; ss.
XX
XX Synthetic.
XX
XX CA2104649-A.
XX
XX 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-02104649.
XX
XX 25-AUG-1992; 92JP-00248796.
XX
XX 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
XX
XX Seki M, Honda Y, Yamada E;
XX
XX WPI; 1994-151836/19.
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX
XX Claim 5; Page 156; 262pp; English.
XX

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```

XX This oligonucleotide is an example of a preferred antisense compound i.e.
XX it has a base sequence of 15-30 bases which is included within the 49
XX bases from G at position 127 to C at position 175 of AA064913 and which
XX contains at least 7 bases from C at position 147 to C at position 153.
XX The antisense oligonucleotide is useful for inhibiting translation of HCV
XX genes
XX
XX Sequence 16 BP; 1 A; 2 C; 11 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 16;
XX Best Local Similarity 83.3%; Pred. No. 3.5e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGGGUCUCUGAG 12
XX ||||:|||||
XX 4 GGGGTCTCTGGAG 15
XX
XX RESULT 27
XX AAT90622
XX ID AAT90622 standard; RNA; 16 BP.
XX
XX AC AAT90622;
XX
XX 07-APR-1998 (first entry)
XX
XX Hepatitis C virus recognition sequence 32 for ribozyme cleavage.
XX
XX Recognition sequence; HCV; ribozyme; 5' untranslated region;
XX nucleocapsid coding region; hairpin ribozyme; RNA cleavage; treatment;
XX HCV infection; HCV contamination; ss.
XX
XX Hepatitis C virus.
XX
XX Key Location/Qualifiers
XX FH 1..4
XX FT misc_feature /*tag= a
XX FT /note= "complementary to the CNR2 ribozyme"
XX FT misc_feature 6
XX FT /*tag= b
XX FT /note= "cleavage site corresponding to position 120 of
XX FT the (-) strand, counting from 3' end"
XX FT misc_feature 9..16
XX FT /*tag= c
XX FT /note= "complementary to the CNR2 ribozyme"
XX
XX WO9732018-A2.
XX
XX 04-SEP-1997.
XX
XX 27-FEB-1997; 97WO-US003304.
XX
XX 29-FEB-1996; 96US-00608862.
XX
XX (IMMU-) IMMUSOL INC.
XX
XX Barber JR, Welch PJ, Tritz R, Yel S, Yu M;
XX
XX WPI; 1997-470461/43.
XX
XX Ribozyme(s) directed against hepatitis C virus - for prevention and
XX treatment of viral infection, and detection of HCV contamination of
XX blood.
XX
XX Example 1; Page 17; 98pp; English.
XX
XX AAT90621-650 represent recognition sequences found in the positive (-)
XX strand of the Hepatitis C virus (HCV) RNA. The sequences are recognised
XX by novel ribozymes which inhibit replication, infectivity or gene
XX expression of HCV. The present sequence is located within the 5' UTR.
XX Hairpin ribozymes of the present invention were designed based on
XX sequences adjacent to the GUC sequence recognition feature. The ribozymes
XX

```

CC are directed against conserved regions of the genome and so should be  
CC active against many strains of HCV. The ribozymes, when optionally  
CC expressed from a vector, cleave the RNA of HCV and so are useful for  
CC treatment and prevention of HCV infection. They can also be used to  
CC detect HCV contamination of blood or for clinical diagnosis

XX  
SQ Sequence 16 BP; 1 A; 3 C; 10 G; 0 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUCGAG 12  
|||  
3 GGGGUCUCGAG 14

DB 3 GGGGUCUCGAG 14

RESULT 28

AAA13439 standard; RNA; 16 BP.

AC AAA13439;

DT 17-JUL-2000 (first entry)

DE Hepatitis C virus hairpin ribozyme recognition sequence SEQ ID NO:39.

KW Hepatitis C virus; HCV; hairpin ribozyme; cleavage; recognition site;

KW infection; virucide; hepatotropic; antiinflammatory;

OS replication inhibitor; gene expression inhibitor; ss.

XX Hepatitis C virus.

XX US6043077-A.

XX 28-MAR-2000.

XX 20-OCT-1997; 97US-00954210.

XX 29-FEB-1996; 97US-00608862.

XX 27-FEB-1997; 97WO-US003504.

XX (IMMU-) IMMUSOL INC.

XX Tritz R, Yei S, Yu M, Barber JR, Welch PJ;

XX WPI; 2000-270342/23.

XX Ribozyme capable of inhibiting replication, infectivity or gene

XX expression of hepatitis C virus, useful for treating or preventing

XX hepatitis C virus infection.

XX Claim 1; Col 13; 57pp; English.

XX The present invention describes ribozymes (I) capable of inhibiting

XX replication, infectivity or gene expression of a hepatitis C virus (HCV),

XX directed to target sequences AAA13438 to AAA13444, AAA13454 and AAA13465.

XX (I) have virucide, hepatotropic and antiinflammatory activities. (I), or

XX vectors comprising nucleotide sequences encoding (I), are useful for

XX interfering with the replication or gene expression of HCV in a human

XX cell. (I) are useful for diagnosis, prevention and treatment of HCV

XX infection or disease in a mammals especially humans. Nucleotide sequences

XX encoding (I) are useful for preventing hepatitis C viral infection in a

XX cell. AAA13401 to AAA13405 represent examples of the briefest

XX requirements for hairpin ribozyme; AAA13406 and AAA13407 represent PCR

XX primers used in the amplification of the HCV capsid sequence; AAA13408 to

XX AAA13467 represent HCV hairpin ribozyme recognition sites; and AAA13468

XX to AAA13473 represent oligonucleotides used in the construction of HCV

XX hairpin ribozymes, all these sequences are used in the exemplification of

XX the present invention

XX Sequence 16 BP; 1 A; 3 C; 10 G; 0 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUCGAG 12  
|||  
3 GGGGUCUCGAG 14

DB 3 GGGGUCUCGAG 14

RESULT 29

ABX74358 standard; RNA; 16 BP.

AC ABX74358;

DT 24-MAR-2003 (first entry)

DE Hepatitis C recognition sequence for ribozyme CN2.

KW Hairpin ribozyme; ss; hepatitis C infection; HCV; gene therapy; virucide.

OS Hepatitis C virus.

XX US6458567-B1.

XX 01-OCT-2002.

XX 01-NOV-1999; 99US-00431419.

XX 29-FEB-1996; 96US-00608862.

XX 20-OCT-1997; 97US-00954210.

XX (IMMU-) IMMUSOL INC.

XX Barber JR, Welch PJ, Tritz R, Yei S, Yu M;

XX WPI; 2003-155536/15.

XX New ribozyme having the ability to inhibit replication, infectivity or

XX gene expression of a Hepatitis C Virus (HCV), useful for treating or

XX preventing HCV infection.

XX Example 1; Col 12; 48pp; English.

XX The invention relates to a new ribozyme with the ability to inhibit

XX replication, infectivity or gene expression of a Hepatitis C Virus (HCV)

XX by cleaving the positive strand genomic RNA of HCV at a sequence having

XX 16 bp. Also included are a nucleic acid encoding the ribozyme, a host

XX cell containing the ribozyme or vector, a vector comprising a promoter

XX operably linked to the nucleic acid, producing a ribozyme, interfering

XX with HCV replication or gene expression in a cell infected in a cell

XX culture with HCV or a composition comprising the ribozyme and a carrier

XX or diluent. The ribozyme is useful for treating or preventing HCV

XX infection. The present sequence is an HCV -ve strand recognition sequence

XX for a ribozyme of the invention

XX Sequence 16 BP; 1 A; 3 C; 10 G; 0 T; 2 U; 0 Other;

XX Query Match 66.7%; Score 12; DB 8; Length 16;

XX Best Local Similarity 100.0%; Pred. No. 3.5e+03;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OY 1 GGGGUCUCGAG 12

XX |||

XX 3 GGGGUCUCGAG 14

XX DB 3 GGGGUCUCGAG 14

XX RESULT 30

XX AAO65126 standard; DNA; 17 BP.

XX ID AAO65126

XX AC AAO65126;

XX XX

DT 21-DEC-1994 (first entry)  
XX  
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX  
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
KM inhibition; viral protein precursor; ss.  
XX  
OS Synthetic.  
XX  
FN CA2104649-A.  
XX  
PD 26-FEB-1994.  
XX  
PF 23-AUG-1993; 93CA-02104649.  
XX  
PR 25-AUG-1992; 92JP-00248796.  
PR 03-MAR-1993; 93JP-00042736.  
XX  
PA (SEKI/) SEKI M.  
XX  
PI Seki M, Honda Y, Yamada E;  
XX  
DR WPI; 1994-151836/19.  
XX  
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
PT genome - are useful as antiviral agents.  
XX  
PS Claim 5; Page 157; 262pp; English.  
XX  
CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AA064913 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 17 BP; 2 A; 2 C; 11 G; 2 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 17;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGGGUCGCGAG 12  
Db 5 GGGGTCTCGAG 16  
RESULT 31  
AA065142  
ID AA065142 standard; DNA; 17 BP.  
XX  
AC AA065142;  
XX  
DT 21-DEC-1994 (first entry)  
XX  
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX  
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
KM inhibition; viral protein precursor; ss.  
XX  
OS Synthetic.  
XX  
FN CA2104649-A.  
XX  
PD 26-FEB-1994.  
XX  
PF 23-AUG-1993; 93CA-02104649.  
XX  
PR 25-AUG-1992; 92JP-00248796.  
PR 03-MAR-1993; 93JP-00042736.  
XX  
PA (SEKI/) SEKI M.

PI Seki M, Honda Y, Yamada E;  
XX  
DR WPI; 1994-151836/19.  
XX  
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
PT genome - are useful as antiviral agents.  
XX  
PS Claim 5; Page 164; 262pp; English.  
XX  
CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AA064913 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 17 BP; 2 A; 2 C; 11 G; 2 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 17;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGGGUCGCGAG 12  
Db 6 GGGGTCTCGAG 17  
RESULT 32  
AA065111  
ID AA065111 standard; DNA; 17 BP.  
XX  
AC AA065111;  
XX  
DT 21-DEC-1994 (first entry)  
XX  
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX  
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
KM inhibition; viral protein precursor; ss.  
XX  
OS Synthetic.  
XX  
FN CA2104649-A.  
XX  
PD 26-FEB-1994.  
XX  
PF 23-AUG-1993; 93CA-02104649.  
XX  
PR 25-AUG-1992; 92JP-00248796.  
PR 03-MAR-1993; 93JP-00042736.  
XX  
PA (SEKI/) SEKI M.  
XX  
PI Seki M, Honda Y, Yamada E;  
XX  
DR WPI; 1994-151836/19.  
XX  
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
PT genome - are useful as antiviral agents.  
XX  
PS Claim 5; Page 150; 262pp; English.  
XX  
CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AA064913 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 17 BP; 1 A; 3 C; 11 G; 2 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 17;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
 |||||:  
 Db 4 GGGGCTCTGGAG 15

RESULT 33  
 ACD65845  
 ID ACD65845 standard; RNA, 17 BP.

XX ACD65845;

XX 30-SEP-2003 (first entry)

DE HCV minus strand DNAzyme substrate sequence #2252.

KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;  
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.

XX Hepatitis C virus.

XX WO200281494-A1.

PD 17-OCT-2002.

PF 26-MAR-2002; 2002WO-US009187.

PR 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MACE/) MACEJAK D.

PA (MCSW/) MCSWIGEN J.

PA (MORR/) MORRISSEY D.

PA (PAVC/) PAVCO P.

PA (LEBP/) LEE P.

PA (DRAP/) DRAPER K.

PA (ROBE/) ROBERTS E.

PI Blatt L, Macejak D, Mcswigen J, Morrissey D, Pavco P, Lee P;

PI Draper K, Roberts E;

DR WPI; 2003-229207/22.

PT Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.

PS Claim 1; Page 315; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNAzymes,  
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and

CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HCV  
 CC DNAzyme or minus strand DNAzyme sequences disclosed in the present  
 CC invention

XX SQ Sequence 17 BP; 2 A; 2 C; 11 G; 0 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 8; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
 |||||:  
 Db 6 GGGGCTCTGGAG 17

RESULT 34  
 ACD56830/C  
 ID ACD56830 standard; RNA, 17 BP.

XX ACD56830;

XX 23-SEP-2003 (first entry)

DT HCV DNAzyme substrate sequence #26.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;  
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.

OS Hepatitis C virus.

XX WO200281494-A1.

PD 17-OCT-2002.

PF 26-MAR-2002; 2002WO-US009187.

PR 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.

PR 08-JUN-2001; 2001US-0296876P.

PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MACE/) MACEJAK D.

PA (MCSW/) MCSWIGEN J.

PA (MORR/) MORRISSEY D.

PA (PAVC/) PAVCO P.

PA (LEBP/) LEE P.

PA (DRAP/) DRAPER K.

PA (ROBE/) ROBERTS E.

PI Blatt L, Macejak D, Mcswigen J, Morrissey D, Pavco P, Lee P;

PI Draper K, Roberts E;

DR WPI; 2003-229207/22.

PT Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.

PS Claim 1; Page 234; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate

Query Match	66.7%	Score 12;	DB 8;	Length 17;
Best Local Similarity	83.3%	Pred. No. 3.5e+03;		
Matches 10; Conservative	2;	Mismatches 0;	Indels 0;	Gaps 0

RESULT 35  
ADL18587/c  
ID ADL18587 standard; DNA; 17 BP.

KM DNA storage; DNA analysis; virus identification; bacteria identification

PN US2003134312-A1.

PD 17-JUL-2003.

PF 15-NOV-2002; 2002US-00298255.

PR 15-NOV-2001; 2001US-0336005P.

PA (WHAT-) WHATMAN INC.

PI Burgoyne LA;

DR WPI; 2003-843261/78.

PT New device comprising a filter layer comprising a dry solid medium

PT storing and analyzing a nucleic acid containing moiety.

PS Example 1; SEQ ID NO 4; 14pp; English

CC The invention relates to a device for storage and analysis of a nucleic acid sample.

CC layer comprising a dry solid medium comprising a hydrophilic solid

CC neutral solid matrix attached to a composition comprising a detergent.

CC sample comprises applying a biological sample to the filter layer,

CC layer to the isolation layer, retaining the nucleic acid components in

Query Match	66.7%	Score 12;	DB 10;	Length 17;
Best Local Similarity	83.3%	Pred. No.	3.5e+03;	
Matches 10;	Conservative 2;	Mismatches 0;	Indels 0;	Gaps 0

RESULT 36  
ADI87283  
ID ADI87283 standard; RNA; 17 BP.

DT	03-JUN-2004	(first entry)
XX		
DE	HCV DNase	substrate sequence #4529

KM ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV,  
KM HCV infection; type I interferon; DNasezyme.

OS Hepatitis C virus.

PN US2003125270-A1

03-JUL-2003 PD

PF 18-DEC-2000; 2000US-00740332.

PR 18-DEC-2000; 2000US-00740332.

PA (BLAT/) BLATT L.

PA (ROBE/) ROBERTS E.

PA (MACE/) MACEJACK D

PI Blatt L, McSwiggen J, Roberts E, Pavco PA, Macejack D;

DR WPI; 2004-031273/03.

PT Enzymatic nucleic acid molecules which specifically cleave RNA derived

PT especially in combination with type I interferon therapy.

PS Claim 1; SEQ ID NO 4529; 198pp; English

CC The invention relates to an enzymatic nucleic acid molecule which

CC the binding arms of the enzymatic nucleic acid molecule comprises

CC in the specification. The nucleic acid molecule may be administered for

CC interferons. The present sequence represents a HCV DNAzyme substrate

XX

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

Best Local Similarity 100.0%; Pred. No. 3.5e+03;

QY 1 GGGGUCGAG 12  
 DB 6 GGGGUCGAG 17

## RESULT 37

AD182780/c  
 ID AD182780 standard; RNA, 17 BP.

AC AD182780;

DT 03-JUN-2004 (first entry)

XX HCV DNAzyme substrate sequence #26.

KW ss; enzymatic nucleic acid; RNA cleavage; hepatitis C virus; HCV;  
 KM HCV infection; type I interferon; DNAzyme.

OS Hepatitis C virus.

PN US2003125270-A1.

PD 03-JUL-2003.

PF 18-DEC-2000; 2000US-00740332.

PR 18-DEC-2000; 2000US-00740332.

PA (BLAT/) BLAT L.

PA (MCSM/) MCSMIGEN J.

PA (ROBE/) ROBERTS E.

PA (PACV/) PACCO P A.

PA (MACE/) MACEJACK D.

PI Blact L, Mcswiggen J, Roberts E, Pavco PA, Macejack D;

DR WPI; 2004-031273/03.

XX Enzymatic nucleic acid molecules which specifically cleave RNA derived

PT from hepatitis C virus (HCV), useful for the treatment of HCV infections,

PT especially in combination with type I interferon therapy.

XX Claim 1; SEQ ID NO 26; 198bp; English.

PS The invention relates to an enzymatic nucleic acid molecule which

CC specifically cleaves RNA derived from hepatitis C virus (HCV), in which

CC the binding arms of the enzymatic nucleic acid molecule comprises

CC sequences complementary to any of the defined substrate sequences given

CC in the specification. The nucleic acid molecule may be administered for

CC the treatment of HCV infections, especially in combination with type I

CC interferons. The present sequence represents a HCV DNAzyme substrate

CC sequence.

XX Sequence 17 BP; 2 A; 11 C; 2 G; 0 T; 2 U; 0 Other;

QY Query Match 66.7%; Score 12; DB 12; Length 17;

DB Best Local Similarity 83.3%; Pred. No. 3.5e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12

DB 13 GGGGUCGAG 2

RESULT 38

AA065127

ID AA065127 standard; DNA, 18 BP.

AC AA065127;

XX 21-DEC-1994 (first entry)

DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KM inhibition; viral protein precursor; ss.  
 XX Synthetic.

XX CA2104649-A.

PN 26-FEB-1994.

PD 23-AUG-1993; 93CA-02104649.

PF 25-AUG-1992; 92JP-00248796.

PR 03-MAR-1993; 93JP-00042736.

XX (SEKI/) SEKI M.

PI Seki M, Honda Y, Yamada E;

DR WPI; 1994-151836/19.

XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus

PT genome - are useful as antiviral agents.

PS Claim 5; Page 157; 262bp; English.

XX This oligonucleotide is an example of a preferred antisense compound i.e.

CC it has a base sequence of 15-30 bases which is included within the 49

CC bases from G at position 127 to C at position 175 of AA064913 and which

CC contains at least 7 bases from C at position 147 to C at position 153.

CC The antisense oligonucleotide is useful for inhibiting translation of HCV

CC genes

XX Sequence 18 BP; 2 A; 2 C; 12 G; 2 T; 0 U; 0 Other;

QY Query Match 66.7%; Score 12; DB 2; Length 18;

DB Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12

DB 6 GGGGUCGAG 17

RESULT 39

AA065112

ID AA065112 standard; DNA, 18 BP.

AC AA065112;

XX 21-DEC-1994 (first entry)

XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.

XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;

XX inhibition; viral protein precursor; ss.

XX Synthetic.

XX CA2104649-A.

PN 26-FEB-1994.

PF 23-AUG-1993; 93CA-02104649.

PR 25-AUG-1992; 92JP-00248796.

PR 03-MAR-1993; 93JP-00042736.

XX (SEKI/) SEKI M.

XX Seki M, Honda Y, Yamada E;

PI 21-DEC-1994 (first entry)

DR WPI; 1994-151836/19.  
 XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
 PT genome - are useful as antiviral agents.  
 XX  
 PS Claim 5; Page 151; 262pp; English.  
 CC This oligonucleotide is an example of a preferred antisense compound i.e.  
 CC it has a base sequence of 15-30 bases which is included within the 49  
 CC bases from G at position 127 to C at position 175 of AA064913 and which  
 CC contains at least 7 bases from C at position 147 to C at position 153.  
 CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 CC genes  
 XX  
 SQ Sequence 18 BP; 2 A; 3 C; 11 G; 2 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 12; DB 2; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GGGGUCCUGAG 12  
 Db 5 GGGGTCTCGAG 16  
 RESULT 40  
 AA065098  
 ID AA065098 standard; DNA; 18 BP.  
 XX  
 AC AA065098;  
 XX  
 DT 20-DEC-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 XX  
 KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KM inhibition; viral protein precursor; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN CA2104649-A.  
 XX  
 PD 26-FEB-1994.  
 XX  
 PF 23-AUG-1993; 93CA-02104649.  
 XX  
 PR 25-AUG-1992; 92JP-00248796.  
 PR 03-MAR-1993; 93JP-00042736.  
 XX  
 PA (SEKI/) SEKI M.  
 XX  
 PI Seki M, Honda Y, Yamada E;  
 XX  
 DR WPI; 1994-151836/19.  
 XX  
 PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
 PT genome - are useful as antiviral agents.  
 XX  
 PS Claim 5; Page 144; 262pp; English.  
 CC This oligonucleotide is an example of a preferred antisense compound i.e.  
 CC it has a base sequence of 15-30 bases which is included within the 49  
 CC bases from G at position 127 to C at position 175 of AA064913 and which  
 CC contains at least 7 bases from C at position 147 to C at position 153.  
 CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 CC genes  
 XX  
 SQ Sequence 18 BP; 1 A; 3 C; 11 G; 3 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 12; DB 2; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCCUGAG 12  
 Db 4 GGGGTCTCGAG 15  
 RESULT 41  
 AA065143  
 ID AA065143 standard; DNA; 18 BP.  
 XX  
 AC AA065143;  
 XX  
 DT 21-DEC-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 XX  
 KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KM inhibition; viral protein precursor; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN CA2104649-A.  
 XX  
 PD 26-FEB-1994.  
 XX  
 PF 23-AUG-1993; 93CA-02104649.  
 XX  
 PR 25-AUG-1992; 92JP-00248796.  
 PR 03-MAR-1993; 93JP-00042736.  
 XX  
 PA (SEKI/) SEKI M.  
 XX  
 PI Seki M, Honda Y, Yamada E;  
 XX  
 DR WPI; 1994-151836/19.  
 XX  
 PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
 PT genome - are useful as antiviral agents.  
 XX  
 PS Claim 5; Page 164; 262pp; English.  
 CC This oligonucleotide is an example of a preferred antisense compound i.e.  
 CC it has a base sequence of 15-30 bases which is included within the 49  
 CC bases from G at position 127 to C at position 175 of AA064913 and which  
 CC contains at least 7 bases from C at position 147 to C at position 153.  
 CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 CC genes  
 XX  
 SQ Sequence 18 BP; 2 A; 2 C; 12 G; 2 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 12; DB 2; Length 18;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GGGGUCCUGAG 12  
 Db 7 GGGGTCTCGAG 18  
 RESULT 42  
 AAT80255  
 ID AAT80255 standard; DNA; 18 BP.  
 XX  
 AC AAT80255;  
 XX  
 DT 15-OCT-1997 (first entry)  
 XX  
 DE Oligo HCV61, targeted to HCV region +4 to +9.  
 XX  
 KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KM inhibition; replication; expression; detection; chronic hepatitis;  
 KM acute hepatitis; hepatocarcinoma; ss.  
 XX  
 OS Synthetic.

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XX Key Location/Qualifiers
FH modified_base 1..12
FT /*tag= a
FT /note= "2' Ome modified"
FT modified_base 13..18
FT /*tag= b
FT /note= "Phosphorothioate linkages"
XX
XX PN MO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX PD 04-JUN-1996; 96WO-EP002427.
XX
XX PF 06-JUN-1995; 95US-00471968.
XX
XX PR (HOFF) :HOFFMANN LA ROCHE & CO AG F.
XX PA (HYBR-) HYBRIDON INC.
XX
XX PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA,
XX PI Roberts PC, Walthers DM, Wolfe JL;
XX DR WPI; 1997-043122/04.
XX
XX PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX PT carcinoma.
XX
XX PS Claim 19; Page 31; 100pp; English.
XX
XX CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX CC which are complementary to a portion of the 5' untranslated region (UTR)
XX CC of hepatitis C virus (HCV). These sequences may be used in a
XX CC pharmaceutical composition for the control or prevention of HCV
XX CC infection. They may be used to inhibit replication or expression of HCV
XX CC or for detecting the presence of HCV in a sample. They may be used to
XX CC inhibit HCV replication in a cell and are therefore useful in the
XX CC treatment of HCV infections such as chronic and acute hepatitis and
XX CC hepatocarcinoma. This oligo was used in a luciferase assay to determine
XX CC whether it binds successfully to its target
XX
XX SQ Sequence 18 BP; 1 A; 4 C; 9 G; 2 T; 2 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGGUCUCCUGAG 12
XX |||||
XX 1 GGGGUCUCCUGAG 12
XX
XX DB
XX
XX RESULT 43
XX AAT80250
XX ID AAT80250 standard; DNA; 18 BP.
XX
XX AC AAT80250;
XX
XX DT 15-OCT-1997 (first entry)
XX
XX DE Oligo HCV54, targeted to HCV region -9 to -4.
XX
XX KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX KW inhibition; replication; expression; detection; chronic hepatitis;
XX KW acute hepatitis; hepatocarcinoma; ss.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX FH modified_base 1..6
XX FT /*tag= b
XX FT /note= "Phosphorothioate linkages"
XX

```

```

FT modified_base 7..18
FT /*tag= a
FT /note= "2' Ome modified"
FT modified_base 13..18
FT /*tag= b
FT /note= "Phosphorothioate linkages"
XX
XX PN MO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX PD 04-JUN-1996; 96WO-EP002427.
XX
XX PF 06-JUN-1995; 95US-00471968.
XX
XX PR (HOFF) :HOFFMANN LA ROCHE & CO AG F.
XX PA (HYBR-) HYBRIDON INC.
XX
XX PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
XX PI Roberts PC, Walthers DM, Wolfe JL;
XX DR WPI; 1997-043122/04.
XX
XX PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX PT carcinoma.
XX
XX PS Claim 19; Page 31; 100pp; English.
XX
XX CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX CC which are complementary to a portion of the 5' untranslated region (UTR)
XX CC of hepatitis C virus (HCV). These sequences may be used in a
XX CC pharmaceutical composition for the control or prevention of HCV
XX CC infection. They may be used to inhibit replication or expression of HCV
XX CC or for detecting the presence of HCV in a sample. They may be used to
XX CC inhibit HCV replication in a cell and are therefore useful in the
XX CC treatment of HCV infections such as chronic and acute hepatitis and
XX CC hepatocarcinoma. This oligo was used in a luciferase assay to determine
XX CC whether it binds successfully to its target
XX
XX SQ Sequence 18 BP; 2 A; 4 C; 10 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGGUCUCCUGAG 12
XX |||||
XX 7 GGGGUCUCCUGAG 18
XX
XX DB
XX
XX RESULT 44
XX AAT80261
XX ID AAT80261 standard; DNA; 18 BP.
XX
XX AC AAT80261;
XX
XX DT 15-OCT-1997 (first entry)
XX
XX DE Oligo HCV93, targeted to HCV region +1 to +6.
XX
XX KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX KW inhibition; replication; expression; detection; chronic hepatitis;
XX KW acute hepatitis; hepatocarcinoma; ss.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX FH modified_base 1..12
XX FT /*tag= a
XX FT /note= "2' Ome modified"
XX FT modified_base 13..18
XX FT /*tag= b
XX FT /note= "Phosphorothioate linkages"
XX
XX PN MO9639500-A2.
XX

```



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XX 12-DEC-1996.
PD 04-JUN-1996; 96WO-EP002427.
PF 06-JUN-1995; 95US-00471968.
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
PA Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PI Roberts PC, Walthers DM, Wolfe JL;
XX WPI; 1997-043122/04.
DR
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT carcinoma.
XX
XX Claim 19; Page 31; 100pp; English.
PS
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC which are complementary to a portion of the 5' untranslated region (UTR)
CC of hepatitis C virus (HCV). These sequences may be used in a
CC pharmaceutical composition for the control or prevention of HCV
CC infection. They may be used to inhibit replication or expression of HCV
CC or for detecting the presence of HCV in a sample. They may be used to
CC inhibit HCV replication in a cell and are therefore useful in the
CC treatment of HCV infections such as chronic and acute hepatitis and
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine
CC whether it binds successfully to its target
XX
XX Sequence 18 BP; 2 A; 4 C; 8 G; 2 T; 2 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCGCGAG 12
DB 1 GGGGUCGCGAG 12

```

```

PR 06-JUN-1995; 95US-00471968.
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
PA Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PI Roberts PC, Walthers DM, Wolfe JL;
XX WPI; 1997-043122/04.
DR
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT carcinoma.
XX
XX Claim 19; Page 31; 100pp; English.
PS
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC which are complementary to a portion of the 5' untranslated region (UTR)
CC of hepatitis C virus (HCV). These sequences may be used in a
CC pharmaceutical composition for the control or prevention of HCV
CC infection. They may be used to inhibit replication or expression of HCV
CC or for detecting the presence of HCV in a sample. They may be used to
CC inhibit HCV replication in a cell and are therefore useful in the
CC treatment of HCV infections such as chronic and acute hepatitis and
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine
CC whether it binds successfully to its target
XX
XX Sequence 18 BP; 2 A; 3 C; 9 G; 2 T; 2 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCGCGAG 12
DB 1 GGGGUCGCGAG 12

```

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RESULT 45
AAT80253
ID AAT80253 standard; DNA; 18 BP.
XX
XX AAT80253;
AC
XX
XX 15-OCT-1997 (first entry)
DT
XX
XX Oligo HCV59, targeted to HCV region -3 to +3.
DE
XX
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KM inhibition; replication; expression; detection; chronic hepatitis;
KM acute hepatitis; hepatocarcinoma; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..12 /*tag= a
FT modified_base 13..18 /*tag= "2'OMe modified"
FT modified_base 13..18 /*tag= b
FT /*tag= "Phosphorothioate linkages"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX
XX
XX

```

```

RESULT 46
AAT80256
ID AAT80256 standard; DNA; 18 BP.
XX
XX AAT80256;
AC
XX
XX 15-OCT-1997 (first entry)
DT
XX
XX Oligo HCV62, targeted to HCV region +4 to +9.
DE
XX
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KM inhibition; replication; expression; detection; chronic hepatitis;
KM acute hepatitis; hepatocarcinoma; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..6 /*tag= b
FT modified_base 7..18 /*tag= "Phosphorothioate linkages"
FT modified_base 7..18 /*tag= a
FT /*tag= "2'OMe modified"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
XX
XX

```

PI	Frank BL, Goodchild J, Hamlin HA, Kilukskie RE, Roberts NA;
PT	Roberts PC, Walther DM, Wolfe JL;
XX	
DR	WPI; 1997-043122/04.
XX	
PS	Claim 19; Page 31; 100pp; English.
XX	
CC	The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC	which are complementary to a portion of the 5' untranslated region (UTR)
CC	of hepatitis C virus (HCV). These sequences may be used in a
CC	pharmacological composition for the control or prevention of HCV
CC	infection. They may be used to inhibit replication or expression of HCV
CC	or for detecting the presence of HCV in a sample. They may be used to
CC	inhibit HCV replication in a cell and are therefore useful in the
CC	treatment of HCV infections such as chronic and acute hepatitis and
CC	hepatocarcinoma. This oligo was used in a luciferase assay to determine
CC	whether it binds successfully to its target
XX	
SO	Sequence 18 BP; 1 A; 4 C; 9 G; 2 T; 2 U; 0 Other;
QY	Query Match 66.7%; Score 12; DB 2; Length 18;
	Best Local Similarity 100.0%; Pred.No. 3.4e+03;
Db	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	1 GGGGHCUCGAG 12
	7 GGGGUCUCGAG 18
RESULT 47	
AAT80264	
ID	AAT80264 standard; DNA; 18 BP.
XX	
AC	AAT80264;
XX	
DT	15-OCT-1997 (first entry)
XX	
DE	Oligo HCV97, targeted to HCV region +7 to +12.
XX	
KW	Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW	inhibition; replication; expression; detection; chronic hepatitis;
KW	acute hepatitis; hepatocarcinoma; ss.
XX	
OS	Synthetic.
XX	
PH	Key
FT	Location/Qualifiers
FT	modified_base 1..6
FT	/*tag= b
FT	/note= "Phosphorothioate linkages"
FT	7..18
FT	/*tag= a
FT	/note= "2'OME modified"
XX	
PN	WO9639500-A2.
XX	
PD	12-DEC-1996.
XX	
PF	04-JUN-1996; 96WO-EP002427.
XX	
PR	06-JUN-1995; 95US-00471968.
XX	
PA	(HOEF ) HOFMANN IA ROCHE & CO AG F.
XX	
PA	(HYBR-) HYBRIDON INC.
XX	
PI	Frank BL, Goodchild J, Hamlin HA, Kilukskie RE, Roberts NA;
PI	Roberts PC, Walther DM, Wolfe JL;
XX	
XX	WPI; 1997-043122/04.
XX	

PT	Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in the treatment and detection of HCV infection, esp. hepatitis and hepatocarcinoma.
PS	Claim 19; Page 32; 100pp; English.
XX	The sequences given in AAT80211-382 represent synthetic oligonucleotides which are complementary to a portion of the 5' untranslated region (UTR) of hepatitis C virus (HCV). These sequences may be used in a pharmaceutical composition for the control or prevention of HCV infection. They may be used to inhibit replication or expression of HCV or for detecting the presence of HCV in a sample. They may be used to inhibit HCV replication in a cell and are therefore useful in the treatment of HCV infections such as chronic and acute hepatitis and hepatocarcinoma. This oligo was used in a luciferase assay to determine whether it binds successfully to its target
SQ	Sequence 18 BP; 2 A; 3 C; 8 G; 3 T; 2 U; 0 Other;
Query Match	66.7%; Score 12; DB 2; Length 18;
Best Local Similarity	100.0%; Pred. No. 3,4e+03;
Matches 12; Conservative	0; Mismatches 0; Indels 0; Gaps 0
Dy	1 GGCGUCCUGGAG 12       7 GGCGUCUGGAG 18
Db	
RESULT 48	
AAT80353	AAT80353 standard; DNA; 18 BP.
AC	AAT80353;
XX	16-OCP-1997 (first entry)
DT	
DE	Oligo HCV-205, targeted to HCV mRNA position +20 to +25.
XX	Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW	inhibition; replication; expression; detection; chronic hepatitis;
KM	acute hepatitis; hepatocarcinoma; sv.
XX	
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	modified_base 1..6
FT	/tag= b
FT	/note= "Comprises phosphorothioate linkages"
FT	modified_base 7..18
FT	/tag= a
FT	/note= "2'-OME RNA"
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XX	WC9639500-A2.
PN	
PD	12-DEC-1996.
XX	
PE	04-JUN-1996; 96WO-BP002427.
XX	
PR	06-JUN-1995; 95US-00471968.
XX	
PA	(HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA	(HYBR-) HYBRIDON INC.
PI	Frank BU, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PT	Roberts FC, Walcher DW, Wolfe JL;
DR	WPI; 1997-043122/04.
XX	
XX	Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in the treatment and detection of HCV infection, esp. hepatitis and hepatocarcinoma.
XX	Claim 20; Page 20; 100pp; English.

XX The sequences given in AAT80211-382 represent synthetic oligonucleotides  
 CC which are complementary to a portion of the 5' untranslated region (UTR)  
 CC of hepatitis C virus (HCV). These sequences may be used in a  
 CC pharmaceutical composition for the control or prevention of HCV  
 CC infection. They may be used to inhibit replication or expression of HCV  
 CC or for detecting the presence of HCV in a sample. They may be used to  
 CC inhibit HCV replication in a cell and are therefore useful in the  
 CC treatment of HCV infections such as chronic and acute hepatitis and  
 CC hepatocarcinoma. This sequence binds to two non-contiguous regions of the  
 CC HCV genome. This sequence is anchored at position -219 to -230 and is  
 CC targeted to position +20 to +25

SQ Sequence 18 BP; 2 A; 2 C; 9 G; 3 T; 2 U; 0 Other;

QY Query Match 66.7%; Score 12; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GGGGUCGCGAG 12  
 7 GGGGUCGCGAG 18

RESULT 49  
 AAT80355  
 ID AAT80355 standard; DNA; 18 BP.  
 XX AAT80355;  
 AC  
 XX 16-OCT-1997 (first entry)  
 DT  
 XX Oligo HCV-213, targeted to HCV mRNA position +230 to +235.  
 DE  
 XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KM inhibition; replication; expression; detection; chronic hepatitis;  
 KM acute hepatitis; hepatocarcinoma; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH modified\_base 1..12  
 FT /\*tag= a  
 FT /note= "2'-Ome RNA"  
 FT modified\_base 13..18  
 FT /\*tag= b  
 FT /note= "Comprises phosphorothioate linkages"  
 XX  
 XX W09639500-A2.  
 PN  
 XX 12-DEC-1996.  
 PD  
 XX 04-JUN-1996; 96WO-EP002427.  
 PF  
 XX 06-JUN-1995; 95US-00471968.  
 PR  
 XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PA (HYBR-) HYBRIDON INC.  
 XX  
 XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
 PI Roberts PC, Walther DM, Wolfe JL;  
 XX  
 XX WPI; 1997-043122/04.  
 DR  
 XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
 PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
 PT carcinoma.  
 PT  
 XX Claim 20; Page 20; 100pp; English.  
 PS  
 XX The sequences given in AAT80211-382 represent synthetic oligonucleotides  
 CC which are complementary to a portion of the 5' untranslated region (UTR)  
 CC of hepatitis C virus (HCV). These sequences may be used in a

CC pharmaceutical composition for the control or prevention of HCV  
 CC infection. They may be used to inhibit replication or expression of HCV  
 CC or for detecting the presence of HCV in a sample. They may be used to  
 CC inhibit HCV replication in a cell and are therefore useful in the  
 CC treatment of HCV infections such as chronic and acute hepatitis and  
 CC hepatocarcinoma. This sequence binds to two non-contiguous regions of the  
 CC HCV genome. This sequence is anchored at position -219 to -230 and is  
 CC targeted to position +230 to +235

SQ Sequence 18 BP; 2 A; 3 C; 10 G; 1 T; 2 U; 0 Other;

QY Query Match 66.7%; Score 12; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GGGGUCGCGAG 12  
 1 GGGGUCGCGAG 12

RESULT 50  
 AAT80263  
 ID AAT80263 standard; DNA; 18 BP.  
 XX AAT80263;  
 AC  
 XX 15-OCT-1997 (first entry)  
 DT  
 XX Oligo HCV96, targeted to HCV region +7 to +12.  
 DE  
 XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KM inhibition; replication; expression; detection; chronic hepatitis;  
 KM acute hepatitis; hepatocarcinoma; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH modified\_base 1..12  
 FT /\*tag= a  
 FT /note= "2'Ome modified"  
 FT modified\_base 13..18  
 FT /\*tag= b  
 FT /note= "Phosphorothioate linkages"  
 XX  
 XX W09639500-A2.  
 PN  
 XX 12-DEC-1996.  
 PD  
 XX 04-JUN-1996; 96WO-EP002427.  
 PF  
 XX 06-JUN-1995; 95US-00471968.  
 PR  
 XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PA (HYBR-) HYBRIDON INC.  
 XX  
 XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
 PI Roberts PC, Walther DM, Wolfe JL;  
 XX  
 XX WPI; 1997-043122/04.  
 DR  
 XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
 PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
 PT carcinoma.  
 PT  
 XX Claim 19; Page 32; 100pp; English.  
 PS  
 XX The sequences given in AAT80211-382 represent synthetic oligonucleotides  
 CC which are complementary to a portion of the 5' untranslated region (UTR)  
 CC of hepatitis C virus (HCV). These sequences may be used in a  
 CC pharmaceutical composition for the control or prevention of HCV  
 CC infection. They may be used to inhibit replication or expression of HCV  
 CC or for detecting the presence of HCV in a sample. They may be used to  
 CC inhibit HCV replication in a cell and are therefore useful in the

CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine  
CC whether it binds successfully to its target  
XX  
SQ Sequence 18 BP; 2 A; 3 C; 8 G; 3 T; 2 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUCGAG 12  
Db 1 GGGGUCUCGAG 12  
RESULT 51  
ID AAT80357 standard; DNA; 18 BP.  
XX AAT80357;  
AC  
XX 16-OCT-1997 (first entry)  
DT  
XX  
DE Oligo HCV-219, targeted to HCV mRNA position +240 to +245.  
XX  
KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KM inhibition; replication; expression; detection; chronic hepatitis;  
KM acute hepatitis; hepatocarcinoma; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..12  
FT /\*tag= a  
FT /note= "2'-Ome RNA"  
FT 13..18  
FT /\*tag= b  
FT /note= "Comprises phosphorothioate linkages"  
XX  
XX MO9639500-A2.  
PN  
XX 12-DEC-1996.  
PD  
XX  
PF 04-JUN-1996; 96WO-EP002427.  
XX  
XX 06-JUN-1995; 95US-00471968.  
PR  
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.  
PA (HYBR-) HYBRIDON INC.  
XX  
XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
PI Roberts PC, Walther DM, Wolfe JL;  
XX  
XX WPI; 1997-043122/04.  
DR  
XX  
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
XX Claim 20; Page 20; 100pp; English.  
PS  
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This sequence binds to two non-contiguous regions of the  
CC HCV genome. This sequence is anchored at position -219 to -230 and is  
CC targeted to position +240 to +245  
XX

SQ Sequence 18 BP; 3 A; 2 C; 10 G; 1 T; 2 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUCGAG 12  
Db 1 GGGGUCUCGAG 12  
RESULT 52  
ID AAT80254 standard; DNA; 18 BP.  
XX AAT80254;  
AC  
XX 15-OCT-1997 (first entry)  
DT  
XX  
DE Oligo HCV60, targeted to HCV region -3 to +3.  
XX  
KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KM inhibition; replication; expression; detection; chronic hepatitis;  
KM acute hepatitis; hepatocarcinoma; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..6  
FT /\*tag= b  
FT /note= "Phosphorothioate linkages"  
FT 7..18  
FT /\*tag= a  
FT /note= "2'Ome modified"  
XX  
XX MO9639500-A2.  
PN  
XX 12-DEC-1996.  
PD  
XX  
PF 04-JUN-1996; 96WO-EP002427.  
XX  
XX 06-JUN-1995; 95US-00471968.  
PR  
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.  
PA (HYBR-) HYBRIDON INC.  
XX  
XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
PI Roberts PC, Walther DM, Wolfe JL;  
XX  
XX WPI; 1997-043122/04.  
DR  
XX  
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
XX Claim 19; Page 31; 100pp; English.  
PS  
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine  
CC whether it binds successfully to its target  
XX  
SQ Sequence 18 BP; 2 A; 3 C; 9 G; 2 T; 2 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
 ID 7 GGGGUCGAG 18  
 Db

## RESULT 53

AAT80252  
 ID AAT80252 standard; DNA; 18 BP.

AC AAT80252;

DT 15-OCT-1997 (first entry)

DE Oligo HCV56, targeted to HCV region +10 to +15.

XX  
 KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KM inhibition; replication; expression; detection; chronic hepatitis;  
 KM acute hepatitis; hepatocarcinoma; ss.

OS Synthetic.

XX  
 FH Key Location/Qualifiers

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

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FT modified\_base

RESULT 54  
 AAT80352  
 ID AAT80352 standard; DNA; 18 BP.

AC AAT80352;

DT 16-OCT-1997 (first entry)

DE Oligo HCV-201, targeted to HCV mRNA position +15 to +20.

XX  
 KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KM inhibition; replication; expression; detection; chronic hepatitis;  
 KM acute hepatitis; hepatocarcinoma; ss.

OS Synthetic.

XX  
 FH Key Location/Qualifiers

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

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FT modified\_base

RESULT 55  
 AAT80249  
 ID AAT80249 standard; DNA; 18 BP.

AC AAT80249;

DT 16-OCT-1997 (first entry)

DE Oligo HCV-201, targeted to HCV mRNA position +15 to +20.

XX  
 KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
 KM inhibition; replication; expression; detection; chronic hepatitis;  
 KM acute hepatitis; hepatocarcinoma; ss.

OS Synthetic.

XX  
 FH Key Location/Qualifiers

FT modified\_base

FT modified\_base

FT modified\_base

FT modified\_base

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FT modified\_base

```

XX AC AAT80249;
XX DT 15-OCT-1997 (first entry)
XX DE Oligo HCV53, targeted to HCV region -9 to -4.
XX KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX KM inhibition; replication; expression; detection; chronic hepatitis;
XX KM acute hepatitis; hepatocarcinoma; ss.
XX OS Synthetic.
XX FT Key Location/Qualifiers
XX FT modified_base 1..12
XX FT /*tag= a
XX FT /note= "Optionally 2' OMe modified"
XX PN WO9639500-A2.
XX PD 12-DEC-1996.
XX PF 04-JUN-1996; 96WO-EP002427.
XX PR 06-JUN-1995; 95US-00471968.
XX PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PA (HYBR-) HYBRIDON INC.
XX PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
XX PI Roberts PC, Walther DM, Wolfe JL;
XX DR WPI; 1997-043122/04.
XX PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX PT carcinoma.
XX PS Claim 19; Page 31; 100pp; English.
XX CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX CC which are complementary to a portion of the 5' untranslated region (UTR)
XX CC of hepatitis C virus (HCV). These sequences may be used in a
XX CC pharmaceutical composition for the control or prevention of HCV
XX CC infection. They may be used to inhibit replication or expression of HCV
XX CC or for detecting the presence of HCV in a sample. They may be used to
XX CC inhibit HCV replication in a cell and are therefore useful in the
XX CC treatment of HCV infections such as chronic and acute hepatitis and
XX CC hepatocarcinoma. This oligo was used in a luciferase assay to determine
XX CC whether it binds successfully to its target
XX SQ Sequence 18 BP; 2 A; 4 C; 10 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCUCUGAG 12
Db 1 GGGGUCUCUGAG 12

```

```

XX KM inhibition; replication; expression; detection; chronic hepatitis;
XX KM acute hepatitis; hepatocarcinoma; ss.
XX OS Synthetic.
XX FT Key Location/Qualifiers
XX FT modified_base 1..12
XX FT /*tag= a
XX FT /note= "2'-OMe RNA"
XX FT modified_base 13..18
XX FT /*tag= b
XX FT /note= "Comprises phosphorothioate linkages"
XX PN WO9639500-A2.
XX PD 12-DEC-1996.
XX PF 04-JUN-1996; 96WO-EP002427.
XX PR 06-JUN-1995; 95US-00471968.
XX PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PA (HYBR-) HYBRIDON INC.
XX PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
XX PI Roberts PC, Walther DM, Wolfe JL;
XX DR WPI; 1997-043122/04.
XX PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX PT carcinoma.
XX PS Claim 20; Page 20; 100pp; English.
XX CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX CC which are complementary to a portion of the 5' untranslated region (UTR)
XX CC of hepatitis C virus (HCV). These sequences may be used in a
XX CC pharmaceutical composition for the control or prevention of HCV
XX CC infection. They may be used to inhibit replication or expression of HCV
XX CC or for detecting the presence of HCV in a sample. They may be used to
XX CC inhibit HCV replication in a cell and are therefore useful in the
XX CC treatment of HCV infections such as chronic and acute hepatitis and
XX CC hepatocarcinoma. This sequence binds to two non-contiguous regions of the
XX CC HCV genome. This sequence is anchored at position -219 to -230 and is
XX CC targeted to position +235 to +240
XX SQ Sequence 18 BP; 2 A; 5 C; 9 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCUCUGAG 12
Db 1 GGGGUCUCUGAG 12

```

```

RESULT 56
AAT80356
ID AAT80356 standard; DNA; 18 BP.
XX AAT80356;
XX
XX 16-OCT-1997 (first entry)
XX
XX Oligo HCV-216, targeted to HCV mRNA position +235 to +240.
XX
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX
XX Synthetic.

```

```

RESULT 57
AAT80251
ID AAT80251 standard; DNA; 18 BP.
XX AAT80251;
XX
XX 15-OCT-1997 (first entry)
XX
XX Oligo HCV55, targeted to HCV region +10 to +15.
XX
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX KM inhibition; replication; expression; detection; chronic hepatitis;
XX KM acute hepatitis; hepatocarcinoma; ss.
XX
XX Synthetic.

```

```

XX Key Location/Qualifiers
FH modified_base 1..12
FT /*tag= a
FT /note= "2'OME modified"
FT modified_base 13..18
FT /*tag= b
FT /note= "Phosphorothioate linkages"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOFF ) HOPFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
XX
XX Frank BL, Goodchild J, Hamlin HA, Kiluskie RE, Roberts NA;
XX Roberts PC, Walther DM, Wolfe JL;
XX
XX WPI; 1997-043122/04.
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX carcinoma.
XX
XX Claim 19; Page 31; 100pp; English.
XX
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX which are complementary to a portion of the 5' untranslated region (UTR)
XX of hepatitis C virus (HCV). These sequences may be used in a
XX pharmaceutical composition for the control or prevention of HCV
XX infection. They may be used to inhibit replication or expression of HCV
XX or for detecting the presence of HCV in a sample. They may be used to
XX inhibit HCV replication in a cell and are therefore useful in the
XX treatment of HCV infections such as chronic and acute hepatitis and
XX hepatocarcinoma. This oligo was used in a luciferase assay to determine
XX whether it binds successfully to its target
XX
XX Sequence 18 BP; 3 A; 2 C; 9 G; 2 T; 2 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCGUGAG 12
Db 1 GGGGUCGUGAG 12

```

```

FT modified_base 7..18
FT /*tag= a
FT /note= "2'-OME RNA"
XX
XX WO9639500-A2.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP002427.
XX
XX 06-JUN-1995; 95US-00471968.
XX
XX (HOFF ) HOPFMANN LA ROCHE & CO AG F.
XX (HYBR-) HYBRIDON INC.
XX
XX Frank BL, Goodchild J, Hamlin HA, Kiluskie RE, Roberts NA;
XX Roberts PC, Walther DM, Wolfe JL;
XX
XX WPI; 1997-043122/04.
XX
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX carcinoma.
XX
XX Claim 20; Page 20; 100pp; English.
XX
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX which are complementary to a portion of the 5' untranslated region (UTR)
XX of hepatitis C virus (HCV). These sequences may be used in a
XX pharmaceutical composition for the control or prevention of HCV
XX infection. They may be used to inhibit replication or expression of HCV
XX or for detecting the presence of HCV in a sample. They may be used to
XX inhibit HCV replication in a cell and are therefore useful in the
XX treatment of HCV infections such as chronic and acute hepatitis and
XX hepatocarcinoma. This sequence binds to two non-contiguous regions of the
XX HCV genome. This sequence is anchored at position -219 to -230 and is
XX targeted to position -18 to -13
XX
XX Sequence 18 BP; 4 A; 3 C; 9 G; 0 T; 2 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCGUGAG 12
Db 7 GGGGUCGUGAG 18

```

```

RESULT 58
AAT80351
ID AAT80351 standard; DNA; 18 BP.
XX
XX AAT80351;
XX
XX 16-OCT-1997 (first entry)
XX
XX Oligo HCV-197, targeted to HCV mRNA position -18 to -13.
XX
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX inhibition; replication; expression; detection; chronic hepatitis;
XX acute hepatitis; hepatocarcinoma; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..6
FT /*tag= b
FT /note= "Comprises phosphorothioate linkages"
FT

```

```

RESULT 59
AAT80259
ID AAT80259 standard; DNA; 18 BP.
XX
XX AAT80259;
XX
XX 15-OCT-1997 (first entry)
XX
XX Oligo HCV90, targeted to HCV region -1 to -6.
XX
XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX inhibition; replication; expression; detection; chronic hepatitis;
XX acute hepatitis; hepatocarcinoma; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..12
FT /*tag= a
FT /note= "2'OME modified"
FT modified_base 13..18
FT /*tag= b
FT /note= "Phosphorothioate linkages"
XX

```

PN WO9639500-A2.  
XX  
PD 12-DEC-1996.  
XX  
PF 04-JUN-1996; 96WO-EP002427.  
XX  
PR 06-JUN-1995; 95US-00471968.  
XX  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
XX (HYBR-) HYBRIDON INC.  
PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
PI Roberts PC, Walthers DM, Wolfe JL;  
DR WPI; 1997-043122/04.  
XX  
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
PS Claim 19; Page 31; 100pp; English.  
XX  
CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine  
CC whether it binds successfully to its target  
XX  
SO Sequence 18 BP; 2 A; 3 C; 10 G; 1 T; 2 U; 0 Other;  
XX  
Query Match 66.7%; Score 12; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUCUGAG 12  
Db 1 GGGGUCUCUGAG 12  
XX  
RESULT 60  
AAT80260  
ID AAT80260 standard; DNA; 18 BP.  
XX  
AC AAT80260;  
XX  
DT 15-OCT-1997 (first entry)  
XX  
DE Oligo HCV91, targeted to HCV region -1 to -6.  
XX  
KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KW inhibition; replication; expression; detection; chronic hepatitis;  
KW acute hepatitis; hepatocarcinoma; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..6  
FT /\*tag= b  
FT /note= "Phosphorothioate linkages"  
FT 7..18  
FT /\*tag= a  
FT /note= "2'-Ome modified"  
XX  
XX WO9639500-A2.  
XX  
PD 12-DEC-1996.  
XX  
PR 04-JUN-1996; 96WO-EP002427.  
XX  
PF 04-JUN-1996; 96WO-EP002427.  
XX

XX  
PR 06-JUN-1995; 95US-00471968.  
XX  
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
XX (HYBR-) HYBRIDON INC.  
PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
PI Roberts PC, Walthers DM, Wolfe JL;  
DR WPI; 1997-043122/04.  
XX  
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
PS Claim 19; Page 31; 100pp; English.  
XX  
CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine  
CC whether it binds successfully to its target  
XX  
SQ Sequence 18 BP; 2 A; 3 C; 10 G; 1 T; 2 U; 0 Other;  
XX  
Query Match 66.7%; Score 12; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUCUGAG 12  
Db 7 GGGGUCUCUGAG 18  
XX  
RESULT 61  
AAT80354  
ID AAT80354 standard; DNA; 18 BP.  
XX  
AC AAT80354;  
XX  
DT 16-OCT-1997 (first entry)  
XX  
DE Oligo HCV-209, targeted to HCV mRNA position +25 to +30.  
XX  
KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KW inhibition; replication; expression; detection; chronic hepatitis;  
KW acute hepatitis; hepatocarcinoma; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..6  
FT /\*tag= b  
FT /note= "Comprises phosphorothioate linkages"  
FT 7..18  
FT /\*tag= a  
FT /note= "2'-Ome RNA"  
XX  
XX WO9639500-A2.  
XX  
PD 12-DEC-1996.  
XX  
PR 04-JUN-1996; 96WO-EP002427.  
XX  
PF 06-JUN-1995; 95US-00471968.  
XX  
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
XX (HYBR-) HYBRIDON INC.  
XX



ID	Sequence	Location/Qualifiers
XX	Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA,	
PI	Roberts PC, Walther DM, Wolfe JL,	
XX		
DR	WPI, 1997-043122/04.	
XX		
PT	Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in	
PT	the treatment and detection of HCV infection, esp. hepatitis and hepato-	
PT	carcinoma.	
XX		
PS	Claim 20; Page 20; 100pp; English.	
CC		
CC	The sequences given in AAT80211-382 represent synthetic oligonucleotides	
CC	which are complementary to a portion of the 5' untranslated region (UTR)	
CC	of hepatitis C virus (HCV). These sequences may be used in a	
CC	pharmaceutical composition for the control or prevention of HCV	
CC	infection. They may be used to inhibit replication or expression of HCV	
CC	or for detecting the presence of HCV in a sample. They may be used to	
CC	inhibit HCV replication in a cell and are therefore useful in the	
CC	treatment of HCV infections such as chronic and acute hepatitis and	
CC	hepatocarcinoma. This sequence binds to two non-contiguous regions of the	
CC	HCV genome. This sequence is anchored at position -219 to -230 and is	
CC	targeted to position +25 to +30	
XX		
SQ	Sequence 18 BP; 1 A; 3 C; 7 G; 5 T; 2 U; 0 Other;	
	Query Match 66.7%; Score 12; DB 2; Length 18;	
	Best Local Similarity 100.0%; Pred. No. 3.4e+03;	
	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0.	
OY	1 GGGGUCUCUGAG 12	
DB	7 GGGGUCUCUGAG 18	
RESULT 62		
AAT80262		
ID	AAT80262 standard; DNA; 18 BP.	
XX		
AC	AAT80262;	
XX		
DT	15-OCT-1997 (first entry)	
XX		
DE	Oligo HCV94, targeted to HCV region +1 to +6.	
XX		
KW	Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;	
KW	inhibition; replication; expression; detection; chronic hepatitis;	
XX	acute hepatitis; hepatocarcinoma; ss.	
XX		
OS	Synthetic.	
XX		
FT	Key modified_base	Location/Qualifiers
FT		1..6
FT	modified_base	/*tag= b
FT		/note= "Phosphorochioate linkages"
FT		7..18
FT		/*tag= a
FT		/note= "2'Ome modified"
XX		
PN	WO9639500-A2.	
XX		
PD	12-DEC-1996.	
XX		
PF	04-JUN-1996; 96WO-EP002427.	
XX		
PR	06-JUN-1995; 95US-00471968.	
XX		
XX	(HOFF ) HOFFMANN LA ROCHE & CO AG F.	
PA	(HYBR-) HYBRIDON INC.	
XX		
PI	Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;	
PI	Roberts PC, Walther DM, Wolfe JL,	
XX		

```

XX WP1; 1997-043122/04.
PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT carcinoma.
XX
PS Claim 19; Page 31; 100pp; English.
XX
CC The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC which are complementary to a portion of the 5' untranslated region (UTR)
CC of hepatitis C virus (HCV). These sequences may be used in a
CC pharmaceutical composition for the control or prevention of HCV
CC infection. They may be used to inhibit replication or expression of HCV
CC or for detecting the presence of HCV in a sample. They may be used to
CC inhibit HCV replication in a cell and are therefore useful in the
CC treatment of HCV infections such as chronic and acute hepatitis and
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine
CC whether it binds successfully to its target
XX
SQ Sequence 18 BP; 2 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
XX
Query Match 66.7%; Score 12; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0
OY 1 GGGGUCUCUGAG 12
   |||||
   |||||
DB 7 GGGGTCCTGGAG 18
XX
RESULT 63
ABS65834
ID ABS65834 standard; DNA; 18 BP.
XX
AC ABS65834;
XX
DT 15-NOV-2002 (first entry)
XX
DE Inhibitory oligonucleotide specific for hepatitis C virus #40.
XX
KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
KW non-B hepatitis; acute hepatitis; chronic hepatitis;
KW hepatocellular carcinoma; virulence; cytostatic; antitense therapy;
KW gene therapy; ss; DNA-RNA hybrid.
XX
OS Synthetic.
XX
FN US2002081577-A1.
XX
PD 27-JUN-2002.
XX
PE 02-JUL-1997; 97US-00887505.
XX
PR 06-JUN-1995; 95US-00471968.
XX
PR 02-JUL-1996; 96US-0021104P.
XX
PA (KILK/) KILKUSKIE R. L.
PA (FRANK/) FRANK B. L.
PA (GOOD/) GOODCHILD J.
PA (WOLFE/) WOLFE J. L.
PA (ROBE/) ROBERTS P. C.
PA (HAML/) HAMLIN H. A.
PA (ROBE/) ROBERTS N. A.
PA (WALT/) WALTHER D. M.
XX
F1 Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,
P1 Hamlin HA, Roberts NA, Walther DM;
XX
XX WP1; 2002-537132/57.
XX
PT Synthetic oligonucleotides complementary to a portion of the 5'
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and
PT treating HCV infections and hepatocellular carcinoma.
XX

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XX PS Claim 22; Page 10; 74pp; English.

XX CC The invention describes synthetic oligonucleotides complementary to a

XX CC portion of the 5' untranslated region of hepatitis C virus. The

XX CC oligonucleotides may be used in methods for controlling, preventing, and

XX CC treating hepatitis C virus infection, in antisense technology and gene

XX CC therapy, and of detecting the presence of hepatitis C virus in a sample.

XX CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded

XX CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non

XX CC -B, acute and chronic hepatitis, and has been associated with

XX CC hepatocellular carcinoma. The invention describes methods and kits for

XX CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic

XX CC acid and protein, and for treating HCV infections. This sequence

XX CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting

XX CC HCV replication and expression of HCV

XX SQ Sequence 18 BP; 2 A; 4 C; 10 G; 0 T; 2 U; 0 Other;

XX Query Match 66.7%; Score 12; DB 6; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTUGAG 12

DB 7 GGGGUCCTUGAG 18

RESULT 64

AB565838

ID AB565838 standard; DNA; 18 BP.

XX AC

XX AB565838;

XX DT 15-NOV-2002 (first entry)

XX DE Inhibitory oligonucleotide specific for hepatitis C virus #4.

XX KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;

XX KW non-B hepatitis; acute hepatitis; chronic hepatitis;

XX KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;

XX KW gene therapy; ss; DNA-RNA hybrid.

XX OS Synthetic.

XX PN US2002081577-A1.

XX PD 27-JUN-2002.

XX PF 02-JUL-1997; 97US-00887505.

XX PR 06-JUN-1995; 95US-00471968.

XX PR 02-JUL-1996; 96US-0021104P.

XX PA (KILK/) KILKUSKIE R L.

XX PA (FRAN/) FRANK B L.

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XX PA (ROBE/) ROBERTS P C.

XX PA (HAML/) HAMLIN H A.

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XX PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;

XX PI Hamlin HA, Roberts NA, Walther DM;

XX DR WPI; 2002-537132/57.

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XX CC -B, acute and chronic hepatitis, and has been associated with

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XX CC acid and protein, and for treating HCV infections. This sequence

XX CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting

XX CC HCV replication and expression of HCV

XX SQ Sequence 18 BP; 2 A; 3 C; 9 G; 2 T; 2 U; 0 Other;

XX Query Match 66.7%; Score 12; DB 6; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTUGAG 12

DB 7 GGGGUCCTUGAG 18

RESULT 65

AB565840

ID AB565840 standard; DNA; 18 BP.

XX AC

XX AB565840;

XX DT 15-NOV-2002 (first entry)

XX DE Inhibitory oligonucleotide specific for hepatitis C virus #46.

XX KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;

XX KW non-B hepatitis; acute hepatitis; chronic hepatitis;

XX KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;

XX KW gene therapy; ss; DNA-RNA hybrid.

XX OS Synthetic.

XX PN US2002081577-A1.

XX PD 27-JUN-2002.

XX PF 02-JUL-1997; 97US-00887505.

XX PR 06-JUN-1995; 95US-00471968.

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XX DR WPI; 2002-537132/57.

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XX PS Claim 22; Page 10; 74pp; English.

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CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
CC HCV replication and expression of HCV

SO Sequence 18 BP; 1 A; 4 C; 9 G; 2 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCGCGAG 12  
Db 7 GGGGUCGCGAG 18

RESULT 66  
ABSS5837  
ID ABS65837 standard; DNA; 18 BP.  
AC ABS65837;  
XX  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Inhibitory oligonucleotide specific for hepatitis C virus #43.  
XX  
KM Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
KM non-B hepatitis; acute hepatitis; chronic hepatitis;  
KM hepatocellular carcinoma; viraemia; cytostatic; antisense therapy;  
KM gene therapy; ss; DNA-RNA hybrid.  
XX  
OS Synthetic.  
XX  
PN US2002081577-A1.  
PD 27-JUN-2002.  
XX  
PF 02-JUL-1997; 97US-00887505.  
XX  
PR 06-JUN-1995; 95US-00471968.  
PR 02-JUL-1996; 96US-0021104P.  
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PA (KILK/) KILKUSKIE R L.  
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PA (ROBE/) ROBERTS P C.  
PA (HAML/) HAMLIN H A.  
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PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
PI Hamlin HA, Roberts NA, Walther DM;  
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DR WPI; 2002-537132/57.  
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PT Synthetic oligonucleotides complementary to a portion of the 5'  
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CC The invention describes synthetic oligonucleotides complementary to a  
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CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
CC HCV replication and expression of HCV

SO Sequence 18 BP; 2 A; 3 C; 9 G; 2 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCGCGAG 12  
Db 1 GGGGUCGCGAG 12

RESULT 67  
ABSS5847  
ID ABS65847 standard; DNA; 18 BP.  
AC ABS65847;  
XX  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Inhibitory oligonucleotide specific for hepatitis C virus #53.  
XX  
KM Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
KM non-B hepatitis; acute hepatitis; chronic hepatitis;  
KM hepatocellular carcinoma; viraemia; cytostatic; antisense therapy;  
KM gene therapy; ss; DNA-RNA hybrid.  
XX  
OS Synthetic.  
XX  
PN US2002081577-A1.  
PD 27-JUN-2002.  
XX  
PF 02-JUL-1997; 97US-00887505.  
XX  
PR 06-JUN-1995; 95US-00471968.  
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PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
PI Hamlin HA, Roberts NA, Walther DM;  
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DR WPI; 2002-537132/57.  
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PT Synthetic oligonucleotides complementary to a portion of the 5'  
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
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CC The invention describes synthetic oligonucleotides complementary to a  
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CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
CC HCV replication and expression of HCV  
XX

SO Sequence 18 BP, 2 A, 3 C, 8 G, 3 T, 2 U, 0 Other;  
Query Match 66.7%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3,4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
Db 1 GGGGUCCUGAG 12

RESULT 68  
ABS65941  
ID ABS65941 standard; DNA, 18 BP.  
XX  
AC ABS65941;  
XX  
DT 15-NOV-2002 (first entry)  
XX

DE Inhibitory oligonucleotide specific for hepatitis C virus #147.  
XX  
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
KM non-B hepatitis; acute hepatitis; chronic hepatitis;  
KM hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
KM gene therapy; ss; DNA-RNA hybrid.  
XX  
OS Synthetic.  
XX  
PN US2002081577-A1.  
XX  
PD 27-JUN-2002.  
XX  
PF 02-JUL-1997; 97US-00887505.  
XX  
PR 06-JUN-1995; 95US-00471968.  
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PR 02-JUL-1996; 96US-0021104P.  
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XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,  
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XX WPI; 2002-537132/57.  
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PT Synthetic oligonucleotides complementary to a portion of the 5'  
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
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XX  
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PS Claim 23; Page 7; 74pp; English.  
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CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
CC HCV replication and expression of HCV  
XX

SO Sequence 18 BP, 3 A, 2 C, 10 G, 1 T, 2 U, 0 Other;  
Query Match 66.7%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3,4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
Db 1 GGGGUCCUGAG 12

RESULT 69  
ABS65845  
ID ABS65845 standard; DNA, 18 BP.  
XX  
AC ABS65845;  
XX  
DT 15-NOV-2002 (first entry)  
XX

DE Inhibitory oligonucleotide specific for hepatitis C virus #51.  
XX  
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
KM non-B hepatitis; acute hepatitis; chronic hepatitis;  
KM hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
KM gene therapy; ss; DNA-RNA hybrid.  
XX  
OS Synthetic.  
XX  
PN US2002081577-A1.  
XX  
PD 27-JUN-2002.  
XX  
PF 02-JUL-1997; 97US-00887505.  
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PR 06-JUN-1995; 95US-00471968.  
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PR 02-JUL-1996; 96US-0021104P.  
XX

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PA (ROBE/) ROBERTS N A.  
PA (WALT/) WALTHER D M.  
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XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,  
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XX WPI; 2002-537132/57.  
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CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
CC HCV replication and expression of HCV

XX Sequence 18 BP; 2 A; 4 C; 8 G; 2 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
1 GGGGUCGAG 12  
Db 1 GGGGUCGAG 12

RESULT 70

AB865839  
ID AB865839 standard; DNA; 18 BP.

XX  
AC AB865839;

DT 15-NOV-2002 (first entry)

DE Inhibitory oligonucleotide specific for hepatitis C virus #45.

XX Hepatitis C virus; HCV, hepatocyte infection; non-A hepatitis;  
KM non-B hepatitis; acute hepatitis; chronic hepatitis;  
KM hepatocellular carcinoma; virolicide; cytostatic; antisense therapy;  
KM gene therapy; ss; DNA-RNA hybrid.

XX Synthetic.

PN US2002081577-A1.

PD 27-JUN-2002.

PF 02-JUL-1997; 97US-00887505.

PR 06-JUN-1995; 95US-00471968.

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PI Hamlin HA, Roberts NA, Walther DM;

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XX Sequence 18 BP; 1 A; 4 C; 9 G; 2 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
1 GGGGUCGAG 12  
Db 1 GGGGUCGAG 12

RESULT 71

AB865936  
ID AB865936 standard; DNA; 18 BP.

XX  
AC AB865936;

DT 15-NOV-2002 (first entry)

DE Inhibitory oligonucleotide specific for hepatitis C virus #142.

XX Hepatitis C virus; HCV, hepatocyte infection; non-A hepatitis;  
KM non-B hepatitis; acute hepatitis; chronic hepatitis;  
KM hepatocellular carcinoma; virolicide; cytostatic; antisense therapy;  
KM gene therapy; ss; DNA-RNA hybrid.

XX Synthetic.

PN US2002081577-A1.

PD 27-JUN-2002.

PF 02-JUL-1997; 97US-00887505.

PR 06-JUN-1995; 95US-00471968.

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PI Hamlin HA, Roberts NA, Walther DM;

DR WPI; 2002-537132/57.

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XX Sequence 18 BP; 2 A; 2 C; 9 G; 3 T; 2 U; 0 Other;  
SQ  
Query Match 66.7%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGUCUCGAG 12  
Db 7 GGGGUCUCGAG 18  
RESULT 72  
ID ABS65835  
AB 65835 standard; DNA; 18 BP.  
AC ABS65835;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Inhibitory oligonucleotide specific for hepatitis C virus #41.  
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
XX non-B hepatitis; acute hepatitis; chronic hepatitis;  
XX hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
XX gene therapy; ss; DNA-RNA hybrid.  
XX  
XX Synthetic.  
XX OS  
XX US2002081577-A1.  
XX PN  
XX 27-JUN-2002.  
XX PD  
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XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC,  
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XX HCV replication and expression of HCV  
XX  
XX Sequence 18 BP; 3 A; 2 C; 9 G; 2 T; 2 U; 0 Other;

XX Query Match 66.7%; Score 12; DB 6; Length 18;  
SQ Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGUCUCGAG 12  
Db 1 GGGGUCUCGAG 12  
RESULT 73  
ID ABS65846  
AB 65846 standard; DNA; 18 BP.  
AC ABS65846;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Inhibitory oligonucleotide specific for hepatitis C virus #52.  
XX  
XX Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
XX non-B hepatitis; acute hepatitis; chronic hepatitis;  
XX hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
XX gene therapy; ss.  
XX  
XX Synthetic.  
XX OS  
XX US2002081577-A1.  
XX PN  
XX 27-JUN-2002.  
XX PD  
XX 02-JUL-1997; 97US-00887505.  
XX PF  
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XX PR 02-JUL-1996; 96US-0021104P.  
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XX Hamlin HA, Roberts NA, Walther DM;  
XX WPI; 2002-537132/57.  
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XX untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
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XX  
XX The invention describes synthetic oligonucleotides complementary to a  
XX portion of the 5' untranslated region of hepatitis C virus. The  
XX oligonucleotides may be used in methods for controlling, preventing, and  
XX treating hepatitis C virus infection, in antisense technology and gene  
XX therapy, and of detecting the presence of hepatitis C virus in a sample.  
XX Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
XX RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
XX -B, acute and chronic hepatitis, and has been associated with  
XX hepatocellular carcinoma. The invention describes methods and kits for  
XX inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
XX acid and protein, and for treating HCV infections. This sequence  
XX represents a synthetic oligonucleotide used for inhibiting HCV  
XX replication and expression of HCV  
XX  
XX Query Match 66.7%; Score 12; DB 6; Length 18;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
Db 7 GGGGUCUGAG 18

## RESULT 74

AB65935  
ID ABS65935 standard; DNA, 18 BP.

AC ABS65935;

DT 15-NOV-2002 (first entry)

DE Inhibitory oligonucleotide specific for hepatitis C virus #141.

KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;

KW non-B hepatitis; acute hepatitis; chronic hepatitis;

KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;

XX gene therapy; ss; DNA-RNA hybrid.

XX Synthetic.

XX US2002081577-A1.

XX 27-JUN-2002.

XX 02-JUL-1997; 97US-00887505.

XX 06-JUN-1995; 95US-00471968.

XX 02-JUL-1996; 96US-0021104P.

XX (KILK/) KILKUSKIE R L.

XX (FRAN/) FRANK B L.

XX (GOOD/) GOODCHILD J.

XX (WOLF/) WOLFE J L.

XX (ROBE/) ROBERTS P C.

XX (HAML/) HAMLIN H A.

XX (ROBE/) ROBERTS N A.

XX (WALT/) WALTHER D M.

XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;

XX Hamlin HA, Roberts NA, Walther DM;

XX WPI; 2002-537132/57.

XX Synthetic oligonucleotides complementary to a portion of the 5'

XX untranslated region of hepatitis C virus (HCV), useful for diagnosing and

XX treating HCV infections and hepatocellular carcinoma.

XX Claim 23; Page 7; 74pp; English.

XX The invention describes synthetic oligonucleotides complementary to a

XX portion of the 5' untranslated region of hepatitis C virus. The

XX oligonucleotides may be used in methods for controlling, preventing, and

XX treating hepatitis C virus infection, in antisense technology and gene

XX therapy, and of detecting the presence of hepatitis C virus in a sample.

XX Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded

XX RNA virus which infects hepatocytes. HCV is the major cause of non-A, non

XX -B, acute and chronic hepatitis, and has been associated with

XX hepatocellular carcinoma. The invention describes methods and kits for

XX inhibiting replication of HCV, inhibiting the expression of HCV nucleic

XX acid and protein, and for treating HCV infections. This sequence

XX represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting

XX HCV replication and expression of HCV

XX Sequence 18 BP; 4 A; 3 C; 9 G; 0 T; 2 U; 0 Other;

XX Query Match 66.7%; Score 12; DB 6; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12

Db 7 GGGGUCUGAG 18

## RESULT 75

AB65937  
ID ABS65937 standard; DNA, 18 BP.

AC ABS65937;

DT 15-NOV-2002 (first entry)

DE Inhibitory oligonucleotide specific for hepatitis C virus #143.

KW Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;

KW non-B hepatitis; acute hepatitis; chronic hepatitis;

KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;

XX gene therapy; ss; DNA-RNA hybrid.

XX Synthetic.

XX US2002081577-A1.

XX 27-JUN-2002.

XX 02-JUL-1997; 97US-00887505.

XX 06-JUN-1995; 95US-00471968.

XX 02-JUL-1996; 96US-0021104P.

XX (KILK/) KILKUSKIE R L.

XX (FRAN/) FRANK B L.

XX (GOOD/) GOODCHILD J.

XX (WOLF/) WOLFE J L.

XX (ROBE/) ROBERTS P C.

XX (HAML/) HAMLIN H A.

XX (ROBE/) ROBERTS N A.

XX (WALT/) WALTHER D M.

XX Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;

XX Hamlin HA, Roberts NA, Walther DM;

XX WPI; 2002-537132/57.

XX Synthetic oligonucleotides complementary to a portion of the 5'

XX untranslated region of hepatitis C virus (HCV), useful for diagnosing and

XX treating HCV infections and hepatocellular carcinoma.

XX Claim 23; Page 7; 74pp; English.

XX The invention describes synthetic oligonucleotides complementary to a

XX portion of the 5' untranslated region of hepatitis C virus. The

XX oligonucleotides may be used in methods for controlling, preventing, and

XX treating hepatitis C virus infection, in antisense technology and gene

XX therapy, and of detecting the presence of hepatitis C virus in a sample.

XX Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded

XX RNA virus which infects hepatocytes. HCV is the major cause of non-A, non

XX -B, acute and chronic hepatitis, and has been associated with

XX hepatocellular carcinoma. The invention describes methods and kits for

XX inhibiting replication of HCV, inhibiting the expression of HCV nucleic

XX acid and protein, and for treating HCV infections. This sequence

XX represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting

XX HCV replication and expression of HCV

XX Sequence 18 BP; 2 A; 2 C; 9 G; 3 T; 2 U; 0 Other;

XX Query Match 66.7%; Score 12; DB 6; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 3.4e+03;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 GGGGUCUGAG 12

Db 7 GGGGUCUGGAG 18

```
RESULT 76
ABS65938
ID ABS65938 standard; DNA; 18 BP.
XX
AC ABS65938;
XX
DT 15-NOV-2002 (first entry)
XX
DE Inhibitory oligonucleotide specific for hepatitis C virus #144.
XX
KW Hepatitis C virus; HCV, hepatocyte infection; non-A hepatitis;
KM non-B hepatitis; acute hepatitis; chronic hepatitis;
KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;
KM gene therapy; ss; DNA-RNA hybrid.
XX
OS Synthetic.
XX
PN US2002081577-A1.
XX
PD 27-JUN-2002.
XX
PF 02-JUL-1997; 97US-00887505.
XX
PR 06-JUN-1995; 95US-00471968.
PR 02-JUL-1996; 96US-0021104P.
XX
PA (KILK/) KILKUSKIE R L.
PA (FRAN/) FRANK B L.
PA (GOOD/) GOODCHILD J.
PA (WOLF/) WOLFE J L.
PA (ROBE/) ROBERTS P C.
PA (HAML/) HAMLIN H A.
PA (ROBE/) ROBERTS N A.
PA (WALT/) WALTHER D M.
XX
PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
PI Hamlin HA, Roberts NA, Walther DM;
XX
DR WPI; 2002-537132/57.
XX
PT Synthetic oligonucleotides complementary to a portion of the 5'
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and
PT treating HCV infections and hepatocellular carcinoma.
XX
PS Claim 23; Page 7; 74pp; English.
XX
CC The invention describes synthetic oligonucleotides complementary to a
CC portion of the 5' untranslated region of hepatitis C virus. The
CC oligonucleotides may be used in methods for controlling, preventing, and
CC treating hepatitis C virus infection, in antisense technology and gene
CC therapy, and of detecting the presence of hepatitis C virus in a sample.
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
CC -B, acute and chronic hepatitis, and has been associated with
CC hepatocellular carcinoma. The invention describes methods and kits for
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic
CC acid and protein, and for treating HCV infections. This sequence
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting
CC HCV replication and expression of HCV
XX
SQ Sequence 18 BP; 1 A; 3 C; 7 G; 5 T; 2 U; 0 Other;
Query Match 66.7%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 77
ABS65848
ID ABS65848 standard; DNA; 18 BP.
XX
AC ABS65848;
XX
DT 15-NOV-2002 (first entry)
XX
DE Inhibitory oligonucleotide specific for hepatitis C virus #54.
XX
KW Hepatitis C virus; HCV, hepatocyte infection; non-A hepatitis;
KM non-B hepatitis; acute hepatitis; chronic hepatitis;
KW hepatocellular carcinoma; virucide; cytostatic; antisense therapy;
KM gene therapy; ss; DNA-RNA hybrid.
XX
OS Synthetic.
XX
PN US2002081577-A1.
XX
PD 27-JUN-2002.
XX
PF 02-JUL-1997; 97US-00887505.
XX
PR 06-JUN-1995; 95US-00471968.
PR 02-JUL-1996; 96US-0021104P.
XX
PA (KILK/) KILKUSKIE R L.
PA (FRAN/) FRANK B L.
PA (GOOD/) GOODCHILD J.
PA (WOLF/) WOLFE J L.
PA (ROBE/) ROBERTS P C.
PA (HAML/) HAMLIN H A.
PA (ROBE/) ROBERTS N A.
PA (WALT/) WALTHER D M.
XX
PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
PI Hamlin HA, Roberts NA, Walther DM;
XX
DR WPI; 2002-537132/57.
XX
PT Synthetic oligonucleotides complementary to a portion of the 5'
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and
PT treating HCV infections and hepatocellular carcinoma.
XX
PS Claim 22; Page 11; 74pp; English.
XX
CC The invention describes synthetic oligonucleotides complementary to a
CC portion of the 5' untranslated region of hepatitis C virus. The
CC oligonucleotides may be used in methods for controlling, preventing, and
CC treating hepatitis C virus infection, in antisense technology and gene
CC therapy, and of detecting the presence of hepatitis C virus in a sample.
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
CC -B, acute and chronic hepatitis, and has been associated with
CC hepatocellular carcinoma. The invention describes methods and kits for
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic
CC acid and protein, and for treating HCV infections. This sequence
CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting
CC HCV replication and expression of HCV
XX
SQ Sequence 18 BP; 2 A; 3 C; 8 G; 3 T; 2 U; 0 Other;
Query Match 66.7%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```

RESULT 79
ABSS65939
ID      ABS65939 standard; DNA; 18 BP.
XX      AC
XX      ABS65939;
XX      DT
XX      15-NOV-2002 (first entry)
XX      DE
XX      Inhibitory oligonucleotide specific for hepatitis C virus #145.
XX      KW
XX      Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
XX      non-B hepatitis; acute hepatitis; chronic hepatitis;
XX      hepatocellular carcinoma; virinide; cyrostatic; antisense therapy;
XX      gene therapy; ss; DNA-RNA hybrid.
XX      OS
XX      Synthetic.
XX      PN
XX      US2002081577-A1.
XX      PD
XX      27-JUN-2002.
XX      PF
XX      02-JUL-1997; 97US-00887505.
XX      PR
XX      06-JUN-1995; 95US-00471968.
XX      PR
XX      02-JUL-1996; 96US-0021104P.
XX      PA
XX      (KILK/) KILKUSKIE R L.
XX      PA
XX      (FRAN/) FRANK B L.
XX      PA
XX      (GOOD/) GOODCHILD J.
XX      PA
XX      (MOLE/) MOLEFE J L.
XX      PA
XX      (ROBE/) ROBERTS P C.
XX      PA
XX      (HAML/) HAMLIN H A.
XX      PA
XX      (ROBE/) ROBERTS N A.
XX      PA
XX      (WALT/) WALTHER D M.
XX      PI
XX      Kiljuetkie RL, Frank BL, Goodchild J, Wole JL, Roberts PC;
XX      Hamlin HA, Roberts NA, Walthier DM;
XX      DR
XX      WPI; 2002-537132/57.
XX      PT
XX      Synthetic oligonucleotides complementary to a portion of the 5'
XX      untranslated region of hepatitis C virus (HCV), useful for diagnosing and
XX      treating HCV infections and hepatocellular carcinoma.
XX      PS
XX      Claim 23; Page 7; 74pp; English.
XX      CC
XX      The invention describes synthetic oligonucleotides complementary to a
XX      portion of the 5' untranslated region of hepatitis C virus. The
XX      oligonucleotides may be used in methods for controlling, preventing, and
XX      treating hepatitis C virus infection, in antisense technology and gene
XX      therapy, and of detecting the presence of hepatitis C virus in a sample.
XX      Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
XX      RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
XX      -B, acute and chronic hepatitis, and has been associated with
XX      hepatocellular carcinoma. The invention describes methods and kits for
XX      inhibiting replication of HCV, inhibiting the expression of HCV nucleic
XX      acid and protein, and for treating HCV infections. This sequence
XX      CC
XX      represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting
XX      HCV replication and expression of HCV
XX      SQ
XX      Sequence 18 BP; 2 A; 3 C; 10 G; 1 T; 2 U; 0 Other;
OY      Query Match      66.7%; Score 12; DB 6; Length 18;
DB      Best Local Similarity 100.0%; Pred. No. 3.4e+03;
        Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0
        1 GGGGUCUCUGAG 12
        1 GGGGUCUCUGAG 12
ABSS65836

```

ID	AB865836 standard; DNA; 18 BP.
XX	
AC	AB865836;
XX	
DT	15-NOV-2002 (first entry)
DE	Inhibitory oligonucleotide specific for hepatitis C virus #42.
KX	Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
KW	non-B hepatitis; acute hepatitis; chronic hepatitis;
KM	hepatocellular carcinoma; viraemia; cytostatic; antisense therapy;
KV	gene therapy; ss; DNA-RNA hybrid.
XX	
OS	Synthetic.
PN	US2002081577-A1.
PD	27-JUN-2002.
PF	02-JUL-1997; 97US-00887505.
PR	06-JUN-1995; 95US-00471968.
PR	02-JUL-1996; 96US-0021104P.
PA	(KILK/) KILKSKIE R L.
PA	(FRAN/) FRANK B L.
PA	(GOOD/) GOODCHILD J.
PA	(WOLF/) WOLFE J L.
PA	(ROBE/) ROBERTS P C.
PA	(HAML/) HAMLIN H A.
PA	(ROBE/) ROBERTS N A.
PA	(WALT/) WALTHER D M.
PI	KilKuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
PI	Hamlin HA, Roberts NA, Walther DM;
DR	WPI; 2002-537132/57.
PT	Synthetic oligonucleotides complementary to a portion of the 5'
PT	untranslated region of hepatitis C virus (HCV), useful for diagnosing and
PT	treating HCV infections and hepatocellular carcinoma.
XX	
PS	Claim 22; Page 10; 74pp; English.
CC	The invention describes synthetic oligonucleotides complementary to a
CC	portion of the 5' untranslated region of hepatitis C virus. The
CC	oligonucleotides may be used in methods for controlling, preventing, and
CC	treating hepatitis C virus infection. In antisense technology and gene
CC	therapy, and of detecting the presence of hepatitis C virus in a sample,
CC	Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
CC	RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
CC	-B, acute and chronic hepatitis, and has been associated with
CC	hepatocellular carcinoma. The invention describes methods and kits for
CC	inhibiting replication of HCV, inhibiting the expression of HCV nucleic
CC	acid and protein, and for treating HCV infections. This sequence
CC	represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting
CC	HCV replication and expression of HCV
SO	Sequence 18 BP; 3 A; 2 C; 9 G; 2 T; 2 U; 0 Other;
QY	Query Match 66.7%; Score 12; DB 6; Length 18;
Db	Beat Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY	1 GGAGUCCUGGAG 12       
DB	7 GGAGUCCUGGAG 18
RESULT 80	
AB865843	
ID	AB865843 standard; DNA; 18 BP.
XX	

```

AC  ABS65843;
XX
XX  15-NOV-2002 (first entry)
DE  Inhibitory oligonucleotide specific for hepatitis C virus #49.
XX
XX  Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
XX  non-B hepatitis; acute hepatitis; chronic hepatitis;
XX  hepatocellular carcinoma; virucide; cytostatic; antisense therapy;
XX  gene therapy; ss; DNA-RNA hybrid.
XX
XX  Synthetic.
XX
XX  US2002081577-A1.
XX
XX  27-JUN-2002.
XX
XX  02-JUL-1997; 97US-00887505.
XX
XX  06-JUN-1995; 95US-00471968.
XX  02-JUL-1996; 96US-0021104P.
XX
XX  (KILK/) KILKUSKIE R L.
XX  (FRAN/) FRANK B L.
XX  (GOOD/) GOODCHILD J.
XX  (WOLF/) WOLFE J L.
XX  (ROBE/) ROBERTS P C.
XX  (HAML/) HAMLIN H A.
XX  (ROBE/) ROBERTS N A.
XX  (WALT/) WALTHER D M.
XX
XX  Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
XX  Hamlin HA, Roberts NA, Walther DM;
XX
XX  WPI; 2002-537132/57.
XX
XX  Synthetic oligonucleotides complementary to a portion of the 5'
XX  untranslated region of hepatitis C virus (HCV), useful for diagnosing and
XX  treating HCV infections and hepatocellular carcinoma.
XX
XX  Claim 22; Page 11; 74pp; English.
XX
XX  The invention describes synthetic oligonucleotides complementary to a
XX  portion of the 5' untranslated region of hepatitis C virus. The
XX  oligonucleotides may be used in methods for controlling, preventing, and
XX  treating hepatitis C virus infection, in antisense technology and gene
XX  therapy, and of detecting the presence of hepatitis C virus in a sample.
XX  Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
XX  RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
XX  -B, acute and chronic hepatitis. HCV is the major cause of non-A, non
XX  hepatocellular carcinoma. The invention describes methods and kits for
XX  inhibiting replication of HCV, inhibiting the expression of HCV nucleic
XX  acid and protein, and for treating HCV infections. This sequence
XX  represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting
XX  HCV replication and expression of HCV
XX
XX  Sequence 18 BP; 2 A; 3 C; 10 G; 1 T; 2 U; 0 Other;
XX
XX  Query Match 66.7%; Score 12; DB 6; Length 18;
XX  Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  1 GGGGUCUCUGAG 12
XX  |||||
XX  1 GGGGUCUCUGAG 12
Db

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```

DT  15-NOV-2002 (first entry)
XX
XX  Inhibitory oligonucleotide specific for hepatitis C virus #50.
DE
XX
XX  Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;
XX  non-B hepatitis; acute hepatitis; chronic hepatitis;
XX  hepatocellular carcinoma; virucide; cytostatic; antisense therapy;
XX  gene therapy; ss; DNA-RNA hybrid.
XX
XX  Synthetic.
XX
XX  US2002081577-A1.
XX
XX  27-JUN-2002.
XX
XX  02-JUL-1997; 97US-00887505.
XX
XX  06-JUN-1995; 95US-00471968.
XX  02-JUL-1996; 96US-0021104P.
XX
XX  (KILK/) KILKUSKIE R L.
XX  (FRAN/) FRANK B L.
XX  (GOOD/) GOODCHILD J.
XX  (WOLF/) WOLFE J L.
XX  (ROBE/) ROBERTS P C.
XX  (HAML/) HAMLIN H A.
XX  (ROBE/) ROBERTS N A.
XX  (WALT/) WALTHER D M.
XX
XX  Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;
XX  Hamlin HA, Roberts NA, Walther DM;
XX
XX  WPI; 2002-537132/57.
XX
XX  Synthetic oligonucleotides complementary to a portion of the 5'
XX  untranslated region of hepatitis C virus (HCV), useful for diagnosing and
XX  treating HCV infections and hepatocellular carcinoma.
XX
XX  Claim 22; Page 11; 74pp; English.
XX
XX  The invention describes synthetic oligonucleotides complementary to a
XX  portion of the 5' untranslated region of hepatitis C virus. The
XX  oligonucleotides may be used in methods for controlling, preventing, and
XX  treating hepatitis C virus infection, in antisense technology and gene
XX  therapy, and of detecting the presence of hepatitis C virus in a sample.
XX  Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded
XX  RNA virus which infects hepatocytes. HCV is the major cause of non-A, non
XX  -B, acute and chronic hepatitis. HCV is the major cause of non-A, non
XX  hepatocellular carcinoma. The invention describes methods and kits for
XX  inhibiting replication of HCV, inhibiting the expression of HCV nucleic
XX  acid and protein, and for treating HCV infections. This sequence
XX  represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting
XX  HCV replication and expression of HCV
XX
XX  Sequence 18 BP; 2 A; 3 C; 10 G; 1 T; 2 U; 0 Other;
XX
XX  Query Match 66.7%; Score 12; DB 6; Length 18;
XX  Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  1 GGGGUCUCUGAG 12
XX  |||||
XX  7 GGGGUCUCUGAG 18
Db

```

```

RESULT 81
ABS65844
ID  ABS65844 standard; DNA; 18 BP.
XX
XX  ABS65844;
XX
XX

```

```

RESULT 82
ABS65833
ID  ABS65833 standard; DNA; 18 BP.
XX
XX  ABS65833;
XX
XX  15-NOV-2002 (first entry)
XX
XX

```

DE Inhibitory oligonucleotide specific for hepatitis C virus #39.  
 XX Hepatitis C virus; HCV, hepatocyte infection; non-A hepatitis;  
 KM non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KM hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KM gene therapy; ss; DNA-RNA hybrid.  
 XX Synthetic.  
 OS  
 XX US2002081577-A1.  
 PN  
 XX 27-JUN-2002.  
 PD  
 XX 02-JUL-1997; 97US-00887505.  
 PF  
 XX 06-JUN-1995; 95US-00471968.  
 PR  
 XX 02-JUL-1996; 96US-0021104P.  
 XX  
 PA (KILK/) KILKUSKIE R L.  
 PA (FRAN/) FRANK B L.  
 PA (GOOD/) GOODCHILD J.  
 PA (WOLF/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.  
 PA (HAML/) HAMLIN H A.  
 PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.  
 XX  
 PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
 PI Hamlin HA, Roberts NA, Walther DM;  
 XX  
 DR WPI; 2002-537132/57.  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.  
 XX  
 PS Claim 22; Page 10; 74pp; English.  
 XX  
 CC The invention describes synthetic oligonucleotides complementary to a  
 CC portion of the 5' untranslated region of hepatitis C virus. The  
 CC oligonucleotides may be used in methods for controlling, preventing, and  
 CC treating hepatitis C virus infection, in antisense technology and gene  
 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
 CC HCV replication and expression of HCV  
 XX  
 SQ Sequence 18 BP; 2 A; 4 C; 10 G; 0 T; 2 U; 0 Other;  
 XX  
 QY Query Match 66.7%; Score 12; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCUCGAG 12  
 Db 1 GGGGUCUCGAG 12  
 XX  
 RESULT 83  
 ID A865940 standard; DNA; 18 BP.  
 XX A865940;  
 AC A865940;  
 XX  
 DT 15-NOV-2002 (first entry)  
 XX  
 DE Inhibitory oligonucleotide specific for hepatitis C virus #146.  
 XX

KM Hepatitis C virus; HCV, hepatocyte infection; non-A hepatitis;  
 KM non-B hepatitis; acute hepatitis; chronic hepatitis;  
 KM hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
 KM gene therapy; ss; DNA-RNA hybrid.  
 XX Synthetic.  
 OS  
 XX US2002081577-A1.  
 PN  
 XX 27-JUN-2002.  
 PD  
 XX 02-JUL-1997; 97US-00887505.  
 PF  
 XX 06-JUN-1995; 95US-00471968.  
 PR  
 XX 02-JUL-1996; 96US-0021104P.  
 XX  
 PA (KILK/) KILKUSKIE R L.  
 PA (FRAN/) FRANK B L.  
 PA (GOOD/) GOODCHILD J.  
 PA (WOLF/) WOLFE J L.  
 PA (ROBE/) ROBERTS P C.  
 PA (HAML/) HAMLIN H A.  
 PA (ROBE/) ROBERTS N A.  
 PA (WALT/) WALTHER D M.  
 XX  
 PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
 PI Hamlin HA, Roberts NA, Walther DM;  
 XX  
 DR WPI; 2002-537132/57.  
 XX  
 PT Synthetic oligonucleotides complementary to a portion of the 5'  
 PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
 PT treating HCV infections and hepatocellular carcinoma.  
 XX  
 PS Claim 23; Page 7; 74pp; English.  
 XX  
 CC The invention describes synthetic oligonucleotides complementary to a  
 CC portion of the 5' untranslated region of hepatitis C virus. The  
 CC oligonucleotides may be used in methods for controlling, preventing, and  
 CC treating hepatitis C virus infection, in antisense technology and gene  
 CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
 CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
 CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
 CC -B, acute and chronic hepatitis, and has been associated with  
 CC hepatocellular carcinoma. The invention describes methods and kits for  
 CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
 CC acid and protein, and for treating HCV infections. This sequence  
 CC represents a synthetic DNA-RNA hybrid oligonucleotide used for inhibiting  
 CC HCV replication and expression of HCV  
 XX  
 SQ Sequence 18 BP; 2 A; 5 C; 9 G; 0 T; 2 U; 0 Other;  
 XX  
 QY Query Match 66.7%; Score 12; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCUCGAG 12  
 Db 1 GGGGUCUCGAG 12  
 XX  
 RESULT 84  
 ID AA065099 standard; DNA; 19 BP.  
 XX AA065099;  
 AC AA065099;  
 XX  
 DT 21-DEC-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 XX  
 KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KM inhibition; viral protein precursor; ss.

```
XX OS Synthetic.
XX PS
XX PN CA2104649-A.
XX CC
XX PD 26-FEB-1994.
XX PF
XX PR 23-AUG-1993; 93CA-02104649.
XX PR 25-AUG-1992; 92JP-00248796.
XX PR 03-MAR-1993; 93JP-00042736.
XX PA (SEKI/) SEKI M.
XX PI Seki M, Honda Y, Yamada E;
XX DR WPI; 1994-151836/19.
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX PS Claim 5; Page 145; 262pp; English.
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX it has a base sequence of 15-30 bases which is included within the 49
XX bases from G at position 127 to C at position 175 of AAQ64913 and which
XX contains at least 7 bases from C at position 147 to C at position 153.
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX genes
XX SQ Sequence 19 BP; 2 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGGUCCTCGAG 12
XX Db 5 GGGGTCTCTGAG 16
XX
XX RESULT 85
XX AAQ65086
XX ID AAQ65086 standard; DNA; 19 BP.
XX AC
XX AAQ65086;
XX AC
XX DT 20-DEC-1994 (first entry)
XX XX
XX DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX XX
XX KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX inhibition; viral protein precursor; ss.
XX OS Synthetic.
XX XX
XX PN CA2104649-A.
XX XX
XX PD 26-FEB-1994.
XX XX
XX PF 23-AUG-1993; 93CA-02104649.
XX XX
XX PR 25-AUG-1992; 92JP-00248796.
XX PR 03-MAR-1993; 93JP-00042736.
XX XX
XX PA (SEKI/) SEKI M.
XX XX
XX PI Seki M, Honda Y, Yamada E;
XX DR WPI; 1994-151836/19.
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
```

```
XX XX Claim 5; Page 139; 262pp; English.
XX XX
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX it has a base sequence of 15-30 bases which is included within the 49
XX bases from G at position 127 to C at position 175 of AAQ64913 and which
XX contains at least 7 bases from C at position 147 to C at position 153.
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX genes
XX SQ Sequence 19 BP; 1 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGGUCCTCGAG 12
XX Db 4 GGGGTCTCTGAG 15
XX
XX RESULT 86
XX AAQ65128
XX ID AAQ65128 standard; DNA; 19 BP.
XX AC
XX AAQ65128;
XX AC
XX DT 21-DEC-1994 (first entry)
XX XX
XX DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX XX
XX KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX inhibition; viral protein precursor; ss.
XX OS Synthetic.
XX XX
XX PN CA2104649-A.
XX XX
XX PD 26-FEB-1994.
XX XX
XX PF 23-AUG-1993; 93CA-02104649.
XX XX
XX PR 25-AUG-1992; 92JP-00248796.
XX PR 03-MAR-1993; 93JP-00042736.
XX XX
XX PA (SEKI/) SEKI M.
XX XX
XX PI Seki M, Honda Y, Yamada E;
XX DR WPI; 1994-151836/19.
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX OS Claim 5; Page 158; 262pp; English.
XX XX
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX it has a base sequence of 15-30 bases which is included within the 49
XX bases from G at position 127 to C at position 175 of AAQ64913 and which
XX contains at least 7 bases from C at position 147 to C at position 153.
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX genes
XX SQ Sequence 19 BP; 2 A; 2 C; 13 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 19;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGGUCCTCGAG 12
XX Db 7 GGGGTCTCTGAG 18
```

```
RESULT 87
AA065144
ID AA065144 standard; DNA; 19 BP.
XX
XX AA065144;
AC
XX
DT 21-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
PN
XX 26-FEB-1994.
PD
XX
XX 23-AUG-1993; 93CA-02104649.
PF
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
PR
XX
PA (SEKI/) SEKI M.
XX
XX Seki M, Honda Y, Yamada E;
PI
XX WPI; 1994-151836/19.
DR
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX Claim 5; Page 165; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
XX Sequence 19 BP; 2 A; 2 C; 13 G; 2 T; 0 U; 0 Other;
SQ
Query Match 66.7%; Score 12; DB 2; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
DB 8 GGGGCTCTGGAG 19
RESULT 88
AA065100
ID AA065100 standard; DNA; 19 BP.
XX
XX AA065100;
AC
XX
XX 21-DEC-1994 (first entry)
DT
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
PN
XX 26-FEB-1994.
PD
XX
```

```
PF 23-AUG-1993; 93CA-02104649.
XX
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
PR
XX
XX (SEKI/) SEKI M.
PA
XX
XX Seki M, Honda Y, Yamada E;
PI
XX WPI; 1994-151836/19.
DR
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX Claim 5; Page 145; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
XX Sequence 19 BP; 2 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
SQ
Query Match 66.7%; Score 12; DB 2; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
DB 5 GGGGCTCTGGAG 16
```

```
RESULT 89
AA065113
ID AA065113 standard; DNA; 19 BP.
XX
XX AA065113;
AC
XX
XX 21-DEC-1994 (first entry)
DT
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
PN
XX 26-FEB-1994.
PD
XX
XX 23-AUG-1993; 93CA-02104649.
PF
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
PR
XX
XX (SEKI/) SEKI M.
PA
XX
XX Seki M, Honda Y, Yamada E;
PI
XX WPI; 1994-151836/19.
DR
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX Claim 5; Page 151; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
```

CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 19 BP; 2 A; 3 C; 12 G; 2 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
DB 6 GGGGTCCTGGAG 17  
RESULT 90  
AA299225  
ID AA299225 standard; DNA; 19 BP.  
XX  
AC AA299225;  
XX  
DT 19-JUN-2000 (first entry)  
XX  
DE Primer for primer-specific and mispair extension analysis of HCV.  
XX  
KW Primer-specific and mispair extension assay; PSMEA;  
KW genotype determination; HCV; gene variation; PCR primer; ss.  
OS Hepatitis C virus.  
PN W0200009745-A1.  
XX  
PD 24-FEB-2000.  
XX  
PF 09-AUG-1999; 99WO-CA000733.  
XX  
PR 13-AUG-1998; 98CA-02245039.  
XX  
PA (CABL-) CANADIAN BLOOD SERVICES.  
PA (HEMA-) HEMA-QUEBEC.  
XX  
PI Hu Y;  
XX  
DR WPI; 2000-224367/19.  
XX  
PT Primer-specific and mispair extension assay for identifying gene  
PT variations, comprises specific primer amplification of unknown nucleic  
PT acid sequences of patients using incomplete dNTP sets.  
XX  
PS Disclosure; Page 13; 65pp; English.  
XX  
CC AA299212-26 represent PCR primers used in a primer-specific and mispair  
CC extension assay (PSMEA) for genotype determination of Hepatitis C virus  
CC (HCV). The method comprises extending an unknown nucleic acid sequence  
CC (from a patient) using a primer specific for particular genotype and  
CC incomplete set of dNTPs under suitable conditions followed by  
CC characterizing and comparing the extension products with known nucleic  
CC acid sequences of various genotypes. The present primers are used for  
CC detecting nucleotide variations in the 5' untranslated region of the HCV  
CC genome. PSMEA is capable of accurately detecting heterozygotes and  
CC nucleotide mutations in a nucleic acid sequence. The PSMEA is useful for  
CC identifying gene variations such as in different genotypes or subtypes  
CC a given genotype, especially Hepatitis C virus genotypes and subtypes  
XX  
SQ Sequence 19 BP; 1 A; 3 C; 10 G; 5 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 3; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
DB 2 GGGGTCCTGGAG 13

RESULT 91  
ADF52572  
ID ADF52572 standard; RNA; 19 BP.  
XX  
AC ADF52572;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus siRNA antisense strand SeqID1162.  
XX  
KW short interfering nucleic acid; siRNA; virus replication inhibition;  
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatocytic; cytosolic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN W02003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JUN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
XX  
DR WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
PS Example 3; SEQ ID NO 1162; 183pp; English.  
XX  
CC This invention relates to novel double-stranded short interfering nucleic  
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA. By RNA  
CC interference. The siRNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siRNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.  
XX  
SQ Sequence 19 BP; 2 A; 2 C; 13 G; 0 T; 2 U; 0 Other;  
Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12

Db 7 GGGGUCGAG 18

RESULT 92

ID ADF51877/c

AC ADF51877; standard; RNA; 19 BP.

XX

XX ADF51877;

DT 12-FEB-2004 (first entry)

DE Hepatitis C virus short interfering nucleic acid sense strand SeqID467.

XX

XX short interfering nucleic acid; siNA; virus replication inhibition;

KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;

KM hepatocytic; cytosolic; RNA interference; HCV infection; liver failure;

KM hepatocellular cancer; cirrhosis; ss.

XX

OS Hepatitis C virus.

PN WO2003070750-A2.

PD 28-AUG-2003.

XX

XX 20-FEB-2003; 2003WO-US005043.

PF

XX 20-FEB-2002; 2002US-0358580P.

PR 11-MAR-2002; 2002US-0363124P.

PR 26-MAR-2002; 2002WO-US009187.

PR 06-JUN-2002; 2002US-0386782P.

PR 05-AUG-2002; 2002US-0401104P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409293P.

PR 15-JAN-2003; 2003US-0440129P.

XX

PA (SIRN-) SIRNA THERAPEUTICS INC.

PI Mewswigen J, Beigelman L, Macejak D, Morrissey D;

XX

DR WPI; 2003-689778/65.

XX

PT New double-stranded short interfering nucleic acid comprises sugar-

PT modified pyrimidine bases useful for treating infection with hepatitis C

PT virus.

XX

PS Example 3; SEQ ID NO 467; 183bp; English.

XX

XX This invention relates to novel double-stranded short interfering nucleic

CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where

CC one strand is an antisense strand (ASS) that is complementary to (part

CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to

CC ASS, and where most of the pyrimidine nucleotides comprise a sugar

CC modification. The invention may allow development of compounds with

CC virucide, antiinflammatory, hepatotropic or cytostatic activities by

CC modulation (inhibition) of expression or activity of HCV RNA, by RNA

CC interference. The siNA's of the invention may be used to inhibit

CC replication of HCV, in cells, tissue explants or organisms, for treating

CC HCV infection and its consequences (liver failure; hepatocellular cancer

CC and cirrhosis), and also for drug screening, diagnosis, target

CC identification and validation, genetic engineering, pharmacogenomics,

CC studying gene function and gene mapping (for example of single-nucleotide

CC polymorphisms). The chemical modification improves stability, activity,

CC cellular uptake and/or binding affinity. The siNA can be directed to

CC conserved regions of HCV genes, so are active against many different

CC strains.

XX

XX Sequence 19 BP; 2 A; 13 C; 2 G; 0 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 10; Length 19;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12

Db 12 GGGGUCGAG 1

RESULT 93

ID ADF51948/c

AC ADF51948; standard; RNA; 19 BP.

XX

XX ADF51948;

DT 12-FEB-2004 (first entry)

DE Hepatitis C virus short interfering nucleic acid sense strand SeqID538.

XX

XX short interfering nucleic acid; siNA; virus replication inhibition;

KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;

KM hepatocytic; cytosolic; RNA interference; HCV infection; liver failure;

KM hepatocellular cancer; cirrhosis; ss.

XX

OS Hepatitis C virus.

PN WO2003070750-A2.

PD 28-AUG-2003.

XX

XX 20-FEB-2003; 2003WO-US005043.

PF

XX 20-FEB-2002; 2002US-0358580P.

PR 11-MAR-2002; 2002US-0363124P.

PR 26-MAR-2002; 2002WO-US009187.

PR 06-JUN-2002; 2002US-0386782P.

PR 05-AUG-2002; 2002US-0401104P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409293P.

PR 15-JAN-2003; 2003US-0440129P.

XX

PA (SIRN-) SIRNA THERAPEUTICS INC.

PI Mewswigen J, Beigelman L, Macejak D, Morrissey D;

XX

DR WPI; 2003-689778/65.

XX

PT New double-stranded short interfering nucleic acid comprises sugar-

PT modified pyrimidine bases useful for treating infection with hepatitis C

PT virus.

XX

PS Example 3; SEQ ID NO 538; 183bp; English.

XX

XX This invention relates to novel double-stranded short interfering nucleic

CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where

CC one strand is an antisense strand (ASS) that is complementary to (part

CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to

CC ASS, and where most of the pyrimidine nucleotides comprise a sugar

CC modification. The invention may allow development of compounds with

CC virucide, antiinflammatory, hepatotropic or cytostatic activities by

CC modulation (inhibition) of expression or activity of HCV RNA, by RNA

CC interference. The siNA's of the invention may be used to inhibit

CC replication of HCV, in cells, tissue explants or organisms, for treating

CC HCV infection and its consequences (liver failure; hepatocellular cancer

CC and cirrhosis), and also for drug screening, diagnosis, target

CC identification and validation, genetic engineering, pharmacogenomics,

CC studying gene function and gene mapping (for example of single-nucleotide

CC polymorphisms). The chemical modification improves stability, activity,

CC cellular uptake and/or binding affinity. The siNA can be directed to

CC conserved regions of HCV genes, so are active against many different

CC strains.

XX

XX Sequence 19 BP; 3 A; 10 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 10; Length 19;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUUGAG 12  
 |||||  
 Db 18 GGGGCTCTGAG 7

RESULT 94  
 ID ADF52651 standard; RNA; 19 BP.  
 AC ADF52651;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Hepatitis C virus siNA antisense strand SegID1241.  
 XX  
 KW short interfering nucleic acid; siNA; virus replication inhibition;  
 KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
 KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
 KW hepatocellular cancer; cirrhosis; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO2003070750-A2.  
 XX  
 PD 28-AUG-2003.  
 XX  
 PF 20-FEB-2003; 2003WO-US005043.  
 XX  
 PR 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 26-MAR-2002; 2002WO-US009187.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 05-AUG-2002; 2002US-0401104P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX  
 PA (SIRN-) SIRNA THERAPEUTICS INC.  
 XX  
 PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
 XX  
 DR WPI; 2003-689778/65.  
 XX  
 PT New double-stranded short interfering nucleic acid comprises sugar-  
 PT modified pyrimidine bases useful for treating infection with hepatitis C  
 PT virus.  
 XX  
 PS Example 3; SEQ ID NO 1241; 183pp; English.  
 XX  
 CC This invention relates to novel double-stranded short interfering nucleic  
 CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
 CC one strand is an antisense strand (ASS) that is complementary to (part  
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
 CC modification. The invention may allow development of compounds with  
 CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
 CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
 CC interference. The siNA's of the invention may be used to inhibit  
 CC replication of HCV, in cells, tissue explants or organisms, for treating  
 CC HCV infection and its consequences (liver failure; hepatocellular cancer  
 CC and cirrhosis), and also for drug screening, diagnosis, target  
 CC identification and validation, genetic engineering, pharmacogenomics,  
 CC studying gene function and gene mapping (for example of single-nucleotide  
 CC polymorphisms). The chemical modification improves stability, activity,  
 CC cellular uptake and/or binding affinity. The siNA can be directed to  
 CC conserved regions of HCV genes, so are active against many different  
 CC strains.  
 XX  
 SQ Sequence 19 BP; 1 A; 4 C; 11 G; 0 T; 3 U; 0 Other;

Query Match 66.7%; Score 12; DB 10; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUUGAG 12  
 |||||  
 Db 3 GGGGCTCTGAG 14

RESULT 95  
 ID ADF52606 standard; RNA; 19 BP.  
 AC ADF52606;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Hepatitis C virus siNA antisense strand SegID1196.  
 XX  
 KW short interfering nucleic acid; siNA; virus replication inhibition;  
 KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
 KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
 KW hepatocellular cancer; cirrhosis; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO2003070750-A2.  
 XX  
 PD 28-AUG-2003.  
 XX  
 PF 20-FEB-2003; 2003WO-US005043.  
 XX  
 PR 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 26-MAR-2002; 2002WO-US009187.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 05-AUG-2002; 2002US-0401104P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX  
 PA (SIRN-) SIRNA THERAPEUTICS INC.  
 XX  
 PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
 XX  
 DR WPI; 2003-689778/65.  
 XX  
 PT New double-stranded short interfering nucleic acid comprises sugar-  
 PT modified pyrimidine bases useful for treating infection with hepatitis C  
 PT virus.  
 XX  
 PS Example 3; SEQ ID NO 1196; 183pp; English.  
 XX  
 CC This invention relates to novel double-stranded short interfering nucleic  
 CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
 CC one strand is an antisense strand (ASS) that is complementary to (part  
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
 CC modification. The invention may allow development of compounds with  
 CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
 CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
 CC interference. The siNA's of the invention may be used to inhibit  
 CC replication of HCV, in cells, tissue explants or organisms, for treating  
 CC HCV infection and its consequences (liver failure; hepatocellular cancer  
 CC and cirrhosis), and also for drug screening, diagnosis, target  
 CC identification and validation, genetic engineering, pharmacogenomics,  
 CC studying gene function and gene mapping (for example of single-nucleotide  
 CC polymorphisms). The chemical modification improves stability, activity,  
 CC cellular uptake and/or binding affinity. The siNA can be directed to  
 CC conserved regions of HCV genes, so are active against many different  
 CC strains.  
 XX



SQ Sequence 19 BP; 2 A; 3 C; 12 G; 0 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 10; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
 |||||  
 Db 6 GGGGUCUUGAG 17

RESULT 96  
 ADF52644  
 ID ADF52644 standard; RNA; 19 BP.  
 AC ADF52644;  
 XX  
 XX 12-FEB-2004 (first entry)  
 DT  
 XX  
 DE Hepatitis C virus sRNA antisense strand SeqID1234.  
 XX  
 KM short interfering nucleic acid; sRNA; virus replication inhibition;  
 KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
 KM hepatotropic; cytosstatic; RNA interference; HCV infection; liver failure;  
 KM hepatocellular cancer; cirrhosis; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO2003070750-A2.  
 PD 28-AUG-2003.  
 XX  
 PF 20-FEB-2003; 2003WO-US005043.  
 XX  
 PR 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 26-MAR-2002; 2002WO-US009187.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 05-AUG-2002; 2002US-0401104P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX  
 PA (SIRN-) SIRNA THERAPEUTICS INC.  
 XX  
 PI Mcswigen J, Beigelman L, Macejak D, Morrissey D;  
 XX  
 DR WPI; 2003-669778/65.  
 DR  
 PT New double-stranded short interfering nucleic acid comprises sugar-  
 PT modified pyrimidine bases useful for treating infection with hepatitis C  
 PT virus.  
 XX  
 PS Example 3; SEQ ID NO 1234; 183bp; English.  
 XX

This invention relates to novel double-stranded short interfering nucleic acid (siRNA) that inhibits replication of hepatitis C virus (HCV), where one strand is an antisense strand (ASS) that is complementary to (part of) an HCV RNA (portion) and a sense strand (SS) that is complementary to ASS, and where most of the pyrimidine nucleotides comprise a sugar virucide, antiinflammatory, hepatotropic or cytosstatic activities by modulation (inhibition) of expression or activity of HCV RNA, by RNA interference. The siRNA's of the invention may be used to inhibit replication of HCV, in cells, tissue explants or organisms, for treating HCV infection and its consequences (liver failure; hepatocellular cancer and cirrhosis), and also for drug screening, diagnosis, target identification and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (for example of single-nucleotide polymorphisms). The chemical modification improves stability, activity, cellular uptake and/or binding affinity. The siRNA can be directed to conserved regions of HCV genes, so are active against many different

CC strains.

SQ Sequence 19 BP; 2 A; 4 C; 10 G; 0 T; 3 U; 0 Other;

Query Match 66.7%; Score 12; DB 10; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
 |||||  
 Db 2 GGGGUCUUGAG 13

RESULT 97  
 ADF51912/C  
 ID ADF51912 standard; RNA; 19 BP.  
 AC ADF51912;  
 XX  
 XX 12-FEB-2004 (first entry)  
 DT  
 XX  
 DE Hepatitis C virus short interfering nucleic acid sense strand SeqID502.  
 XX  
 KM short interfering nucleic acid; siRNA; virus replication inhibition;  
 KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
 KM hepatotropic; cytosstatic; RNA interference; HCV infection; liver failure;  
 KM hepatocellular cancer; cirrhosis; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO2003070750-A2.  
 PD 28-AUG-2003.  
 XX  
 PF 20-FEB-2003; 2003WO-US005043.  
 XX  
 PR 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 26-MAR-2002; 2002WO-US009187.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 05-AUG-2002; 2002US-0401104P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX  
 PA (SIRN-) SIRNA THERAPEUTICS INC.  
 XX  
 PI Mcswigen J, Beigelman L, Macejak D, Morrissey D;  
 XX  
 DR WPI; 2003-669778/65.  
 DR  
 PT New double-stranded short interfering nucleic acid comprises sugar-  
 PT modified pyrimidine bases useful for treating infection with hepatitis C  
 PT virus.  
 XX  
 PS Example 3; SEQ ID NO 502; 183bp; English.  
 XX

This invention relates to novel double-stranded short interfering nucleic acid (siRNA) that inhibits replication of hepatitis C virus (HCV), where one strand is an antisense strand (ASS) that is complementary to (part of) an HCV RNA (portion) and a sense strand (SS) that is complementary to ASS, and where most of the pyrimidine nucleotides comprise a sugar virucide, antiinflammatory, hepatotropic or cytosstatic activities by modulation (inhibition) of expression or activity of HCV RNA, by RNA interference. The siRNA's of the invention may be used to inhibit replication of HCV, in cells, tissue explants or organisms, for treating HCV infection and its consequences (liver failure; hepatocellular cancer and cirrhosis), and also for drug screening, diagnosis, target identification and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (for example of single-nucleotide polymorphisms). The chemical modification improves stability, activity,

CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.  
XX  
SQ Sequence 19 BP; 3 A; 11 C; 3 G; 0 T; 2 U; 0 Other;  
Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
Db 15 GGGGTCTCTGAG 4  
RESULT 98  
ADFS1876/c  
ID ADFS1876 standard; RNA; 19 BP.  
XX  
AC ADFS1876;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus short interfering nucleic acid sense strand SeqID466.  
XX  
KM short interfering nucleic acid; siNA; virus replication inhibition;  
KM hepatitis C virus; HCV; sugar modification; viraemia; anti-inflammatory;  
KM hepatotropic; cytosolic; RNA interference; HCV infection; liver failure;  
KM hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-036782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswigen J, Beigelman L, Macejak D, Morrissey D;  
XX  
DR WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
PS Example 3; SEQ ID NO 466; 183bp; English.  
XX  
CC This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC viraemic, anti-inflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,

CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.  
XX  
SQ Sequence 19 BP; 2 A; 13 C; 2 G; 0 T; 2 U; 0 Other;  
Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
Db 13 GGGGTCTCTGAG 2  
RESULT 99  
ADFS1910/c  
ID ADFS1910 standard; RNA; 19 BP.  
XX  
AC ADFS1910;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus short interfering nucleic acid sense strand SeqID500.  
XX  
KM short interfering nucleic acid; siNA; virus replication inhibition;  
KM hepatitis C virus; HCV; sugar modification; viraemia; anti-inflammatory;  
KM hepatotropic; cytosolic; RNA interference; HCV infection; liver failure;  
KM hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-036782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswigen J, Beigelman L, Macejak D, Morrissey D;  
XX  
DR WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
PS Example 3; SEQ ID NO 500; 183bp; English.  
XX  
CC This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC viraemic, anti-inflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer

CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.

XX  
SQ Sequence 19 BP; 2 A; 12 C; 3 G; 0 T; 2 U; 0 Other;

Qy Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Dy 1 GGGGUCGCGAG 12  
14 GGGGCTCTGAG 3

RESULT 100  
ADFS1954/C  
ID ADFS1954 standard; RNA; 19 BP.  
XX  
AC ADFS1954;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus short interfering nucleic acid sense strand SegID544.  
XX  
KM short interfering nucleic acid; siNA; virus replication inhibition;  
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KM hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Meswigen J, Beigelman L, Macejak D, Morrissey D;  
XX  
DR WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
PS Example 3; SEQ ID NO 544; 183bp; English.  
XX  
XX This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (AS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC AS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siNA's of the invention may be used to inhibit

CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure, hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.

XX  
SQ Sequence 19 BP; 3 A; 9 C; 5 G; 0 T; 2 U; 0 Other;

Qy Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Dy 1 GGGGUCGCGAG 12  
19 GGGGCTCTGAG 8

RESULT 101  
ADFS2650  
ID ADFS2650 standard; RNA; 19 BP.  
XX  
AC ADFS2650;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus siNA antisense strand SegID1240.  
XX  
KM short interfering nucleic acid; siNA; virus replication inhibition;  
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KM hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
XX (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Meswigen J, Beigelman L, Macejak D, Morrissey D;  
XX  
DR WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
PS Example 3; SEQ ID NO 1240; 183bp; English.  
XX  
XX This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (AS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC AS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by

CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siNA's of the invention may be used to inhibit  
CC infection of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.  
CC  
SQ Sequence 19 BP; 2 A; 5 C; 9 G; 0 T; 3 U; 0 Other;  
XX  
XX  
Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
1 GGGGUCCUGAG 12  
Db 1 GGGGUCCUGAG 12  
RESULT 102  
ADFS2573  
ID ADFS2573 standard; RNA; 19 BP.  
XX  
AC ADFS2573;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus siNA antisense strand SeqID1163.  
XX  
XX short interfering nucleic acid; siNA; virus replication inhibition;  
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatotropic; cytosstatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 29-AUG-2002; 2002US-0401104P.  
PR 05-SEP-2002; 2002US-0406784P.  
PR 09-SEP-2002; 2002US-0408378P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
PI WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
XX Example 3; SEQ ID NO 1163; 183bp; English.  
XX  
PS This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar

CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytosstatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure; hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.  
CC  
SQ Sequence 19 BP; 2 A; 2 C; 13 G; 0 T; 2 U; 0 Other;  
XX  
XX  
Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
1 GGGGUCCUGAG 12  
Db 8 GGGGUCCUGAG 19  
RESULT 103  
ADFS1908/C  
ID ADFS1908 standard; RNA; 19 BP.  
XX  
AC ADFS1908;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus short interfering nucleic acid sense strand SeqID498.  
XX  
XX short interfering nucleic acid; siNA; virus replication inhibition;  
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KW hepatotropic; cytosstatic; RNA interference; HCV infection; liver failure;  
KW hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 29-AUG-2002; 2002US-0401104P.  
PR 05-SEP-2002; 2002US-0406784P.  
PR 09-SEP-2002; 2002US-0408378P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;  
PI WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
PT virus.  
XX  
XX Example 3; SEQ ID NO 498; 183bp; English.  
XX  
PS This invention relates to novel double-stranded short interfering nucleic  
CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part

CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siRNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure, hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siRNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.  
XX  
SQ Sequence 19 BP; 3 A; 12 C; 3 G; 0 T; 1 U; 0 Other;  
Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
Db 16 GGGGTCTCGAG 5  
RESULT 104  
ADFS2608  
ID ADFS2608 standard; RNA; 19 BP.  
XX  
AC ADFS2608;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus siNA antisense strand SegID1198.  
XX  
KM short interfering nucleic acid; siNA; virus replication inhibition;  
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KM hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KM hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-036782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI McSwiggen J, Beigelman L, Macejak D, Morrissey D,  
XX  
DR WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
XX  
PS Example 3; SEQ ID NO 1198; 183bp; English.  
XX  
CC This invention relates to novel double-stranded short interfering nucleic

CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
CC one strand is an antisense strand (ASS) that is complementary to (part  
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
CC modification. The invention may allow development of compounds with  
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by  
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
CC interference. The siRNA's of the invention may be used to inhibit  
CC replication of HCV, in cells, tissue explants or organisms, for treating  
CC HCV infection and its consequences (liver failure, hepatocellular cancer  
CC and cirrhosis), and also for drug screening, diagnosis, target  
CC identification and validation, genetic engineering, pharmacogenomics,  
CC studying gene function and gene mapping (for example of single-nucleotide  
CC polymorphisms). The chemical modification improves stability, activity,  
CC cellular uptake and/or binding affinity. The siNA can be directed to  
CC conserved regions of HCV genes, so are active against many different  
CC strains.  
XX  
SQ Sequence 19 BP; 2 A; 3 C; 11 G; 0 T; 3 U; 0 Other;  
Query Match 66.7%; Score 12; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
Db 5 GGGGUCCTGGAG 16  
RESULT 105  
ADFS1955/c  
ID ADFS1955 standard; RNA; 19 BP.  
XX  
AC ADFS1955;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Hepatitis C virus short interfering nucleic acid sense strand SegID545.  
XX  
KM short interfering nucleic acid; siNA; virus replication inhibition;  
KM hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
KM hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
KM hepatocellular cancer; cirrhosis; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN WO2003070750-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 20-FEB-2003; 2003WO-US005043.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 26-MAR-2002; 2002WO-US009187.  
PR 06-JUN-2002; 2002US-036782P.  
PR 05-AUG-2002; 2002US-0401104P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI McSwiggen J, Beigelman L, Macejak D, Morrissey D,  
XX  
DR WPI; 2003-689778/65.  
XX  
PT New double-stranded short interfering nucleic acid comprises sugar-  
PT modified pyrimidine bases useful for treating infection with hepatitis C  
XX  
PS Example 3; SEQ ID NO 545; 183bp; English.  
XX

XX This invention relates to novel double-stranded short interfering nucleic  
 CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
 CC one strand is an antisense strand (ASS) that is complementary to (part  
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
 CC modification. The invention may allow development of compounds with  
 CC antiviral, antiinflammatory, hepatotropic or cytostatic activities by  
 CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
 CC interference. The siNA's of the invention may be used to inhibit  
 CC replication of HCV, in cells, tissue explants or organisms, for treating  
 CC HCV infection and its consequences (liver failure, hepatocellular cancer  
 CC and cirrhosis), and also for drug screening, diagnosis, target  
 CC identification and validation, genetic engineering, pharmacogenomics,  
 CC studying gene function and gene mapping (for example of single-nucleotide  
 CC polymorphisms). The chemical modification improves stability, activity,  
 CC cellular uptake and/or binding affinity. The siNA can be directed to  
 CC conserved regions of HCV genes, so are active against many different  
 CC strains.

SO Sequence 19 BP; 3 A; 11 C; 4 G; 0 T; 1 U; 0 Other;

Query Match 66.7%; Score 12; DB 10; Length 19;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
 Db 17 GGGGCTCTGAG 6

RESULT 106  
 ADF52604  
 ID ADF52604 standard; RNA; 19 BP.

XX ADF52604;

DT 12-FEB-2004 (first entry)

DE Hepatitis C virus siNA antisense strand SeqID1194.

KW short interfering nucleic acid; siNA; virus replication inhibition;  
 KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;  
 KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;  
 KW hepatocellular cancer; cirrhosis; ss.

OS Hepatitis C virus.

PN WO2003070750-A2.

PD 28-AUG-2003.

PF 20-FEB-2003; 2003WO-US005043.

PR 20-FEB-2002; 2002US-0358580P.

PR 11-MAR-2002; 2002US-0363124P.

PR 26-MAR-2002; 2002WO-US009187P.

PR 06-JUN-2002; 2002US-0386782P.

PR 05-AUG-2002; 2002US-0401104P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409293P.

PR 15-JAN-2003; 2003US-0440129P.

XX (SIRNA-) SIRNA THERAPEUTICS INC.  
 XX PI Mcswigen J, Beigelman L, Macejak D, Morrissey D;  
 XX DR WPI; 2003-689778/65.  
 XX New double-stranded short interfering nucleic acid comprises sugar-  
 PT modified pyrimidine bases useful for treating infection with hepatitis C  
 PT virus.

XX Example 3; SEQ ID NO 1194; 183bp; English.

PS This invention relates to novel double-stranded short interfering nucleic  
 XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where  
 CC one strand is an antisense strand (ASS) that is complementary to (part  
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to  
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar  
 CC modification. The invention may allow development of compounds with  
 CC antiviral, antiinflammatory, hepatotropic or cytostatic activities by  
 CC modulation (inhibition) of expression or activity of HCV RNA, by RNA  
 CC interference. The siNA's of the invention may be used to inhibit  
 CC replication of HCV, in cells, tissue explants or organisms, for treating  
 CC HCV infection and its consequences (liver failure, hepatocellular cancer  
 CC and cirrhosis), and also for drug screening, diagnosis, target  
 CC identification and validation, genetic engineering, pharmacogenomics,  
 CC studying gene function and gene mapping (for example of single-nucleotide  
 CC polymorphisms). The chemical modification improves stability, activity,  
 CC cellular uptake and/or binding affinity. The siNA can be directed to  
 CC conserved regions of HCV genes, so are active against many different  
 CC strains.

SO Sequence 19 BP; 1 A; 3 C; 12 G; 0 T; 3 U; 0 Other;

Query Match 66.7%; Score 12; DB 10; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
 Db 4 GGGGUCGAG 15

RESULT 107  
 ADJ53727/c  
 ID ADJ53727 standard; DNA; 19 BP.

XX ADJ53727;

DT 06-MAY-2004 (first entry)

DE HCV specific oligonucleotide #7.

KW ss; capture oligonucleotide; HBV; HIV-1; HCV; donated blood screening;  
 KW DNA-RNA hybrid.

OS Hepatitis C virus.

PN WO2003106714-A1.

PD 24-DEC-2003.

PF 13-JUN-2003; 2003WO-US018993.

PR 14-JUN-2002; 2002US-0389393P.

PR (GENP-) GEN-PROBE INC.

PR Linnen JM, Kolk DP, Dockter JM, Getman DK, Yoshimura T;  
 PI Ho-Sing-Loy M, Stringfellow LA;  
 XX WPI; 2004-082210/08.

PT Capture oligonucleotide composition useful for detection of hepatitis B  
 PT virus (HBV), comprising polynucleotide having HBV-complementary sequence  
 PT which is immobilized on solid support.  
 XX Example 7; SEQ ID NO 121; 112bp; English.

XX The invention relates to a capture oligonucleotide composition comprising  
 CC an hepatitis B virus (HBV)-complementary sequence polynucleotide  
 CC immobilised to a solid support. The composition is useful for detecting  
 CC nucleic acids of HBV and/of HIV-1 and/or HCV in biological sample such as

CC blood, serum, plasma or other body fluid or tissue to be tested. The  
 CC composition can be used either in diagnostic application or for screening  
 CC donated blood and that products or other tissues that may contain  
 CC infectious particles. The composition facilitates detection of very low  
 CC levels of HBV nucleic acids. The composition allows selective detection  
 CC of nucleic acids of HBV and/or HIV and/or HCV. The present sequence is  
 CC used in the exemplification of the invention.

XX  
 SQ Sequence 19 BP, 3 A, 11 C, 3 G, 1 T, 1 U, 0 Other;

Query Match 66.7%; Score 12; DB 12; Length 19;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCCTCGAG 12  
 |||||:  
 Db 15 GGGGCTCTCGAG 4

RESULT 108  
 ADR81222/c  
 ID ADR81222 standard; DNA; 19 BP.

XX  
 AC ADR81222;

XX  
 DT 16-DEC-2004 (first entry)

XX  
 DE Hepatitis C virus (HCV) oligonucleotide seqid 5721.

XX  
 KM antiHepemic; cardiatic; vasotropic; antiarteriosclerotic; antidiabetic;  
 KM cytosaratic; anticonvulsant; nootropic; muscular; anti-HIV;  
 KM RNA interference; iRNA; antisense technology; lipid metabolism;  
 KM cholesterol imbalance; dyslipidaemia hypercholesterolaemia;  
 KM coronary artery disease; CAD; coronary heart disease; CHD;  
 KM atherosclerosis; hepatic glucose production;  
 KM glucose-metabolism-related disorder; diabetes; cancer; breast cancer;  
 KM colon cancer; lung cancer; neurological disease; Huntington disease;  
 KM spinocerebellar ataxia; viral disease; AIDS; hepatitis C virus; HCV; ss.

XX  
 OS Hepatitis C virus.

XX  
 PN WO2004080406-A2.

XX  
 PD 23-SEP-2004.

XX  
 PF 08-MAR-2004; 2004WO-US007070.

XX  
 PR 07-MAR-2003; 2003US-0452682P.  
 PR 12-MAR-2003; 2003US-0454265P.  
 PR 13-MAR-2003; 2003US-0454962P.  
 PR 13-MAR-2003; 2003US-0455050P.  
 PR 14-APR-2003; 2003US-0462894P.  
 PR 17-APR-2003; 2003US-0463772P.  
 PR 25-APR-2003; 2003US-0465655P.  
 PR 25-APR-2003; 2003US-0465802P.  
 PR 09-MAY-2003; 2003US-0459612P.  
 PR 08-AUG-2003; 2003US-0459686P.  
 PR 11-AUG-2003; 2003US-0494597P.  
 PR 26-SEP-2003; 2003US-0506341P.  
 PR 09-OCT-2003; 2003US-0510246P.  
 PR 10-OCT-2003; 2003US-0510318P.  
 PR 07-NOV-2003; 2003US-0518453P.

XX  
 PA (ALINY-) ALNYTAM PHARM.

XX  
 PI Manoharan M, Bumcrot D;

XX  
 DR WPI; 2004-677362/66.

XX  
 PT Interference RNA agent useful for treating dyslipidemia; coronary artery  
 PT disease, diabetes, cancer or neurological disease, comprises sense  
 PT sequence and antisense sequence which has specific modifications.

PS Example 5; SEQ ID NO 5721; 378bp; English.

XX  
 CC The invention describes a RNA interference (iRNA) agent (I) comprising a  
 CC sense sequence and an antisense sequence, where the sense sequences have  
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense  
 CC sequences have one or more asymmetrical phosphorothioate modifications  
 CC and the antisense sequence targets a human gene sequence. Also described  
 CC are: a pharmaceutical preparation comprising (I); reducing (MI) apob-100  
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);  
 CC stabilising (I), involves selecting a sequence with activity and  
 CC introducing one or more asymmetrical modification in the sequence, where  
 CC the modification decreases nuclease sensitivity while not decreasing its  
 CC activity; a kit comprising (I) and instruction for its use; and a device  
 CC that can be dispense or administer a composition comprising (I). (I) is  
 CC useful for reducing apob-100 levels or glucose-6-phosphatase levels.  
 CC is useful for reducing apob-100 levels or glucose-6-phosphatase levels.  
 CC The subject is suffering from a disorder characterised by elevated or  
 CC otherwise unwanted expression of apob-100, elevated or otherwise unwanted  
 CC levels of cholesterol and/or dysregulation of lipid metabolism. The  
 CC disorder is chosen from the HDL/LDL cholesterol imbalance,  
 CC dyslipidemia, hypercholesterolaemia, statin-resistant  
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart  
 CC disease (CHD) and atherosclerosis. (I) is administered to a subject to  
 CC inhibit hepatic glucose production or for treating glucose-metabolism-  
 CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for  
 CC treating the diseases as mentioned above, cancer (e.g. breast, colon or  
 CC lung cancer), neurological disease (e.g., Huntington disease or  
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence  
 CC represents a hepatitis C virus (HCV) antisense oligonucleotide that can  
 CC be used to control HCV gene expression.

XX  
 SQ Sequence 19 BP, 3 A, 9 C, 5 G, 2 T, 0 U, 0 Other;

Query Match 66.7%; Score 12; DB 13; Length 19;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCCTCGAG 12  
 |||||:  
 Db 19 GGGGCTCTCGAG 8

RESULT 109  
 ADR81223/c  
 ID ADR81223 standard; DNA; 19 BP.

XX  
 AC ADR81223;

XX  
 DT 16-DEC-2004 (first entry)

XX  
 DE Hepatitis C virus (HCV) oligonucleotide seqid 5722.

XX  
 KM antiHepemic; cardiatic; vasotropic; antiarteriosclerotic; antidiabetic;  
 KM cytosaratic; anticonvulsant; nootropic; muscular; anti-HIV;  
 KM RNA interference; iRNA; antisense technology; lipid metabolism;  
 KM cholesterol imbalance; dyslipidaemia hypercholesterolaemia;  
 KM coronary artery disease; CAD; coronary heart disease; CHD;  
 KM atherosclerosis; hepatic glucose production;  
 KM glucose-metabolism-related disorder; diabetes; cancer; breast cancer;  
 KM colon cancer; lung cancer; neurological disease; Huntington disease;  
 KM spinocerebellar ataxia; viral disease; AIDS; hepatitis C virus; HCV; ss.

XX  
 OS Hepatitis C virus.

XX  
 PN WO2004080406-A2.

XX  
 PD 23-SEP-2004.

XX  
 PF 08-MAR-2004; 2004WO-US007070.

XX  
 PR 07-MAR-2003; 2003US-0452682P.  
 PR 12-MAR-2003; 2003US-0454265P.  
 PR 13-MAR-2003; 2003US-0454962P.

PR 13-MAR-2003; 2003US-0455050P.  
 PR 14-APR-2003; 2003US-0462894P.  
 PR 17-APR-2003; 2003US-0463772P.  
 PR 25-APR-2003; 2003US-0465665P.  
 PR 09-MAY-2003; 2003US-0465802P.  
 PR 08-AUG-2003; 2003US-0469612P.  
 PR 11-AUG-2003; 2003US-0493986P.  
 PR 26-SEP-2003; 2003US-0494597P.  
 PR 09-OCT-2003; 2003US-0506341P.  
 PR 10-OCT-2003; 2003US-0510246P.  
 PR 07-NOV-2003; 2003US-0518453P.  
 XX  
 PA (ALNTV-) ALNTVLM PHARM.  
 XX Manoharan M, Bumcrot D;  
 XX WPI; 2004-677362/66.  
 DR  
 XX  
 PT Interference RNA agent useful for treating dyslipidemias, coronary artery  
 PT disease, diabetes, cancer or neurological disease, comprises sense  
 PT sequence and antisense sequence which has specific modifications.  
 XX  
 PS Example 5; SEQ ID NO 5722; 378bp; English.  
 XX  
 CC The invention describes a RNA interference (iRNA) agent (I) comprising a  
 CC sense sequence and an antisense sequence, where the sense sequences have  
 CC one or more asymmetrical 2'-O alkyl modifications, the antisense  
 CC sequences have one or more asymmetrical phosphorothioate modifications  
 CC and the antisense sequence targets a human gene sequence. Also described  
 CC are: a pharmaceutical preparation comprising (II): reducing (MI) apob-100  
 CC levels or glucose-6-phosphatase levels in a subject; producing (I);  
 CC stabilizing (I); involves selecting a sequence with activity and  
 CC introducing one or more asymmetrical modification in the sequence, where  
 CC the modification decreases nuclease sensitivity while not decreasing its  
 CC activity; a kit comprising (I) and instruction for its use; and a device  
 CC that can be dispense or administer a composition comprising (I). (I) is  
 CC useful for reducing apob-100 levels or glucose-6-phosphatase levels. (MI)  
 CC is useful for reducing apob-100 levels or glucose-6-phosphatase levels.  
 CC The subject is suffering from a disorder characterized by elevated or  
 CC otherwise unwanted expression of apob-100, elevated or otherwise unwanted  
 CC levels of cholesterol, and/or dysregulation of lipid metabolism. The  
 CC disorder is chosen from the HDL/LDL cholesterol imbalance,  
 CC dyslipidemias, hypercholesterolaemia, statin-resistant  
 CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart  
 CC disease (CHD) and atherosclerosis. (I) is administered to a subject to  
 CC inhibit hepatic glucose production or for treating glucose-metabolism-  
 CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for  
 CC treating the diseases as mentioned above, cancer (e.g. breast, colon or  
 CC lung cancer), neurological disease (e.g., Huntington disease or  
 CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence  
 CC represents a hepatitis C virus (HCV) antisense oligonucleotide that can  
 CC be used to control HCV gene expression.  
 XX  
 SQ Sequence 19 BP; 3 A; 10 C; 4 G; 2 T; 0 U; 0 Other;  
 XX  
 Query Match 66.7%; Score 12; DB 13; Length 19;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTCGAG 12  
 DB 18 GGGGTCCTCGAG 7  
 XX  
 RESULT 110  
 AA032979/c  
 ID AA032979 standard; DNA; 20 BP.  
 XX  
 AC AA032979;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 14-MAY-1993 (first entry)

XX  
 DE HCV probe NC (+) (-235- -216).  
 XX  
 KM PCR; amplification; prototype; HCV pt; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9221759-A1.  
 XX  
 PD 10-DEC-1992.  
 XX  
 PF 04-JUN-1992; 92WO-FR000501.  
 XX  
 PR 06-JUN-1991; 91FR-00006882.  
 XX  
 PA (INSP) INST PASTEUR.  
 XX  
 PI Brechot C, Kremsdorf D, Porchon C;  
 XX  
 DR WPI; 1992-433657/52.  
 XX  
 PT New nucleotide and peptide sequences - specific for French isolate of  
 PT hepatitis C virus and useful in diagnosing and treating related  
 PT infections.  
 XX  
 PS Disclosure; Page 11; 50pp; French.  
 XX  
 CC RNA was extracted from the serum of an HCV-positive blood donor, subjected  
 CC to reverse transcription and the cDNA formed amplified by PCR.  
 CC Amplification products were cloned, screened with a probe derived from the  
 CC HCV prototype and inserts sequenced. The results showed marked  
 CC conservation in the non-coding region, significant variability in the  
 CC structural region (encoding envelope proteins) and reduced variability in  
 CC the non-structural region. The primer and probe sequences and positions  
 CC correspond to the HCV prototype (HCV pt) (EP-A-O 318 216 and WO-A-  
 CC 90/14436). (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 20 BP; 3 A; 10 C; 5 G; 2 T; 0 U; 0 Other;  
 XX  
 Query Match 66.7%; Score 12; DB 2; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTCGAG 12  
 DB 19 GGGGTCCTCGAG 8  
 XX  
 RESULT 111  
 AA065145  
 ID AA065145 standard; DNA; 20 BP.  
 XX  
 AC AA065145;  
 XX  
 DT 21-DEC-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 XX  
 KM Hepatitis C virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KM inhibition; viral protein precursor; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN CA2104649-A.  
 XX  
 PD 26-FEB-1994.  
 XX  
 PF 23-AUG-1993; 93CA-02104649.  
 XX  
 PR 25-AUG-1992; 92JP-00248796.  
 PR 03-MAR-1993; 93JP-00042736.  
 XX  
 PA (SEKI) SEKI M.



```
XX Seki M, Honda Y, Yamada E;
XX WPI; 1994-151836/19.
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX
XX Claim 5; Page 165; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
XX it has a base sequence of 15-30 bases which is included within the 49
XX bases from G at position 127 to C at position 175 of AA064913 and which
XX contains at least 7 bases from C at position 147 to C at position 153.
XX The antisense oligonucleotide is useful for inhibiting translation of HCV
XX genes
XX
XX Sequence 20 BP; 2 A; 3 C; 13 G; 2 T; 0 U; 0 Other;
XX
XX Query Match
XX Best Local Similarity 83.3%; Score 12; DB 2; Length 20;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGGGUCCTCGAG 12
XX 9 GGGCTCTCGAG 20
XX
XX RESULT 112
XX AA065075
XX ID AA065075 standard; DNA; 20 BP.
XX
XX AA065075;
XX
XX 20-DEC-1994 (first entry)
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX inhibition; viral protein precursor; ss.
XX
XX Synthetic.
XX
XX CA2104649-A.
XX
XX 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-02104649.
XX
XX 25-AUG-1992; 92JP-00248796.
XX 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
XX
XX Seki M, Honda Y, Yamada E;
XX WPI; 1994-151836/19.
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX
XX Claim 5; Page 134; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
XX it has a base sequence of 15-30 bases which is included within the 49
XX bases from G at position 127 to C at position 175 of AA064913 and which
XX contains at least 7 bases from C at position 147 to C at position 153.
XX The antisense oligonucleotide is useful for inhibiting translation of HCV
XX genes
XX
XX Sequence 20 BP; 1 A; 4 C; 12 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 20;
```

```
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGGGUCCTCGAG 12
XX 4 GGGCTCTCGAG 15
XX
XX RESULT 113
XX AA065114
XX ID AA065114 standard; DNA; 20 BP.
XX
XX AA065114;
XX
XX 21-DEC-1994 (first entry)
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX inhibition; viral protein precursor; ss.
XX
XX Synthetic.
XX
XX CA2104649-A.
XX
XX 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-02104649.
XX
XX 25-AUG-1992; 92JP-00248796.
XX 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
XX
XX Seki M, Honda Y, Yamada E;
XX WPI; 1994-151836/19.
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX
XX Claim 5; Page 151; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
XX it has a base sequence of 15-30 bases which is included within the 49
XX bases from G at position 127 to C at position 175 of AA064913 and which
XX contains at least 7 bases from C at position 147 to C at position 153.
XX The antisense oligonucleotide is useful for inhibiting translation of HCV
XX genes
XX
XX Sequence 20 BP; 2 A; 3 C; 13 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 20;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGGGUCCTCGAG 12
XX 7 GGGCTCTCGAG 18
XX
XX RESULT 114
XX AA065129
XX ID AA065129 standard; DNA; 20 BP.
XX
XX AA065129;
XX
XX 21-DEC-1994 (first entry)
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX inhibition; viral protein precursor; ss.
```

XX OS Synthetic.  
XX PS CA2104649-A.  
XX PN 26-FEB-1994.  
XX PD 23-AUG-1993; 93CA-02104649.  
XX PF 25-AUG-1992; 92JP-00248796.  
XX PR 03-MAR-1993; 93JP-00042736.  
XX PA (SEKI/) SEKI M.  
XX PI Seki M, Honda Y, Yamada E;  
XX DR WPI; 1994-151836/19.  
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
XX genome - are useful as antiviral agents.  
XX PS Claim 5; Page 158; 262pp; English.  
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.  
XX CC it has a base sequence of 15-30 bases which is included within the 49  
XX CC bases from G at position 127 to C at position 175 of AAQ64913 and which  
XX CC contains at least 7 bases from C at position 147 to C at position 153.  
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
XX CC genes  
XX SQ Sequence 20 BP; 2 A; 2 C; 14 G; 2 T; 0 U; 0 Other;  
QY Query Match 66.7%; Score 12; DB 2; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
DB 1 GGGGUCCTCGAG 12  
8 GGGGTCTCTGAG 19  
RESULT 115  
AAQ64918  
ID AAQ64918 standard; DNA; 20 BP.  
XX AC AAQ64918;  
XX AC  
XX DT 19-DEC-1994 (first entry)  
XX DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
XX KM inhibition; viral protein precursor; ss.  
XX OS Synthetic.  
XX OS  
XX PN CA2104649-A.  
XX PN  
XX PD 26-FEB-1994.  
XX PF 23-AUG-1993; 93CA-02104649.  
XX PR 25-AUG-1992; 92JP-00248796.  
XX PR 03-MAR-1993; 93JP-00042736.  
XX PA (SEKI/) SEKI M.  
XX PI Seki M, Honda Y, Yamada E;  
XX DR WPI; 1994-151836/19.  
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
PT genome - are useful as antiviral agents.

XX PS Claim 5; Page 66; 262pp; English.  
XX XX  
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.  
XX CC it has a base sequence of 16-24 bases which is included within the 24  
XX CC bases from G at position 127 to C at position 150 of AAQ64913 and which  
XX CC contains at least 16 bases from C at position 131 to A at position 146.  
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
XX CC genes  
XX SQ Sequence 20 BP; 2 A; 5 C; 10 G; 3 T; 0 U; 0 Other;  
QY Query Match 66.7%; Score 12; DB 2; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
DB 1 GGGGUCCTCGAG 12  
1 GGGGTCTCTGAG 16  
RESULT 116  
AAQ65087  
ID AAQ65087 standard; DNA; 20 BP.  
XX AC AAQ65087;  
XX AC  
XX DT 20-DEC-1994 (first entry)  
XX DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
XX KM inhibition; viral protein precursor; ss.  
XX OS Synthetic.  
XX OS  
XX PN CA2104649-A.  
XX PN  
XX PD 26-FEB-1994.  
XX PF 23-AUG-1993; 93CA-02104649.  
XX PR 25-AUG-1992; 92JP-00248796.  
XX PR 03-MAR-1993; 93JP-00042736.  
XX PA (SEKI/) SEKI M.  
XX PI Seki M, Honda Y, Yamada E;  
XX DR WPI; 1994-151836/19.  
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
PT genome - are useful as antiviral agents.  
XX PS Claim 5; Page 140; 262pp; English.  
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.  
XX CC it has a base sequence of 15-30 bases which is included within the 49  
XX CC bases from G at position 127 to C at position 175 of AAQ64913 and which  
XX CC contains at least 7 bases from C at position 147 to C at position 153.  
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
XX CC genes  
XX SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;  
QY Query Match 66.7%; Score 12; DB 2; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
DB 1 GGGGUCCTCGAG 12  
5 GGGGTCTCTGAG 16

```

RESULT 117
AA055282 ID AA055282 standard; DNA; 20 BP.
XX
XX AA055282;
AC
XX 21-DEC-1994 (first entry)
DT
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
PN
XX 26-FEB-1994.
PD
XX
XX 23-AUG-1993; 93CA-02104649.
PF
XX
XX 25-AUG-1992; 92JP-00248796.
PR
XX 03-MAR-1993; 93JP-00042736.
PR
XX
XX (SEKI/) SEKI M.
PA
XX
XX Seki M, Honda Y, Yamada E;
PI
XX
XX WPI; 1994-151836/19.
DR
XX
XX Antisense oligonucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
PT
XX
XX Disclosure; Page 225; 262pp; English.
PS
XX
XX This oligonucleotide is an example of an antisense compound designed to
CC hybridise to a hepatitis C virus sequence. Such antisense
CC oligonucleotides are useful for inhibiting translation of HCV genes. (The
CC patent specification does not contain any references to this sequence)
CC
XX
XX Sequence 20 BP; 2 A; 5 C; 10 G; 3 T; 0 U; 0 Other;
SQ
Query Match 66.7%; Score 12; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
    |||:|||||
Db 2 GGGGCTCTGGAG 13
RESULT 118
AA058400 ID AA058400 standard; DNA; 20 BP.
XX
XX AA058400;
AC
XX
XX 25-MAR-2003 (revised)
DT
XX 04-OCT-1994 (first entry)
DT
XX
DE Antisense oligonucleotide CAS-104 to HCV 5'-untranslated region.
XX
XX Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBHV;
XX antisense oligonucleotide; translation inhibition; therapy; 5'-UTR;
XX 5'-untranslated region; loop C; ss.
XX
XX Synthetic.
OS
XX WO9405813-A1.
PN
XX 17-MAR-1994.
PD
XX

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```

PF 10-SEP-1993; 93WO-JP001293.
XX
XX 10-SEP-1992; 92US-00945289.
PR
XX 14-APR-1993; 93JP-00087195.
PR
XX
XX (MOCH ) MOCHIDA PHARM CO LTD.
PA
XX (KAGA ) CHEMO SERO THERAPEUTIC RES INST.
PA
XX (ISIS-) ISIS PHARM INC.
XX
XX Anderson KP, Hanecak RC, Hoshiko K, Nozaki C, Nishihara T;
PI
XX Nakatake H, Hamada F, Eto T, Furukawa S;
PI
XX
XX WPI; 1994-101217/12.
DR
XX
XX Antisense oligo:nucleotide(s) complementary to hepatitis C viral genome
PT - useful for inhibiting HCV replication, to treat related diseases.
PT
XX
XX Claim 28; Page 24; 91pp; English.
PS
XX
XX Antisense oligonucleotides were synthesised which are complementary to
CC target sequences located at 10-nucleotide intervals from nucleotide 1 to
CC 339 in the HCV RNA 5'-untranslated region. Of these sequences (CAS-1 to
CC CAS-320), oligonucleotide CAS-110 (AA058403), which is complementary to a
CC portion of loop C, was found to cause greater than 80% inhibition of core
CC protein translation. Antisense oligonucleotides which are complementary
CC to the 26 base region from nucleotides 104-129 of HCV RNA showed strong
CC inhibitory activity compared to oligonucleotides complementary to other
CC regions of the 5'-UTR. The oligonucleotides CAS-104, -106 and -108 showed
CC 70% or more inhibition of HCV translation. See AA058388-Q58422, AA044885-
CC Q44892 and AA058383. (Updated on 25-MAR-2003 to correct PN field.)
CC
XX
XX Sequence 20 BP; 2 A; 5 C; 10 G; 3 T; 0 U; 0 Other;
SQ
Query Match 66.7%; Score 12; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
    |||:|||||
Db 1 GGGGCTCTGGAG 12
RESULT 119
AA058401 ID AA058401 standard; DNA; 20 BP.
XX
XX AA058401;
AC
XX
XX 25-MAR-2003 (revised)
DT
XX 04-OCT-1994 (first entry)
DT
XX
DE Antisense oligonucleotide CAS-106 to HCV 5'-untranslated region.
XX
XX Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBHV;
XX antisense oligonucleotide; translation inhibition; therapy; 5'-UTR;
XX 5'-untranslated region; loop C; ss.
XX
XX Synthetic.
OS
XX WO9405813-A1.
PN
XX 17-MAR-1994.
PD
XX
XX 10-SEP-1993; 93WO-JP001293.
XX
XX 10-SEP-1992; 92US-00945289.
PR
XX 14-APR-1993; 93JP-00087195.
PR
XX
XX (MOCH ) MOCHIDA PHARM CO LTD.
PA
XX (KAGA ) CHEMO SERO THERAPEUTIC RES INST.
PA
XX (ISIS-) ISIS PHARM INC.
XX
XX Anderson KP, Hanecak RC, Hoshiko K, Nozaki C, Nishihara T;
PI

```

PI Nakatake H, Hamada F, Eto T, Furukawa S;  
XX  
XX WPI; 1994-101217/12.  
XX  
XX Anti:sense oligo:nucleotide(s) complementary to hepatitis C viral genome  
PT - useful for inhibiting HCV replication, to treat related diseases.  
XX  
XX  
PS Claim 28; Page 24; 91pp; English.  
XX  
CC Antisense oligonucleotides were synthesised which are complementary to  
CC target sequences located at 10-nucleotide intervals from nucleotide 1 to  
CC 339 in the HCV RNA 5'-untranslated region. Of these sequences (CAS-1 to  
CC CAS-320), oligonucleotide CAS-110 (AAQ58403), which is complementary to a  
CC portion of loop C, was found to cause greater than 80% inhibition of core  
CC protein translation. Antisense oligonucleotides which are complementary  
CC to the 26 base region from nucleotides 104-129 of HCV RNA showed strong  
CC inhibitory activity compared to oligonucleotides complementary to other  
CC regions of the 5'-UTR. The oligonucleotides CAS-104, -106 and -108 showed  
CC 70% or more inhibition of HCV translation. See AAQ58388-Q58422, AAQ44885-  
CC Q44892 and AAQ58383. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 20 BP; 2 A; 4 C; 11 G; 3 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUGGAG 12  
DB 3 GGGGTCCTGGAG 14  
RESULT 120  
AAQ58402  
ID AAQ58402 standard; DNA; 20 BP.  
XX  
XX AAQ58402;  
XX  
XX 25-MAR-2003 (revised)  
DT 04-OCT-1994 (first entry)  
XX  
DE Antisense oligonucleotide CAS-108 to HCV 5'-untranslated region.  
XX  
XX Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBHV;  
KW antisense oligonucleotide; translation inhibition; therapy; 5'-UTR;  
KM 5'-untranslated region; loop C; ss.  
XX  
XX Synthetic.  
XX  
XX WO9405813-A1.  
PN 17-MAR-1994.  
XX  
PD 10-SEP-1993; 93WO-JP001293.  
XX  
PF 10-SEP-1992; 92US-00945289.  
PR 14-APR-1993; 93JP-00087195.  
XX  
XX (MOCH) MOCHIDA PHARM CO LTD.  
PA (KAGA) CHEMO SERO THERAPEUTIC RES INST.  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Anderson KP, Hanecek RC, Hoshiko K, Nozaki C, Nishihara T;  
PI Nakatake H, Hamada F, Eto T, Furukawa S;  
XX  
XX WPI; 1994-101217/12.  
XX  
XX  
XX Anti:sense oligo:nucleotide(s) complementary to hepatitis C viral genome  
PT - useful for inhibiting HCV replication, to treat related diseases.  
XX  
XX  
PS Claim 28; Page 24; 91pp; English.  
XX  
CC Antisense oligonucleotides were synthesised which are complementary to

CC target sequences located at 10-nucleotide intervals from nucleotide 1 to  
CC 339 in the HCV RNA 5'-untranslated region. Of these sequences (CAS-1 to  
CC CAS-320), oligonucleotide CAS-110 (AAQ58403), which is complementary to a  
CC portion of loop C, was found to cause greater than 80% inhibition of core  
CC protein translation. Antisense oligonucleotides which are complementary  
CC to the 26 base region from nucleotides 104-129 of HCV RNA showed strong  
CC inhibitory activity compared to oligonucleotides complementary to other  
CC regions of the 5'-UTR. The oligonucleotides CAS-104, -106 and -108 showed  
CC 70% or more inhibition of HCV translation. See AAQ58388-Q58422, AAQ44885-  
CC Q44892 and AAQ58383. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUGGAG 12  
DB 5 GGGGTCCTGGAG 16  
RESULT 121  
AAQ58406  
ID AAQ58406 standard; DNA; 20 BP.  
XX  
XX AAQ58406;  
XX  
XX 25-MAR-2003 (revised)  
DT 04-OCT-1994 (first entry)  
XX  
DE Antisense oligonucleotide CAS-112 to HCV 5'-untranslated region.  
XX  
XX Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBHV;  
KW antisense oligonucleotide; translation inhibition; therapy; 5'-UTR;  
KM 5'-untranslated region; loop C; ss.  
XX  
XX Synthetic.  
XX  
XX WO9405813-A1.  
PN 17-MAR-1994.  
XX  
PD 10-SEP-1993; 93WO-JP001293.  
XX  
PF 10-SEP-1992; 92US-00945289.  
PR 14-APR-1993; 93JP-00087195.  
XX  
XX (MOCH) MOCHIDA PHARM CO LTD.  
PA (KAGA) CHEMO SERO THERAPEUTIC RES INST.  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Anderson KP, Hanecek RC, Hoshiko K, Nozaki C, Nishihara T;  
PI Nakatake H, Hamada F, Eto T, Furukawa S;  
XX  
XX WPI; 1994-101217/12.  
XX  
XX  
XX Anti:sense oligo:nucleotide(s) complementary to hepatitis C viral genome  
PT - useful for inhibiting HCV replication, to treat related diseases.  
XX  
XX  
PS Claim 28; Page 24; 91pp; English.  
XX  
CC Antisense oligonucleotides were synthesised which are complementary to  
CC target sequences located at 10-nucleotide intervals from nucleotide 1 to  
CC 339 in the HCV RNA 5'-untranslated region. Of these sequences (CAS-1 to  
CC CAS-320), oligonucleotide CAS-110 (AAQ58403), which is complementary to a  
CC portion of loop C, was found to cause greater than 80% inhibition of core  
CC protein translation. Antisense oligonucleotides which are complementary  
CC to the 26 base region from nucleotides 104-129 of HCV RNA showed strong  
CC inhibitory activity compared to oligonucleotides complementary to other  
CC regions of the 5'-UTR. See AAQ58388-Q58422, AAQ44885-Q44892 and AAQ58383.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX

Sequence 20 BP; 2 A; 3 C; 13 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 9 GGGGTCTCTGGAG 20

# RESULT 122

AAQ58403 ID AAQ58403 standard; DNA; 20 BP.

AC AAQ58403;

DT 25-MAR-2003 (revised)

DT 04-OCT-1994 (first entry)

DE Antisense oligonucleotide CAS-110 to HCV 5'-untranslated region.

KM Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBHV;

KM antisense oligonucleotide; translation inhibition; therapy; 5'-UTR;

XX 5'-untranslated region; loop C; ss.

OS Synthetic.

PN WO9405813-A1.

PD 17-MAR-1994.

PF 10-SEP-1993; 93WO-JP001293.

PR 10-SEP-1992; 92US-00945289.

PR 14-APR-1993; 93JP-00087195.

PA (MOCH ) MOCHIDA PHARM CO LTD.

PA (KAGA ) CHEMO SERO THERAPEUTIC RES INST.

PA (ISIS-) ISIS PHARM INC.

PI Anderson KP, Hanecak RC, Hoshiko K, Nozaki C, Nishihara T;

PI Nakatake H, Hamada F, Eco T, Furukawa S;

PI WPI; 1994-101217/12.

PT Anti:sense oligo:nucleotide(s) complementary to hepatitis C viral genome

PT - useful for inhibiting HCV replication, to treat related diseases.

PS Claim 28; Page 24; 91pp; English.

CC Antisense oligonucleotides were synthesised which are complementary to

CC target sequences located at 10-nucleotide intervals from nucleotide 1 to

CC 339 in the HCV RNA 5'-untranslated region. Of these sequences (CAS-1 to

CC CAS-120), oligonucleotide CAS-110 (AAQ58403), which is complementary to a

CC portion of loop C, was found to cause greater than 80% inhibition of core

CC protein translation. Antisense oligonucleotides which are complementary

CC to the 26 base region from nucleotides 104-129 of HCV RNA showed strong

CC inhibitory activity compared to oligonucleotides complementary to other

CC regions of the 5'-UTR. See AAQ58388-Q58422, AAQ44885-Q44892 and AAQ58383.

CC (updated on 25-MAR-2003 to correct PN field.)

XX XX Sequence 20 BP; 2 A; 3 C; 13 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 20;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 7 GGGGTCTCTGGAG 18

RESULT 123  
AAT39734/C  
ID AAT39734 standard; DNA; 20 BP.

AC AAT39734;

DT 09-APR-1997 (first entry)

DE Hepatitis C virus PCR primer IN2, based on nucleotides 88-97.

KM Hepatitis C virus; HCV; polymerase chain reaction; amplification;

KM replication; non-lymphoblastoid cell; monkey kidney cell; ss.

OS Synthetic.

PN WO9624662-A1.

PD 15-AUG-1996.

PF 10-FEB-1995; 95WO-IT000016.

PR 10-FEB-1995; 95WO-IT000016.

PA (CNDR ) CONSIGLIO NAZ DELLE RICERCH.

PI Ravagnan G, Battaglia M, Carloni G, Ponzetto A, Iacovacci S;

PI WPI; 1996-384435/38.

PT Replication of hepatitis C virus in non-lymphoblastoid mammalian cells -

PT useful for studies of HCV replication, prodn. of vaccines or viral

PT antigens, etc.

PS Disclosure; Page 8; 25pp; English.

CC Hepatitis C virus can be replicated in non-lymphoblastoid mammalian cells

CC by first incubating an HCV sample with the cells until an infecting

CC amount of HCV has been absorbed. Infected cells are then washed and

CC incubated under growth conditions. In an example, the presence of HCV in

CC culture medium of monkey kidney cells inoculated with HCV-infected serum

CC was verified by PCR amplification using two external primers (OU1 and

CC OU2, see AAT39731 and AAT39732) and two internal primers (IN1 and IN2,

CC see AAT39733 and AAT39734). The amplified products were identified by

CC hybridisation to labelled probe SI (see AAT39735). Small amounts of virus

CC were shown to be released into the culture medium from secondary

CC cultures. Control (non-inoculated) cells were negative for presence of

CC viral genome

XX XX Sequence 20 BP; 3 A; 10 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 20;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 19 GGGGTCTCTGGAG 8

# RESULT 124

AAT80229 ID AAT80229 standard; DNA; 20 BP.

AC AAT80229;

DT 15-OCT-1997 (first entry)

DE Oligo HCV42, targeted to HCV mRNA RNase sensitive region B.

XX Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;

KM inhibition; replication; expression; detection; chronic hepatitis;

KM acute hepatitis; hepatocarcinoma; ss.

```

OS      Synthetic.
XX      Key
FH      Location/Qualifiers
FT      modified_base
FT      1..20
FT      /*tag= a
FT      /note= "Comprises phosphorothioate linkages"
XX      WO9639500-A2.
XX      12-DEC-1996.
XX      PD
XX      04-JUN-1996; 96WO-EP002427.
XX      PF
XX      06-JUN-1995; 95US-00471968.
XX      PR
XX      (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX      (HYBR-) HYBRIDON INC.
XX      PI
XX      Frank BL, Goodchild J, Hamlin HA, Kilukskie RE, Roberts NA;
XX      Roberts PC, Walthers DM, Wolfe JL;
XX      WPI; 1997-043122/04.
XX      DR
XX      Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX      the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX      carcinoma.
XX      PT
XX      Disclosure; Page 25; 100pp; English.
XX      PS
XX      The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX      CC which are complementary to a portion of the 5' untranslated region (UTR)
XX      CC of hepatitis C virus (HCV). These sequences may be used in a
XX      CC pharmaceutical composition for the control or prevention of HCV
XX      CC infection. They may be used to inhibit replication or expression of HCV
XX      CC or for detecting the presence of HCV in a sample. They may be used to
XX      CC inhibit HCV replication in a cell and are therefore useful in the
XX      CC treatment of HCV infections such as chronic and acute hepatitis and
XX      CC hepatocarcinoma. This oligo was used in an RNase H assay to determine
XX      CC whether it binds successfully to its target. Three regions of HCV mRNA
XX      CC were investigated as RNase sensitive sites. This oligo binds to position
XX      CC -237 to -218
XX      SQ
XX      Sequence 20 BP; 2 A; 5 C; 10 G; 3 T; 0 U; 0 Other;
XX
XX      Query Match 66.7%; Score 12; DB 2; Length 20;
XX      Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX      Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY
XX      1 GGGGUCUCCUGAG 12
XX      |||||:|||||
XX      Db 2 GGGGTCTCTGGAG 13
XX
XX      RESULT 125
XX      AAT80230
XX      ID AAT80230 standard; DNA; 20 BP.
XX      AC
XX      AAT80230;
XX      DT
XX      15-OCT-1997 (first entry)
XX      DE
XX      Oligo HCV43, targeted to HCV mRNA RNase sensitive region B.
XX      KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX      KW inhibition; replication; expression; detection; chronic hepatitis;
XX      KW acute hepatitis; hepatocarcinoma; ss.
XX      OS
XX      Synthetic.
XX      Key
XX      Location/Qualifiers
XX      modified_base 1..20
XX      /*tag= a
XX      /note= "Comprises phosphorothioate linkages"

```

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XX      WO9639500-A2.
XX      12-DEC-1996.
XX      PD
XX      04-JUN-1996; 96WO-EP002427.
XX      PF
XX      06-JUN-1995; 95US-00471968.
XX      PR
XX      (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX      (HYBR-) HYBRIDON INC.
XX      PI
XX      Frank BL, Goodchild J, Hamlin HA, Kilukskie RE, Roberts NA;
XX      Roberts PC, Walthers DM, Wolfe JL;
XX      WPI; 1997-043122/04.
XX      DR
XX      Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX      the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX      carcinoma.
XX      PT
XX      Disclosure; Page 25; 100pp; English.
XX      PS
XX      The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX      CC which are complementary to a portion of the 5' untranslated region (UTR)
XX      CC of hepatitis C virus (HCV). These sequences may be used in a
XX      CC pharmaceutical composition for the control or prevention of HCV
XX      CC infection. They may be used to inhibit replication or expression of HCV
XX      CC or for detecting the presence of HCV in a sample. They may be used to
XX      CC inhibit HCV replication in a cell and are therefore useful in the
XX      CC treatment of HCV infections such as chronic and acute hepatitis and
XX      CC hepatocarcinoma. This oligo was used in an RNase H assay to determine
XX      CC whether it binds successfully to its target. Three regions of HCV mRNA
XX      CC were investigated as RNase sensitive sites. This oligo binds to position
XX      CC -233 to -214
XX      SQ
XX      Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
XX
XX      Query Match 66.7%; Score 12; DB 2; Length 20;
XX      Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX      Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY
XX      1 GGGGUCUCCUGAG 12
XX      |||||:|||||
XX      Db 6 GGGGTCTCTGGAG 17
XX
XX      RESULT 126
XX      AAX84019/C
XX      ID AAX84019 standard; CDNA; 20 BP.
XX      AC
XX      AAX84019;
XX      DT
XX      27-AUG-2003 (revised)
XX      DT
XX      26-AUG-1999 (first entry)
XX      DE
XX      Probe for HCV EI coding sequence.
XX      KW HCV EI region; monoclonal antibody; diagnosis; HCV EI-specific antigen;
XX      KW probe; ss.
XX      OS
XX      Synthetic.
XX      OS
XX      Hepatitis C virus.
XX      PN
XX      US5919454-A.
XX      PD
XX      06-JUL-1999.
XX      PF
XX      07-JUN-1995; 95US-00487231.
XX      PR
XX      18-MAR-1993; 93US-00965285.
XX      PA
XX      (INSP ) INST PASTEUR.

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```

XX Porchon C, Brechot C, Kremsdorf D;
XX WPI; 1999-394595/33.
XX Nucleotides and peptides from hepatitis C virus isolate for detecting EI-
XX specific antigens.
XX PS Disclosure; Col 5; 45pp; English.
XX This sequence represents a probe for DNA encoding a hepatitis C virus
XX (HCV) E1 region protein. The invention relates to human or murine
XX monoclonal antibodies directed against a HCV E1 protein sequence. The
XX CC monoclinal antibodies and their fragments are useful for the in vitro
XX CC diagnosis of HCV E1-specific antigens. (Updated on 27-AUG-2003 to correct
XX OS field.)
XX Sequence 20 BP; 3 A; 10 C; 5 G; 2 T; 0 U; 0 Other;
XX
Query Match 66.7%; Score 12; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCGAG 12
Db 19 GGGCTCTGAG 8

```

RESULT 127  
AAx16776/c  
ID AAX16776 standard; DNA; 20 BP.

AC AAX16776;  
XX  
XX 27-APR-1999 (first entry)  
XX  
XX Hepatitis C virus probe NC, bases -235 to -216.  
XX  
XX  
XX E1 region; French Hepatitis C virus; HCV; immunogen; antibody; detection;  
XX immunassay; probe; hybridisation; ss.  
XX  
XX Synthetic.  
XX Hepatitis C virus.  
XX  
XX US5866139-A.  
XX  
XX 02-FEB-1999.  
XX  
XX 07-JUN-1995; 95US-00483695.  
XX  
XX 18-MAR-1993; 93US-00965285.  
XX  
XX (INSP ) INST PASTEUR.  
XX  
XX Porchon C, Kremsdorf D, Brechot C;  
XX WPI; 1999-141865/12.  
XX  
XX New isolated and purified Hepatitis C virus E1 peptides - useful for  
XX vaccine production or diagnostic purposes.  
XX  
XX  
XX Disclosure; Col 5-6; 45pp; English.  
XX  
XX Probes AAX16773-X16777 were used to screen for sequences in the E1, NS1,  
XX NS2, NS3 and NS4 regions from a French Hepatitis C virus (HCV) isolate.  
XX The protein or peptides derived from these regions (see AAX16758-X16761)  
XX can be: (i) conjugated to a carrier protein and used as immunogens for  
XX CC eliciting protective antibodies; or (ii) labelled, and used as  
XX CC immunassay reagents for detecting antibodies specific for HCV E1  
XX  
XX Sequence 20 BP; 3 A; 10 C; 5 G; 2 T; 0 U; 0 Other;  
XX  
Query Match 66.7%; Score 12; DB 2; Length 20;

```

XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCGAG 12
Db 19 GGGCTCTGAG 8

```

RESULT 128  
AAx52565  
ID AAx52565 standard; DNA; 20 BP.

AC AAx52565;  
XX  
XX 27-SEP-2000 (first entry)  
XX  
XX Oligonucleotide SEQ ID NO:3, complementary to HCV RNA bases 97-116.  
XX  
XX Oligonucleotide; HCV genomic RNA; detection; amplification;  
XX reverse transcription inhibition; translation inhibition; antiviral;  
XX gene therapy; antisense; reverse transcription-PCR; RT-PCR primer; probe;  
XX ss.  
XX Hepatitis C virus.  
XX  
XX Key Location/Qualifiers  
XX FT masc\_binding 1..20  
XX FT tag a  
XX PN EPI002878-A2. /bound\_molecy= "HCV genomic RNA, bases 97-116"  
XX  
XX PD 24-MAY-2000.  
XX  
XX 18-NOV-1999; 99EP-00122092.  
XX  
XX 19-NOV-1998; 98JP-00323874.  
XX  
XX (TOYT ) TOSOH CORP.  
XX  
XX Toshiki T, Takahiko I, Juichi S;  
XX WPI; 2000-352431/31.  
XX  
XX Hepatitis C virus RNA-binding single-stranded oligo DNAs useful as  
XX reagents for gene diagnosis involving cleavage, amplification and  
XX detection of RNA and as an inhibitory drugs.  
XX  
XX Claim 3; Page 12; 21pp; English.  
XX  
XX The invention relates to single-stranded antisense oligodeoxynucleotides  
XX (AAx52563-A52568) which bind to various sites on the hepatitis C virus  
XX (HCV) RNA genome, and to sense oligodeoxynucleotides (AAx52569-A52571)  
XX corresponding to sites on the HCV genome. The oligonucleotides are useful  
XX as primers in RT-PCR (reverse transcription-PCR) and the sense  
XX oligonucleotides may also be used as promoter primers. The antisense  
XX oligonucleotides may be used to inhibit translation or reverse  
XX transcription of HCV RNA and may be used as probes for detection of HCV  
XX RNA. Additionally, the antisense oligos may be linked to an RNA-cleaving  
XX cleavage. The invention also encompasses methods of identifying and  
XX preparing single-stranded oligodeoxynucleotides which bind to target  
XX RNAs. The single-stranded oligodeoxynucleotides are useful as reagents  
XX for genetic diagnosis involving cleavage, amplification and detection of  
XX HCV RNA (as primers and probes), and as inhibitors of reverse  
XX transcription or translation of HCV RNA. Sequences AAx52563-A52568  
XX represent the antisense oligodeoxynucleotides of the invention. The  
XX present sequence is complementary to bases 97-116 of HCV genomic RNA  
XX  
XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUGAG 12  
|||:|||||  
Db 6 GGGGTCCTGAG 17

## RESULT 129

AAA52566  
ID AAA52566 standard; DNA; 20 BP.

AAA52566;

DT 27-SEP-2000 (first entry)

DE Oligonucleotide SEQ ID NO:4, complementary to HCV RNA bases 95-114.

XX Oligonucleotide; HCV genomic RNA; detection; amplification;

KM reverse transcription inhibition; translation inhibition; antiviral;

KW gene therapy; antisense; reverse transcription-PCR; RT-PCR primer; probe;

ss.

XX Hepatitis C virus.

OS Hepatitis C virus.

XX Key

FT misc\_binding

FT 1..20

FT /tag= a

FT /bound\_molety= "HCV genomic RNA, bases 95-114"

PN EPI002878-A2.

PD 24-MAY-2000.

PF 18-NOV-1999; 99EP-00122092.

PR 19-NOV-1998; 98UP-00329874.

XX (TOYU ) TOSOH CORP.

PA Toshiki T, Takahiko I, Juichi S;

PI WPI; 2000-352431/31.

DR Hepatitis C virus RNA-binding single-stranded oligo DNAs useful as

PT reagents for gene diagnosis involving cleavage, amplification and

PT detection of RNA and as an inhibitory drugs.

XX Claim 4; Page 13; 21pp; English.

XX The invention relates to single-stranded antisense oligodeoxynucleotides

CC (AAA52563-A52568) which bind to various sites on the hepatitis C virus

CC (HCV) RNA genome, and to sense oligodeoxynucleotides (AAA52569-A52571)

CC corresponding to sites on the HCV genome. The oligonucleotides are useful

CC as primers in RT-PCR (reverse transcription-PCR) and the sense

CC oligonucleotides may also be used as promoter primers. The antisense

CC oligonucleotides may be used to inhibit translation or reverse

CC transcription of HCV RNA and may be used as probes for detection of HCV

CC RNA. Additionally, the antisense oligos may be linked to an RNA-cleaving

CC moiety to target single-stranded RNA cleavage or RNA heteroduplex

CC cleavage. The invention also encompasses methods of identifying and

CC preparing single-stranded oligodeoxynucleotides which bind to target

CC RNAs. The single-stranded oligodeoxynucleotides are useful as reagents

CC for genetic diagnosis involving cleavage, amplification and detection of

CC HCV RNA (as primers and probes), and as inhibitors of reverse

CC transcription or translation of HCV RNA. Sequences AAA42563-A52568

CC represent the antisense oligodeoxynucleotides of the invention. The

CC present sequence is complementary to bases 95-114 of HCV genomic RNA

XX Sequence 20 BP; 1 A; 4 C; 12 G; 3 T; 0 U; 0 Other;

## Query Match

Best Local Similarity 66.7%; Score 12; DB 3; Length 20;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUGAG 12  
|||:|||||

Db 4 GGGGTCCTGAG 15

## RESULT 130

AAA52564  
ID AAA52564 standard; DNA; 20 BP.

AAA52564;

DT 27-SEP-2000 (first entry)

DE Oligonucleotide SEQ ID NO:2, complementary to HCV RNA bases 99-118.

XX Oligonucleotide; HCV genomic RNA; detection; amplification;

KM reverse transcription inhibition; translation inhibition; antiviral;

KW gene therapy; antisense; reverse transcription-PCR; RT-PCR primer; probe;

ss.

XX Hepatitis C virus.

OS Hepatitis C virus.

XX Key

FT misc\_binding

FT 1..20

FT /tag= a

FT /bound\_molety= "HCV genomic RNA, bases 99-118"

PN EPI002878-A2.

PD 24-MAY-2000.

PF 18-NOV-1999; 99EP-00122092.

PR 19-NOV-1998; 98UP-00329874.

XX (TOYU ) TOSOH CORP.

PA Toshiki T, Takahiko I, Juichi S;

PI WPI; 2000-352431/31.

DR Hepatitis C virus RNA-binding single-stranded oligo DNAs useful as

PT reagents for gene diagnosis involving cleavage, amplification and

PT detection of RNA and as an inhibitory drugs.

XX Claim 2; Page 12; 21pp; English.

XX The invention relates to single-stranded antisense oligodeoxynucleotides

CC (AAA52563-A52568) which bind to various sites on the hepatitis C virus

CC (HCV) RNA genome, and to sense oligodeoxynucleotides (AAA52569-A52571)

CC corresponding to sites on the HCV genome. The oligonucleotides are useful

CC as primers in RT-PCR (reverse transcription-PCR) and the sense

CC oligonucleotides may also be used as promoter primers. The antisense

CC oligonucleotides may be used to inhibit translation or reverse

CC transcription of HCV RNA and may be used as probes for detection of HCV

CC RNA. Additionally, the antisense oligos may be linked to an RNA-cleaving

CC moiety to target single-stranded RNA cleavage or RNA heteroduplex

CC cleavage. The invention also encompasses methods of identifying and

CC preparing single-stranded oligodeoxynucleotides which bind to target

CC RNAs. The single-stranded oligodeoxynucleotides are useful as reagents

CC for genetic diagnosis involving cleavage, amplification and detection of

CC HCV RNA (as primers and probes), and as inhibitors of reverse

CC transcription or translation of HCV RNA. Sequences AAA42563-A52568

CC represent the antisense oligodeoxynucleotides of the invention. The

CC present sequence is complementary to bases 99-118 of HCV genomic RNA

XX Sequence 20 BP; 2 A; 2 C; 14 G; 2 T; 0 U; 0 Other;

## Query Match

Best Local Similarity 66.7%; Score 12; DB 3; Length 20;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;



OY 1 GGGGUCUCUGAG 12  
 |||||:  
 DB 8 GGGGTCCTCGAG 19

RESULT 131  
 ID AAK52663/C  
 ABK52663 standard; DNA; 20 BP.

XX AC ABK52663;

XX DT 27-AUG-2002 (first entry)

XX DE Hepatitis C virus DNA real time PCR probe.

XX KM Human; hepatitis C virus; HCV probe; PCR; real-time PCR; antiviral;

XX KM viral replication inhibitor; mitochondrial toxicity; ss.

XX OS Hepatitis C virus.

XX FT Key Location/Qualifiers

XX FT modified\_base 1

XX FT /tag= a  
 /note= "FAM (6-carboxy fluorescein) labelled"

XX FT modified\_base 20

XX FT /tag= b  
 /note= "TAMRA (6-carbo tetramethyl rhodamine) labelled"

XX PN WO200233128-A2.

XX PD 25-APR-2002.

XX PF 18-OCT-2001; 2001WO-US047223.

XX PR 18-OCT-2000; 2000US-0241488P.

XX PR 15-DEC-2000; 2000US-0256067P.

XX PR 06-APR-2001; 2001US-0282156P.

XX PA (PHAR-) PHARMASSET LTD.

XX PI Stuyver L, Watanabe KA;

XX DR WPI; 2002-454613/48.

XX PT Identifying a viral replication inhibitor comprises contacting nucleic acids from a virus infected host with an amplification mixture of two primers and/or probes that provide detectable signals during a polymerase chain reaction.

XX PS Example 16; Page 36; 95pp; English.

XX CC This invention relates to a novel method for identifying an inhibitor of viral replication by contacting nucleic acids from a virus infected host with an amplification mixture having 2 primers and/or probes that provide detectable signals during a polymerase chain reaction. The method of the invention is useful for identifying a compound that inhibits viral replication. Another new method is useful for assessing the toxicity of an anti-viral compound. The method of the invention is economic, non-radioactive, rapid, accurate, reproducible and amenable to large throughput. The second method of the invention is a sensitive and accurate method for determining mitochondrial toxicity of a compound. The present sequence represents a hepatitis C virus (HCV) real time PCR probe used in the method of the invention

XX SQ Sequence 20 BP; 2 A; 14 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 6; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUCUGAG 12  
 |||||:  
 DB 13 GGGGTCCTCGAG 2

RESULT 132

XX ID AAD33151 standard; DNA; 20 BP.

XX AC AAD33151;

XX DT 01-JUL-2002 (first entry)

XX DE GsuI enzyme recognition sequence #2.

XX KM Restriction endonuclease; altered specificity; recognition sequence; GsuI; enzyme; ds.

XX OS Unidentified.

XX PN EP1179596-A1.

XX PD 13-FEB-2002.

XX PF 06-JUL-2001; 2001EP-00305859.

XX PR 10-AUG-2000; 2000GB-00019744.

XX PA (FERM-) FERMENTAS AB.

XX PI Janulaitis A, Rimseleiene R, Lubys A;

XX DR WPI; 2002-229927/29.

XX PT Producing DNA encoding restriction endonuclease with altered specificity, comprises mutagenizing DNA encoding the enzyme and isolating DNA encoding mutated enzyme with specificity for an altered sequence.

XX PS Example; Page 5; 44pp; English.

XX CC The invention relates to a method of producing a polynucleotide encoding a restriction endonuclease with altered specificity. The method involves mutagenizing a polynucleotide encoding restriction endonuclease with specificity for a recognition sequence to produce mutated polynucleotides and isolating from them a polynucleotide encoding mutated restriction endonuclease with specificity for an altered recognition sequence by selecting a polynucleotide expressing a restriction endonuclease with methylase specificity for the altered recognition sequence. The method is useful for producing a polynucleotide encoding a restriction endonuclease comprising Eco571, BcgI, HaeIII or AclI, with an altered specificity. The method allows selection of mutant variants recognising new sequences that differ not only in single nucleotide from wild type enzyme but also for mutants that recognise degenerate sequences or sequences differing in several nucleotides, especially if mutants of altered specificity are taken into the next round of mutagenesis and digestion-selection. The present sequence is recognition sequence of GsuI restriction enzyme

XX SQ Sequence 20 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 14 Other;

Query Match 66.7%; Score 12; DB 6; Length 20;  
 Best Local Similarity 91.7%; Pred. No. 3.4e+03;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 CTGGAGNNNNNN 18  
 |||||:  
 DB 1 CTGGAGNNNNNN 12

RESULT 133

XX ID ABO78212 standard; DNA; 20 BP.

XX AC ABO78212;

XX DT 22-OCT-2002 (first entry)



CC represents a synthetic oligonucleotide used for inhibiting HCV  
CC replication and expression of HCV  
XX  
SQ Sequence 20 BP; 2 A; 5 C; 10 G; 3 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 6; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGGGUCCTGGAG 12  
DB 2 GGGGTCTCTGGAG 13  
RESULT 135  
ABS55814  
ID ABS55814 standard; DNA; 20 BP.  
XX  
AC ABS55814;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Inhibitory oligonucleotide specific for hepatitis C virus #20.  
XX  
KM Hepatitis C virus; HCV; hepatocyte infection; non-A hepatitis;  
KM non-B hepatitis; acute hepatitis; chronic hepatitis;  
KM hepatocellular carcinoma; virucide; cytostatic; antisense therapy;  
KM gene therapy; ss.  
XX  
OS Synthetic.  
XX  
PN US2002081577-A1.  
XX  
PD 27-JUN-2002.  
XX  
PF 02-JUL-1997; 97US-00887505.  
XX  
PR 06-JUN-1995; 95US-00471968.  
PR 02-JUL-1996; 96US-0021104P.  
XX  
PA (KILK/) KILKUSKIE R L.  
PA (FRAN/) FRANK B L.  
PA (GOOD/) GOODCHILD J.  
PA (WOLF/) WOLFE J L.  
PA (ROBE/) ROBERTS P C.  
PA (HAML/) HAMLIN H A.  
PA (ROBE/) ROBERTS N A.  
PA (WALT/) WALTHER D M.  
XX  
PI Kilkuskie RL, Frank BL, Goodchild J, Wolfe JL, Roberts PC;  
PI Hamlin HA, Roberts NA, Walther DM;  
XX  
DR WPI; 2002-537132/57.  
XX  
PT Synthetic oligonucleotides complementary to a portion of the 5'  
PT untranslated region of hepatitis C virus (HCV), useful for diagnosing and  
PT treating HCV infections and hepatocellular carcinoma.  
XX  
PS Disclosure; Page 8; 74pp; English.  
XX  
CC The invention describes synthetic oligonucleotides complementary to a  
CC portion of the 5' untranslated region of hepatitis C virus. The  
CC oligonucleotides may be used in methods for controlling, preventing, and  
CC treating hepatitis C virus infection, in antisense technology and gene  
CC therapy, and of detecting the presence of hepatitis C virus in a sample.  
CC Hepatitis C virus (HCV) is an enveloped, positive sense, single-stranded  
CC RNA virus which infects hepatocytes. HCV is the major cause of non-A, non  
CC -B, acute and chronic hepatitis, and has been associated with  
CC hepatocellular carcinoma. The invention describes methods and kits for  
CC inhibiting replication of HCV, inhibiting the expression of HCV nucleic  
CC acid and protein, and for treating HCV infections. This sequence  
CC represents a synthetic oligonucleotide used for inhibiting HCV  
CC replication and expression of HCV

XX  
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 6; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGGGUCCTGGAG 12  
DB 6 GGGGTCTCTGGAG 17  
RESULT 136  
AAQ65101  
ID AAQ65101 standard; DNA; 21 BP.  
XX  
AC AAQ65101;  
XX  
DT 21-DEC-1994 (first entry)  
XX  
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX  
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
KM inhibition; viral protein precursor; ss.  
XX  
OS Synthetic.  
XX  
PN CA2104649-A.  
XX  
PD 26-FEB-1994.  
XX  
PF 23-AUG-1993; 93CA-02104649.  
XX  
PR 25-AUG-1992; 92JP-00248796.  
PR 03-MAR-1993; 93JP-00042736.  
XX  
PA (SEKI/) SEKI M.  
XX  
PI Seki M, Honda Y, Yamada E;  
XX  
DR WPI; 1994-151836/19.  
XX  
PT Anti-sense oligo:nucleotide(s) complementary to the hepatitis C virus  
PT genome - are useful as antiviral agents.  
XX  
PS Claim 5; Page 146; 262pp; English.  
XX  
CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AAQ64913 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 21 BP; 2 A; 3 C; 13 G; 3 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 21;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGGGUCCTGGAG 12  
DB 7 GGGGTCTCTGGAG 18  
RESULT 137  
AAQ64923  
ID AAQ64923 standard; DNA; 21 BP.  
XX  
AC AAQ64923;  
XX  
DT 19-DEC-1994 (first entry)  
XX

```

DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
PN
XX
XX 26-FEB-1994.
PD
XX
XX 23-AUG-1993; 93CA-02104649.
PF
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
PA
XX Seki M, Honda Y, Yamada E;
PI
XX WPI; 1994-151836/19.
DR
XX
XX Antisense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
PS
XX Claim 5; Page 68; 262pp; English.
PS
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 16-24 bases which is included within the 24
CC bases from G at position 127 to C at position 150 of AAQ64913 and which
CC contains at least 16 bases from C at position 131 to A at position 146.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
XX Sequence 21 BP; 3 A; 5 C; 10 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 21;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTCGAG 12
XX ||||:|||||
Db 1 GGGGTCTCTGAG 12
XX

RESULT 138
AAQ65088
ID AAQ65088 standard; DNA; 21 BP.
XX
XX AAQ65088;
AC
XX
XX 20-DEC-1994 (first entry)
DT
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
PN
XX
XX 26-FEB-1994.
PD
XX
XX 23-AUG-1993; 93CA-02104649.
PF
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
PA
XX Seki M, Honda Y, Yamada E;
PI
XX

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DR WPI; 1994-151836/19.
XX
XX Antisense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
PS
XX Claim 5; Page 140; 262pp; English.
PS
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AAQ64913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
XX Sequence 21 BP; 2 A; 3 C; 13 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 21;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTCGAG 12
XX ||||:|||||
Db 6 GGGGTCTCTGAG 17
XX

RESULT 139
AAQ65130
ID AAQ65130 standard; DNA; 21 BP.
XX
XX AAQ65130;
AC
XX
XX 21-DEC-1994 (first entry)
DT
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
PN
XX
XX 26-FEB-1994.
PD
XX
XX 23-AUG-1993; 93CA-02104649.
PF
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
PA
XX Seki M, Honda Y, Yamada E;
PI
XX WPI; 1994-151836/19.
DR
XX
XX Antisense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
PS
XX Claim 5; Page 158; 262pp; English.
PS
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AAQ64913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
XX Sequence 21 BP; 2 A; 3 C; 14 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 21;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GGGGUCGCGAG 12  
 ||||:||||  
 Db 9 GGGGTCTCGAG 20

RESULT 140  
 AA065115  
 ID AA065115 standard; DNA; 21 BP.

XX AA065115;

XX 21-DEC-1994 (first entry)

DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.

XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 XX Inhibition; viral protein precursor; ss.

OS Synthetic.

PN CA2104649-A.

XX 26-FEB-1994.

PF 23-AUG-1993; 93CA-02104649.

PR 25-AUG-1992; 92JP-00248796.

PR 03-MAR-1993; 93JP-00042736.

PA (SEKI/) SEKI M.

PI Seki M, Honda Y, Yamada E;

XX WPI; 1994-151836/19.

PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
 genome - are useful as antiviral agents.

PS Claim 5; Page 152; 262pp; English.

CC This oligonucleotide is an example of a preferred antisense compound i.e.  
 CC it has a base sequence of 15-30 bases which is included within the 49  
 CC bases from G at position 127 to C at position 175 of AA064913 and which  
 CC contains at least 7 bases from C at position 147 to C at position 153.  
 CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 CC genes

SO Sequence 21 BP; 2 A; 3 C; 14 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 21;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGCGAG 12  
 ||||:||||  
 Db 8 GGGGTCTCGAG 19

RESULT 141

AA065076  
 ID AA065076 standard; DNA; 21 BP.

XX AA065076;

XX 20-DEC-1994 (first entry)

DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.

XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 XX Inhibition; viral protein precursor; ss.

OS Synthetic.

PN CA2104649-A.

XX 26-FEB-1994.

PF 23-AUG-1993; 93CA-02104649.

PR 25-AUG-1992; 92JP-00248796.

PR 03-MAR-1993; 93JP-00042736.

PA (SEKI/) SEKI M.

PI Seki M, Honda Y, Yamada E;

XX WPI; 1994-151836/19.

PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
 genome - are useful as antiviral agents.

PS Claim 5; Page 135; 262pp; English.

CC This oligonucleotide is an example of a preferred antisense compound i.e.  
 CC it has a base sequence of 15-30 bases which is included within the 49  
 CC bases from G at position 127 to C at position 175 of AA064913 and which  
 CC contains at least 7 bases from C at position 147 to C at position 153.  
 CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 CC genes

SO Sequence 21 BP; 2 A; 4 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 21;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGCGAG 12  
 ||||:||||  
 Db 5 GGGGTCTCGAG 16

RESULT 142

AA065146  
 ID AA065146 standard; DNA; 21 BP.

XX AA065146;

XX 21-DEC-1994 (first entry)

DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.

XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 XX Inhibition; viral protein precursor; ss.

OS Synthetic.

PN CA2104649-A.

XX 26-FEB-1994.

PF 23-AUG-1993; 93CA-02104649.

PR 25-AUG-1992; 92JP-00248796.

PR 03-MAR-1993; 93JP-00042736.

PA (SEKI/) SEKI M.

PI Seki M, Honda Y, Yamada E;

XX WPI; 1994-151836/19.

PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
 genome - are useful as antiviral agents.

PS Claim 5; Page 165; 262pp; English.

```

CC This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AAQ64913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
SQ Sequence 21 BP; 2 A; 5 C; 12 G; 2 T; 0 U; 0 Other;

Query Match      66.7%; Score 12; DB 2; Length 21;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12
   |||||:|||||
Db 10 GGGGTCTCGAG 21

RESULT 143
AAQ65065
ID AAQ65065 standard; DNA; 21 BP.
AC AAQ65065;
XX
XX 20-DEC-1994 (first entry)
DT
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX inhibition; viral protein precursor; ss.
XX
XX Synthetic.
XX
XX CA2104649-A.
XX
XX 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-02104649.
XX
XX 25-AUG-1992; 92JP-00248796.
XX 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
XX
XX Seki M, Honda Y, Yamada E;
XX
XX WPI; 1994-151836/19.
XX
XX Anti-sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX
XX Claim 5; Page 130; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
XX it has a base sequence of 15-30 bases which is included within the 49
XX bases from G at position 127 to C at position 175 of AAQ64913 and which
XX contains at least 7 bases from C at position 147 to C at position 153.
XX The antisense oligonucleotide is useful for inhibiting translation of HCV
XX genes
XX
SQ Sequence 21 BP; 2 A; 4 C; 12 G; 3 T; 0 U; 0 Other;

Query Match      66.7%; Score 12; DB 2; Length 21;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12
   |||||:|||||
Db 4 GGGGTCTCGAG 15

RESULT 144
AAQ72991

```

```

ID AAA72991 standard; DNA; 21 BP.
XX
XX AAA72991;
AC
XX 24-NOV-2000 (first entry)
DT
XX
XX Hepatitis C virus antisense oligonucleotide HCV123.
DE
XX
XX Hepatitis C virus; HCV; antisense oligonucleotide; leuciferinase;
XX luciferase; HepG2; medicine; ss.
XX
XX Hepatitis C virus.
OS
XX
XX CN1253138-A.
XX
XX 17-MAY-2000.
XX
XX
XX 09-NOV-1998; 98CN-00124388.
XX
XX
XX 09-NOV-1998; 98CN-00124388.
XX
XX
XX 09-NOV-1998; 98CN-00124388.
XX
XX
XX (RADI-) RADIOMEDICINE ACAD MILITARY MEDICAL SCI.
XX
XX Wang S, Wang X, Zhu B;
XX
XX WPI; 2000-46526/41.
XX
XX
XX Structure and usage of antisense oligonucleotide for treating diseases
XX correlative to hepatitis C virus.
XX
XX
XX Claim 1; Page 1; 20pp; Chinese.
XX
XX
XX The present invention describes antisense oligonucleotides which are
XX designed and synthesised on the basis of the gene structure of hepatitis
XX C virus (HCV) and can be used to suppress the expression of HCV gene. The
XX non-coding region 5' of HCV gene is used to regulate the instantaneous
XX expression system of leuciferinase gene in HepG2 cells and the transgenic
XX cell model HepG2.9706 of luciferase gene. The 15 antisense
XX oligonucleotides (AAV2988 to AAA73002) which are complementary to the
XX non-coding region 5' and translational initiation region of HCV are
XX actively screened and evaluated to discover for the first time the
XX oligonucleotides HCV279, HCV349, HCV363, HCV65 and HCV 313 and their
XX chemical modified objects for suppressing the expression of HCV gene.
XX Thus, the present invention relates to the new medicine for treating the
XX diseases associated with HCV
XX
XX
SQ Sequence 21 BP; 3 A; 5 C; 10 G; 3 T; 0 U; 0 Other;

Query Match      66.7%; Score 12; DB 3; Length 21;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12
   |||||:|||||
Db 1 GGGGTCTCGAG 12

RESULT 145
ADD67935/C
ID ADD67935 standard; DNA; 21 BP.
AC ADD67935;
XX
XX 15-JAN-2004 (first entry)
DT
XX
XX Hepatitis C virus detection probe seq id 7.
DE
XX
XX antiviral; hepatitis C virus; HCV; viral replication inhibitor;
XX replication competent HCV; 3' non-translated region; probe; ss.
XX
XX Hepatitis C virus.
OS
XX
XX US2003125541-A1.
XX
XX

```

```
XX 03-JUL-2003.
PD
XX
PF 27-SEP-2002; 2002US-00259275.
XX
PR 23-DEC-1999; 99US-0171909P.
PR 23-DEC-2000; 2000US-00747419.
PR 27-SEP-2001; 2001US-0325236P.
PR 13-NOV-2001; 2001US-0338123P.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Lemon SM, Y1 M;
XX
DR WPI; 2003-811006/76.
XX
XX Identifying a compound that inhibits replication of a hepatitis C virus
PT (HCV) RNA comprises contacting a cell comprising a replication competent
PT HCV RNA containing a heterologous polynucleotide encoding a
PT transactivator, with a compound.
XX
XX Example 2; SEQ ID NO 7; 95pp; English.
XX
CC The invention describes a method of identifying a compound that inhibits
CC replication of a hepatitis C virus (HCV) RNA. The method comprises
CC contacting a cell comprising a replication competent HCV RNA containing a
CC heterologous polynucleotide having a first coding sequence encoding a
CC transactivator, with a compound. The method is useful for identifying a
CC compound that inhibits replication of HCV RNA. The kit is useful for
CC detecting replication competent HCV RNA. This sequence represents a probe
CC used to detect DNA encoding HCV in order to detect the production of the
CC virus by chimpanzee.
XX
SQ Sequence 21 BP; 3 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 66.7%; Score 12; DB 10; Length 21;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTCGAG 12
Db 21 GGGGCTCTCGAG 10
RESULT 146
ABX10607/c
ID ABX10607 standard; DNA; 21 BP.
XX
AC ABX10607;
XX
DT 11-APR-2003 (first entry)
XX
DE Light Cycler red PCR probe used to detect HCV.
XX
XX PCR; probe; ss; replication competent; hepatitis C virus; HCV;
KM 3' non-translated RNA; 3'NTR; chronic viral hepatitis; hepatic fibrosis;
KM cirrhosis; hepatocellular carcinoma.
XX
XX Hepatitis C virus.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= labelled with Light Cycler Red 640 dye"
XX
PN US2002155582-A1.
XX
PD 24-OCT-2002.
XX
PF 23-DEC-2000; 2000US-00747419.
XX
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PR 23-DEC-1999; 99US-0171909P.
XX
XX (LEMO/) LEMON S M.
PA (Y1M/) Y1 M.
XX
XX Lemon SM, Y1 M;
XX
DR WPI; 2003-182640/18.
XX
XX Novel replication competent hepatitis C virus for producing infectious
PT viral particles and as antigen for detecting hepatitis C virus
PT antibodies, comprises hepatitis C virus genome and heterologous
PT polynucleotide.
XX
XX Example 2; Page 12; 37pp; English.
XX
XX The invention discloses a replication competent hepatitis C virus (HCV)
CC comprising a HCV virus genome and a heterologous polynucleotide, where
CC the HCV genome comprises a 3' non-translated RNA and the heterologous
CC polynucleotide is present in the 3' non-translated RNA. HCV is a cause of
CC chronic viral hepatitis, hepatic fibrosis, cirrhosis and/or the
CC development of hepatocellular carcinoma. A cell comprising the HCV is
CC useful for selecting or detecting a replication competent HCV, for
CC identifying a compound that inhibits replication of HCV, for producing
CC infectious viral particles which are useful as a source of virus
CC particles for various assays, including evaluating methods for
CC inactivating particles, excluding particles from serum, identifying a
CC neutralizing compound and as an antigen for use in detecting anti-HCV
CC antibodies in an animal. The cell comprising the HCV is also useful for
CC identifying a variant HCV. An HCV particle is useful as an antigen, as a
CC positive-control in assays that test for the presence of anti-HCV
CC antibodies, to produce antibodies to detect the presence of viral
CC particles in biological samples (e.g. blood products and cell-free blood
CC products) and as a source of viral antigen to measure the presence and
CC amount of antibody present in an animal. The sequence presented is the
CC Light Cycler PCR red probe which was used to detect HCV
XX
SQ Sequence 21 BP; 3 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 66.7%; Score 12; DB 10; Length 21;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTCGAG 12
Db 21 GGGGCTCTCGAG 10
RESULT 147
AAQ65116
ID AAQ65116 standard; DNA; 22 BP.
XX
AC AAQ65116;
XX
DT 21-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX
XX CA2104649-A.
XX
XX 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-02104649.
XX
XX 25-AUG-1992; 92JP-00248796.
XX
XX 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
PA
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XX PI Seki M, Honda Y, Yamada E;
XX DR WPI; 1994-151836/19.
XX PT Antisense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX PS Claim 5; Page 152; 262pp; English.
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes.
XX SQ Sequence 22 BP; 2 A; 4 C; 14 G; 2 T; 0 U; 0 Other;

Query Match      66.7%; Score 12; DB 2; Length 22;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12
   ||||:|||||
Db 9 GGGGTCTCTGAG 20

RESULT 148
AA065102
ID AA065102 standard; DNA; 22 BP.
XX
AC AA065102;
XX
DT 21-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-02104649.
XX
PR 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
PA (SEKI/) SEKI M.
XX
PI Seki M, Honda Y, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Antisense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
PS Claim 5; Page 146; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes.
XX SQ Sequence 22 BP; 2 A; 3 C; 14 G; 3 T; 0 U; 0 Other;

Query Match      66.7%; Score 12; DB 2; Length 22;

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      Best Local Similarity 83.3%; Pred. No. 3.4e+03;
      Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12
   ||||:|||||
Db 8 GGGGTCTCTGAG 19

RESULT 149
AA065131
ID AA065131 standard; DNA; 22 BP.
XX
AC AA065131;
XX
DT 21-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-02104649.
XX
PR 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
PA (SEKI/) SEKI M.
XX
PI Seki M, Honda Y, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Antisense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
PS Claim 5; Page 159; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes.
XX SQ Sequence 22 BP; 2 A; 4 C; 14 G; 2 T; 0 U; 0 Other;

Query Match      66.7%; Score 12; DB 2; Length 22;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12
   ||||:|||||
Db 10 GGGGTCTCTGAG 21

RESULT 150
AA065066
ID AA065066 standard; DNA; 22 BP.
XX
AC AA065066;
XX
DT 20-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.

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```
XX OS Synthetic.
XX PN CA2104649-A.
XX PD 26-FEB-1994.
XX PF 23-AUG-1993; 93CA-02104649.
XX PR 25-AUG-1992; 92JP-00248796.
XX PR 03-MAR-1993; 93JP-00042736.
XX PA (SEKI/) SEKI M.
XX PI Seki M, Honda Y, Yamada E;
XX DR WPI; 1994-151836/19.
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX PS Claim 5; Page 130; 262pp; English.
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX it has a base sequence of 15-30 bases which is included within the 49
XX bases from G at position 127 to C at position 175 of AA064913 and which
XX contains at least 7 bases from C at position 147 to C at position 153.
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX genes
XX SQ Sequence 22 BP; 3 A; 4 C; 12 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 22;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGGUCCTGGAG 12
XX Db 5 GGGGTCTCTGGAG 16
XX
XX RESULT 151
XX AA065056
XX ID AA065056 standard; DNA; 22 BP.
XX AC AA065056;
XX XX 20-DEC-1994 (first entry)
XX DT
XX DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX inhibition; viral protein precursor; ss.
XX OS Synthetic.
XX PN CA2104649-A.
XX PD 26-FEB-1994.
XX PF 23-AUG-1993; 93CA-02104649.
XX PR 25-AUG-1992; 92JP-00248796.
XX PR 03-MAR-1993; 93JP-00042736.
XX PA (SEKI/) SEKI M.
XX PI Seki M, Honda Y, Yamada E;
XX DR WPI; 1994-151836/19.
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
```

```
XX PS Claim 5; Page 126; 262pp; English.
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX it has a base sequence of 15-30 bases which is included within the 49
XX bases from G at position 127 to C at position 175 of AA064913 and which
XX contains at least 7 bases from C at position 147 to C at position 153.
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX genes
XX SQ Sequence 22 BP; 2 A; 5 C; 12 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 22;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGGUCCTGGAG 12
XX Db 4 GGGGTCTCTGGAG 15
XX
XX RESULT 152
XX AA065077
XX ID AA065077 standard; DNA; 22 BP.
XX AC AA065077;
XX DT 20-DEC-1994 (first entry)
XX DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX inhibition; viral protein precursor; ss.
XX OS Synthetic.
XX PN CA2104649-A.
XX PD 26-FEB-1994.
XX PF 23-AUG-1993; 93CA-02104649.
XX PR 25-AUG-1992; 92JP-00248796.
XX PR 03-MAR-1993; 93JP-00042736.
XX PA (SEKI/) SEKI M.
XX PI Seki M, Honda Y, Yamada E;
XX DR WPI; 1994-151836/19.
XX PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX PS Claim 5; Page 135; 262pp; English.
XX CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX it has a base sequence of 15-30 bases which is included within the 49
XX bases from G at position 127 to C at position 175 of AA064913 and which
XX contains at least 7 bases from C at position 147 to C at position 153.
XX CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX genes
XX SQ Sequence 22 BP; 2 A; 4 C; 13 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 12; DB 2; Length 22;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGGGUCCTGGAG 12
XX Db 6 GGGGTCTCTGGAG 17
```

```

RESULT 153
AAQ65088
ID AAQ65089 standard; DNA; 22 BP.
XX
XX
AC AAQ65089;
XX
XX
DT 20-DEC-1994 (first entry)
XX
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX
XX
OS Inhibition; viral protein precursor; ss.
XX
XX
OS Synthetic.
XX
XX
PN CA2104649-A.
XX
XX
PD 26-FEB-1994.
XX
XX
PF 23-AUG-1993; 93CA-02104649.
XX
XX
PR 25-AUG-1992; 92JP-00248796.
XX
XX
PR 03-MAR-1993; 93JP-00042736.
XX
XX
PA (SEKI/) SEKI M.
XX
XX
PI Seki M, Honda Y, Yamada E;
XX
XX
DR WPI; 1994-151836/19.
XX
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX
XX
PT genome - are useful as antiviral agents.
XX
XX
PS Claim 5; Page 140; 262pp; English.
XX
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX
XX
CC it has a base sequence of 15-30 bases which is included within the 49
XX
XX
CC bases from G at position 127 to C at position 175 of AAQ64913 and which
XX
XX
CC contains at least 7 bases from C at position 147 to C at position 153.
XX
XX
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX
XX
CC genes
XX
XX
SQ Sequence 22 BP; 2 A; 3 C; 14 G; 3 T; 0 U; 0 Other;
XX
XX
Query Match 66.7%; Score 12; DB 2; Length 22;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
Db 7 GGGGTCCTGGAG 18
XX
XX
RESULT 154
AAQ65147
ID AAQ65147 standard; DNA; 22 BP.
XX
XX
AC AAQ65147;
XX
XX
DT 21-DEC-1994 (first entry)
XX
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX
XX
OS Inhibition; viral protein precursor; ss.
XX
XX
OS Synthetic.
XX
XX
PN CA2104649-A.
XX
XX
PD 26-FEB-1994.
XX

```

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PF 23-AUG-1993; 93CA-02104649.
XX
XX
XX 25-AUG-1992; 92JP-00248796.
XX
XX
PR 03-MAR-1993; 93JP-00042736.
XX
XX
PA (SEKI/) SEKI M.
XX
XX
PI Seki M, Honda Y, Yamada E;
XX
XX
DR WPI; 1994-151836/19.
XX
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX
XX
PT genome - are useful as antiviral agents.
XX
XX
PS Claim 5; Page 166; 262pp; English.
XX
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX
XX
CC it has a base sequence of 15-30 bases which is included within the 49
XX
XX
CC bases from G at position 127 to C at position 175 of AAQ64913 and which
XX
XX
CC contains at least 7 bases from C at position 147 to C at position 153.
XX
XX
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
XX
XX
CC genes
XX
XX
SQ Sequence 22 BP; 2 A; 5 C; 13 G; 2 T; 0 U; 0 Other;
XX
XX
Query Match 66.7%; Score 12; DB 2; Length 22;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
Db 11 GGGGTCCTGGAG 22
XX
XX
RESULT 155
AAQ64928
ID AAQ64928 standard; DNA; 22 BP.
XX
XX
AC AAQ64928;
XX
XX
DT 19-DEC-1994 (first entry)
XX
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX
XX
OS Inhibition; viral protein precursor; ss.
XX
XX
OS Synthetic.
XX
XX
PN CA2104649-A.
XX
XX
PD 26-FEB-1994.
XX
XX
PF 23-AUG-1993; 93CA-02104649.
XX
XX
PR 25-AUG-1992; 92JP-00248796.
XX
XX
PR 03-MAR-1993; 93JP-00042736.
XX
XX
PA (SEKI/) SEKI M.
XX
XX
PI Seki M, Honda Y, Yamada E;
XX
XX
DR WPI; 1994-151836/19.
XX
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX
XX
PT genome - are useful as antiviral agents.
XX
XX
PS Claim 5; Page 70; 262pp; English.
XX
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
XX
XX
CC it has a base sequence of 16-24 bases which is included within the 24
XX
XX
CC bases from G at position 127 to C at position 150 of AAQ64913 and which
XX
XX
CC contains at least 16 bases from C at position 131 to A at position 146.
XX

```

CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 CC genes

CC Sequence 22 BP; 3 A; 6 C; 10 G; 3 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 22;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DB 1 GGGGUCCTGGAG 12

1 GGGGUCCTGGAG 12

RESULT 156

AD33107

AD33107

AD33107

01-JUL-2002 (first entry)

Restriction endonuclease; altered specificity; recognition sequence;

Gaui, enzyme; de.

Undentified.

EP1179596-A1.

13-FEB-2002.

06-JUL-2001; 2001EP-00305859.

10-AUG-2000; 2000GB-00019744.

(FERM-) FERMENTAS AB.

Janulaitis A, Rimelene R, Ludys A;

WPI; 2002-229927/29.

Producing DNA encoding restriction endonuclease with altered specificity;

comprises mutagenizing DNA encoding the enzyme and isolating DNA encoding

mutated enzyme with specificity for an altered sequence.

Example; Page 5; 44pp; English.

The invention relates to a method of producing a polynucleotide encoding

a restriction endonuclease with altered specificity. The method involves

mutagenizing a polynucleotide encoding restriction endonuclease with

specificity for a recognition sequence to produce mutated polynucleotides

and isolating from them a polynucleotide encoding mutated restriction

endonuclease with specificity for an altered recognition sequence by

selecting a polynucleotide expressing a restriction endonuclease with

methylester specificity for the altered recognition sequence. The method is

useful for producing a polynucleotide encoding a restriction endonuclease

comprising Eco571, BspI, HaeIII or AclI, with an altered specificity. The

method allows selection of mutant variants recognising new sequences that

differ not only in single nucleotide from wild type enzyme but also for

several nucleotides, especially if mutants of altered specificity are

taken into the next round of mutagenesis and digestion-selection. The

present sequence is recognition sequence of Gaui restriction enzyme

DB 1 CTGGAGNNNNNN 12

RESULT 157

AD145772

AD145772

AD145772

22-APR-2004 (first entry)

Single stranded nucleic acid cleavage method related nucleotide #205.

ss, single-stranded nucleic acid cleavage; restriction endonuclease;

complementation; genetic package; bacteriophage display library;

antibody fragment.

Undentified.

WO200179481-A2.

25-OCT-2001.

17-APR-2001; 2001WO-US012454.

17-APR-2000; 2000US-0198069P.

(DYAX-) DYAX CORP.

Ladner RC, Cohen EH, Natri HG, Rooker KL, Hoet R;

WPI; 2002-011131/01.

Selective cleavage of single-stranded nucleic acid, useful for preparing

display libraries of proteins and peptides, by hybridization with

oligonucleotide and enzymatic restriction.

Disclosure; SEQ ID NO 223; 190pp; English.

The invention relates to a method of cleaving single-stranded (ss)

nucleic acid (I) at a selected location, using an oligonucleotide (ON)

that is complementary to (I) in the target region and a restriction

endonuclease (RE). The ON forms, with its complement in (I), an RE

recognition site that ensures cleavage only at the selected location.

Contact between (I) and ON, and treatment with RE, are done at a

temperature at which (I) (I) is maintained in substantially ss form and

(II) RE is active. ON is (i) single stranded, and includes a sequence

that forms, with its complement in (I), the RE site or (ii) has a double-

stranded (ds) region that includes a recognition site for a type IIS RE

that cleaves at a remote site formed by complementation of (I) and the ss

region of ON. The method is used to construct libraries of genetic

packages (phages) that display diverse families of (poly)peptides and

proteins (A), especially human Fab or other antibody fragments. The

libraries are screened to identify (A) for possible therapeutic use. The

method is not biased to DNAs containing native sequences complementary to

amplification primers and allows any sequences that may be deleterious to

expression to be removed before cloning and display. DNAs are cut only at

a single (constant) site, without the need to build an RE site into the

or synthetic site can be used for cleavage. The use of a partially ds ON

allows cleavage at sites where no restriction sites occur naturally or

can be created. Both methods allow use of 5' and 3' primers for maximum

diversity. This sequence represents a sequence used in the invention.

Sequence 22 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 16 Other;

Query Match 66.7%; Score 12; DB 6; Length 22;

Best Local Similarity 91.7%; Pred. No. 3.4e+03;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 7 CTGGAGNNNNNN 18

1:|||||

1:|||||

Db 1 CTGAGANNNNNN 12

RESULT 158

ABT15975

ID ABT15975 standard; DNA; 22 BP.

XX

AC ABT15975;

XX

DT 28-MAR-2003 (first entry)

XX

DE HCV variant detection related PCR primer SEQ ID No 4.

XX

KW Primer extension chain reaction; reverse; forward; target nucleic acid;

KM variant; HIV; HCV; HBV; Parvovirus B19; PCR primer; ss.

XX

OS Hepatitis C virus.

OS Synthetic.

XX

PN WO200283927-A2.

XX

PD 24-OCT-2002.

XX

PF 17-APR-2002; 2002WO-US012035.

XX

PR 17-APR-2001; 2001US-0284334P.

XX

PA (NYBL-) NEW YORK BLOOD CENT INC.

XX

PI Andrus L, Nichols CN;

XX

DR WPI; 2003-103374/09.

XX

PT Detecting presence of target nucleic acid molecule e.g. human

PT immunodeficiency virus, hepatitis B or C virus in a sample, by using a

PT universal multi-variant detection system.

XX

PS Example; Page 25; 63pp; English.

XX

CC The invention relates to a novel method for a primer extension chain

CC reaction for determining presence of a target nucleic acid molecule in a

CC sample, where the nucleotide at 3' end of the reverse primer hybridises

CC with nucleotide at 5' end of the forward primer extension product or a

CC nucleotide separated from the nucleotide at 5' end of the forward primer

CC extension product by a gap comprising a highly conserved nucleotide

CC sequence. The method is useful for determining presence of a target

CC nucleic acid molecule known to have variant sequences, in a sample. The

CC target nucleic acid is preferably a virus including human

CC immunodeficiency virus (HIV), hepatitis C virus (HCV), hepatitis B virus

CC (HBV) or Parvovirus B19. This polynucleotide sequence represents a PCR

CC primer used in the primer extension chain reaction method of the

CC invention

XX

SQ Sequence 22 BP; 2 A; 5 C; 13 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 8; Length 22;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCCUGAG 12

DB 11 GGGGCTCTGAG 22

RESULT 159

AAD63097

ID AAD63097 standard; DNA; 22 BP.

XX

AC AAD63097;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human tandem tag DNA #31.

XX

KW Tandem tag; concatenated tag; human; ds.

XX

OS Homo sapiens.

XX

PN US2003190618-A1.

XX

PD 09-OCT-2003.

XX

PF 06-MAR-2002; 2002US-00092885.

XX

PR 06-MAR-2002; 2002US-00092885.

XX

PA (SAMA/) SAMAL B.

PA (LIYY/) LI Y.

PA (HERM/) HERMIDA L C.

PA (HOPP/) HOPPA N L.

PA (JOHE/) JOHE K K.

XX

PI Samal B, Li Y, Hermida LC, Hoppa NL, Johe KK;

XX

DR WPI; 2003-831617/77.

XX

PT Generating five prime biased tandem tag libraries of cDNAs by isolating a

PT sample of mRNAs, amplifying the released tags, concatenating the

PT amplified tags to form concatenated tags, amplifying and isolating the

PT concatenated tags.

XX

PS Disclosure; Page 9; 0pp; English.

XX

CC The present invention discloses a method for generating five prime biased

CC tandem tag libraries of cDNAs. The step involves isolating a sample of

CC mRNAs, amplifying the released tags, concatenating the amplified tags to

CC form concatenated tags, amplifying and isolating the concatenated tags.

CC The present sequence is human tandem tag DNA

XX

SQ Sequence 22 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 16 Other;

Query Match 66.7%; Score 12; DB 10; Length 22;

Best Local Similarity 91.7%; Pred. No. 3.4e+03;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGGAGNNNNNN 18

DB 1 CTGAGANNNNNN 12

RESULT 160

ABZ37284

ID ABZ37284 standard; DNA; 22 BP.

XX

AC ABZ37284;

XX

DT 18-FEB-2003 (first entry)

XX

DE Type II restriction enzyme recognition sequence GsuI SEQ ID NO:375.

XX

KW Library; cleavage; display; diverse family; ss.

XX

OS Synthetic.

XX

PN WO200283872-A2.

XX

PD 24-OCT-2002.

XX

PF 17-APR-2002; 2002WO-US012405.

XX

PR 17-APR-2001; 2001US-00837306.

XX

PR 24-OCT-2001; 2001US-00000516.

XX

PR 25-OCT-2001; 2001US-00045674.

XX

PA (LADN/) LADNER R C.

PA (COHE/) COHEN E H.

PA (NASTRI/) NASTRI H G.  
 PA (ROOKEY/) ROOKEY K L.  
 PA (HOET/) HOET R.  
 PA (HOOGE/) HOOGEBOOM H R J M.  
 PI Ladner RC, Cohen EH, Nastri HG, Rookey KL, Hoet R;  
 PI Hoogenboom HRJM;  
 XX WPI: 2003-093015/08.  
 DR  
 XX  
 XX  
 PT Cleaving single-stranded nucleic acid sequences at a desired location by  
 PT contacting the nucleic acid with an single strand oligonucleotide  
 PT complementary to a nucleic acid region where cleavage is desired.  
 XX  
 XX  
 PS Disclosure; Page 370; 485bp; English.  
 XX  
 XX The present invention describes a method for cleaving single-stranded  
 CC nucleic acid sequences at a desired location. Also described: (1) methods  
 CC for displaying or expressing a member of a diverse family of peptides,  
 CC polypeptides or proteins on the surface of a genetic package and  
 CC collectively displaying at least a part of the diversity of the family,  
 CC where the displayed or expressed peptide, polypeptide or protein is  
 CC encoded at least in part by a nucleic acid that has been cleaved at a  
 CC desired location; (2) a method for preparing single-stranded nucleic  
 CC acids; (3) a method for preparing a library comprising a collection of  
 CC genetic packages that display a member of a diverse family of peptides,  
 CC polypeptides or proteins and that collectively display at least a portion  
 CC of the family; (4) a vector comprising a DNA sequence encoding an  
 CC antibody variable region linked to a version of pIII anchor which does  
 CC not mediate infection of phage particles, and wild-type gene III; (5) a  
 CC method for producing a population or a library of immunoglobulin genes;  
 CC and (6) a library of immunoglobulins that comprise members having at  
 CC least one variable domain in which at least one of CDR1 and CDR2 contain  
 CC synthetic diversity and CDR3 diversity is captured from B cells. The  
 CC method is useful for cleaving single-stranded nucleic acid sequences at a  
 CC desired location, which can be subsequently used to produce libraries or  
 CC genetic packages that display and/or express a diverse family of  
 CC peptides, polypeptides or proteins. AB236912 to AB237510 and ABP5564 to  
 CC ABP55499 represent sequences used in the exemplification of the present  
 CC invention  
 CC  
 XX  
 XX Sequence 22 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 16 Other;  
 SQ  
 Query Match 66.7%; Score 12; DB 10; Length 22;  
 Best Local Similarity 91.7%; Pred. No. 3.4e+03;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 CUGGAGNNNNNN 18  
 Db 1 CTGGAGNNNNNN 12  
 RESULT 161  
 ADM29087  
 ID ADM29087 standard; DNA; 22 BP.  
 XX  
 AC ADM29087;  
 XX  
 DT 01-JUL-2004 (first entry)  
 XX  
 DE Hepatitis C virus HCV-R PCR primer SEQ ID NO:37.  
 XX  
 KM DNA vaccine; vaccine; antigen gene; hepatitis C virus; HCV;  
 KM recombinant adenovirus vaccine; adenovirus; HCV infection;  
 KM hepatitis C virus infection; infection; virucide; PCR; primer; ss.  
 XX  
 OS Hepatitis C virus.  
 OS Synthetic.  
 XX  
 XX WO2004028563-A1.  
 PN  
 PD 08-APR-2004.  
 XX

PR 24-SEP-2003; 2003WO-KR001951.  
 XX  
 XX 27-SEP-2002; 2002KR-00058712.  
 PR 06-NOV-2002; 2002KR-00068496.  
 XX  
 XX (GENE-) GENEXINE INC.  
 PA (POST-) POSTECH FOUND.  
 PA (DONG-) DONG-A PHARM CO LTD.  
 PA (DAEW-) DAEWOOONG CO LTD.  
 PA (POSC-) POSCO.  
 PI Sung YC, Yoon J, Yang S, Park S, Lee CG;  
 PI WPI: 2004-305120/28.  
 DR  
 XX  
 XX  
 PT New DNA vaccine comprising plasmid containing 2-6 kb of the total antigen  
 PT gene of hepatitis C virus (HCV), useful in treating or preventing HCV  
 PT infection.  
 XX  
 XX Example 16; SEQ ID NO 37; 165bp; English.  
 XX  
 XX The present invention describes a DNA vaccine which comprises a plasmid  
 CC containing 2-6 kb of the total antigen gene of hepatitis C virus (HCV).  
 CC Also described: (1) a recombinant adenovirus vaccine including an  
 CC adenovirus containing 2-6 kb of total antigen gene of HCV; (2) a vaccine  
 CC administering method; and (3) a method for treating or preventing HCV  
 CC infection. The DNA vaccine has virucide activity. The DNA vaccine is  
 CC useful in treating or preventing HCV infection. The present sequence  
 CC represents a PCR primer for HCV, which is used in an example from the  
 CC present invention.  
 XX  
 XX Sequence 22 BP; 2 A; 5 C; 13 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 66.7%; Score 12; DB 12; Length 22;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTGGAG 12  
 Db 11 GGGGTCCTGGAG 22  
 RESULT 162  
 AAQ65090  
 ID AAQ65090 standard; DNA; 23 BP.  
 XX  
 AC AAQ65090;  
 XX  
 DT 20-DEC-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 XX  
 KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KM inhibition; viral protein precursor; ss.  
 XX  
 OS Synthetic.  
 OS  
 XX CA2104649-A.  
 PN  
 XX 26-FEB-1994.  
 PD  
 XX  
 PF 23-AUG-1993; 93CA-02104649.  
 XX  
 XX 25-AUG-1992; 92JP-00248796.  
 PR 03-MAR-1993; 93JP-00042736.  
 XX  
 PA (SEKI/) SEKI M.  
 XX  
 XX Seki M, Honda Y, Yamada E;  
 PI WPI: 1994-151836/19.  
 DR  
 XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus

PT genome - are useful as antiviral agents.  
XX  
XX Claim 5; Page 141; 262pp; English.  
XX  
XX This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AA064913 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 23 BP; 2 A; 3 C; 15 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 66.7%; Score 12; DB 2; Length 23;  
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTCGAG 12  
DB 8 GGGGTCCTCGAG 19  
XX  
XX RESULT 163  
XX AA065078  
XX ID AA065078 standard; DNA; 23 BP.  
XX  
XX AA065078;  
XX  
XX 20-DEC-1994 (first entry)  
XX  
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX  
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
XX inhibition; viral protein precursor; ss.  
XX  
XX Synthetic.  
XX  
XX CA2104649-A.  
XX  
XX 26-FEB-1994.  
XX  
XX 23-AUG-1993; 93CA-02104649.  
XX  
XX 25-AUG-1992; 92JP-00248796.  
XX  
XX 03-MAR-1993; 93JP-00042736.  
XX  
XX (SEKI/) SEKI M.  
XX  
XX Seki M, Honda Y, Yamada E;  
XX  
XX WPI; 1994-151836/19.  
XX  
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
XX genome - are useful as antiviral agents.  
XX  
XX Claim 5; Page 136; 262pp; English.  
XX  
XX This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AA064913 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 23 BP; 2 A; 4 C; 14 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 66.7%; Score 12; DB 2; Length 23;  
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTCGAG 12  
DB 7 GGGGTCCTCGAG 18

XX  
XX RESULT 164  
XX AA065148  
XX ID AA065148 standard; DNA; 23 BP.  
XX  
XX AA065148;  
XX  
XX 21-DEC-1994 (first entry)  
XX  
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX  
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
XX inhibition; viral protein precursor; ss.  
XX  
XX Synthetic.  
XX  
XX CA2104649-A.  
XX  
XX 26-FEB-1994.  
XX  
XX 23-AUG-1993; 93CA-02104649.  
XX  
XX 25-AUG-1992; 92JP-00248796.  
XX  
XX 03-MAR-1993; 93JP-00042736.  
XX  
XX (SEKI/) SEKI M.  
XX  
XX Seki M, Honda Y, Yamada E;  
XX  
XX WPI; 1994-151836/19.  
XX  
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
XX genome - are useful as antiviral agents.  
XX  
XX Claim 5; Page 166; 262pp; English.  
XX  
XX This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AA064913 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 23 BP; 2 A; 5 C; 13 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 66.7%; Score 12; DB 2; Length 23;  
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTCGAG 12  
DB 12 GGGGTCCTCGAG 23  
XX  
XX RESULT 165  
XX AA065103  
XX ID AA065103 standard; DNA; 23 BP.  
XX  
XX AA065103;  
XX  
XX 21-DEC-1994 (first entry)  
XX  
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX  
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
XX inhibition; viral protein precursor; ss.  
XX  
XX Synthetic.  
XX  
XX CA2104649-A.  
XX  
XX 26-FEB-1994.  
XX

```

XX 23-AUG-1993; 93CA-02104649.
PF 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
PA (SEKI/) SEKI M.
PI Seki M, Honda Y, Yamada E;
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
PS Claim 5; Page 147; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
SQ Sequence 23 BP; 2 A; 4 C; 14 G; 3 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 23;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCUGAG 12
Db 9 GGGGTCTCTGGAG 20

RESULT 166
AA065067
ID AA065067 standard; DNA; 23 BP.
XX
AC AA065067;
XX
DT 20-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-02104649.
XX
PR 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
PA (SEKI/) SEKI M.
PI Seki M, Honda Y, Yamada E;
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
PS Claim 5; Page 131; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC bases from G at position 127 to C at position 175 of AA064913 and which

```

```

CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
SQ Sequence 23 BP; 3 A; 4 C; 13 G; 3 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 23;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCUGAG 12
Db 6 GGGGTCTCTGGAG 17

RESULT 167
AA065117
ID AA065117 standard; DNA; 23 BP.
XX
AC AA065117;
XX
DT 21-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-02104649.
XX
PR 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
PA (SEKI/) SEKI M.
PI Seki M, Honda Y, Yamada E;
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
PS Claim 5; Page 153; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
SQ Sequence 23 BP; 2 A; 5 C; 14 G; 2 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 23;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCUGAG 12
Db 10 GGGGTCTCTGGAG 21

RESULT 168
AA065057
ID AA065057 standard; DNA; 23 BP.
XX
AC AA065057;

```

```

XX 20-DEC-1994 (first entry)
DT
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
PN
XX 26-FEB-1994.
PD
XX
XX 23-AUG-1993; 93CA-02104649.
PF
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
PA
XX Seki M, Honda Y, Yamada E;
PI
XX WPI; 1994-151836/19.
DR
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX Claim 5; Page 127; 262pp; English.
PS
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AAQ64913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
XX Sequence 23 BP; 3 A; 5 C; 12 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 23;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCUCUGAG 12
XX |||||:|||||
Db 5 GGGGTCTGTGAG 16
XX

RESULT 169
AAQ65048
ID AAQ65048 standard; DNA; 23 BP.
XX
XX AAQ65048;
AC
XX
XX 20-DEC-1994 (first entry)
DT
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
PN
XX 26-FEB-1994.
PD
XX
XX 23-AUG-1993; 93CA-02104649.
PF
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
PA
XX

```

```

XX Seki M, Honda Y, Yamada E;
PI
XX WPI; 1994-151836/19.
DR
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX Claim 5; Page 123; 262pp; English.
PS
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AAQ64913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
XX Sequence 23 BP; 2 A; 5 C; 13 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 23;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCUCUGAG 12
XX |||||:|||||
Db 4 GGGGTCTGTGAG 15
XX

RESULT 170
AAQ64933
ID AAQ64933 standard; DNA; 23 BP.
XX
XX AAQ64933;
AC
XX
XX 19-DEC-1994 (first entry)
DT
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
KM inhibition; viral protein precursor; ss.
XX
XX Synthetic.
OS
XX CA2104649-A.
PN
XX 26-FEB-1994.
PD
XX
XX 23-AUG-1993; 93CA-02104649.
PF
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
PA
XX
XX Seki M, Honda Y, Yamada E;
PI
XX WPI; 1994-151836/19.
DR
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX Claim 5; Page 72; 262pp; English.
PS
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 16-24 bases which is included within the 24
CC bases from G at position 127 to C at position 150 of AAQ64913 and which
CC contains at least 16 bases from C at position 131 to A at position 146.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
XX Sequence 23 BP; 4 A; 6 C; 10 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 23;

```



Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
|||:||||  
Db 1 GGGGTCTGTGAG 12

## RESULT 171

AA043906  
ID AA043906 standard; DNA; 23 BP.

AC AAD43906;

DT 14-NOV-2002 (first entry)

DE Bpm I restriction endonuclease recognition motif.

KM Single stranded polynucleotide tag; cleavage agent; gene expression;

OS Unidentified.

XX Key Location/Qualifiers

FT misc\_feature 22..23  
FT /tag= a  
FT /note= "Nicking site"

XX MO200259357-A2.

XX 01-AUG-2002.

XX 24-JAN-2002; 2002MO-DK000052.

XX 24-JAN-2001; 2001DK-00000126.

XX 12-FEB-2001; 2001US-0267704P.

XX (GENO-) GENOMIC EXPRESSION APS.

XX Pedersen ML;

XX WPI: 2002-636542/68.

PT Obtaining single stranded polynucleotide tags from a biological sample,  
PT for analyzing gene expression or diagnosing clinical conditions,  
PT comprises employing nicking endonucleases that cleave complementary  
PT strands.

XX PS Disclosure; Page 88; 302pp; English.

CC The invention relates to a method for obtaining a single stranded  
CC polynucleotide tag from a biological sample by cleaving one of the  
CC complementary strands of a double stranded polynucleotide with a cleavage  
CC agent capable of recognising a double stranded polynucleotide comprising  
CC complementary strands and cleaving only one of the strands of the  
CC polynucleotide in the process of generating a single stranded  
CC polynucleotide tag. The method is useful for separating, analyzing,  
CC quantifying or obtaining single stranded polynucleotides comprising tags  
CC originating partly, and preferably wholly from a source of DNA and/or RNA  
CC in a sample comprising biological cells. The method is particularly for  
CC analyzing gene expression (expression profiling or differential gene  
CC expression), or in diagnosing clinical conditions. The present sequence  
CC is Bpm I restriction endonuclease recognition motif. This sequence is  
CC used to illustrate the method of the invention

XX SQ Sequence 23 BP; 1 A; 1 C; 3 G; 1 T; 0 U; 17 Other;

Query Match 66.7%; Score 12; DB 6; Length 23;

Best Local Similarity 91.7%; Pred. No. 3.4e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGGNNNNNN 18  
|:|||||

Db 1 CTGAGGNNNNNN 12

## RESULT 172

AA065133  
ID AA065133 standard; DNA; 24 BP.

XX AA065133;

XX 21-DEC-1994 (first entry)

DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.

KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
KM inhibition; viral protein precursor; ss.

OS Synthetic.

XX CA2104649-A.

XX 26-FEB-1994.

XX 23-AUG-1993; 93CA-02104649.

XX 25-AUG-1992; 92JP-00248796.  
XX 03-MAR-1993; 93JP-00042736.

XX (SEKI/) SEKI M.

XX Seki M, Honda Y, Yamada E;

XX WPI: 1994-151836/19.

PT Anti-sense oligo:nucleotide(s) complementary to the hepatitis C virus  
PT genome - are useful as antiviral agents.

XX PS Claim 5; Page 160; 262pp; English.

CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AA064913 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes

XX SQ Sequence 24 BP; 2 A; 5 C; 14 G; 3 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 24;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
|||:||||  
Db 12 GGGGTCTGTGAG 23

## RESULT 173

AA065104  
ID AA065104 standard; DNA; 24 BP.

XX AA065104;

XX 21-DEC-1994 (first entry)

DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.

KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
KM inhibition; viral protein precursor; ss.

OS Synthetic.

XX CA2104649-A.

```
PD 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-02104649.
XX
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
XX
XX Seki M, Honda Y, Yamada E;
XX
XX WPI; 1994-151836/19.
XX
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX
XX Claim 5; Page 147; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AAQ64913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
XX Sequence 24 BP; 2 A; 5 C; 14 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 24;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGGGUCCTGGAG 12
XX 10 GGGGTCTGGAG 21
Db
XX
XX RESULT 174
XX AAQ65091
XX ID AAQ65091 standard; DNA; 24 BP.
XX
XX AAQ65091;
XX
XX 20-DEC-1994 (first entry)
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX inhibition; viral protein precursor; ss.
XX
XX Synthetic.
XX
XX CA2104649-A.
XX
XX 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-02104649.
XX
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
XX
XX Seki M, Honda Y, Yamada E;
XX
XX WPI; 1994-151836/19.
XX
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX
XX Claim 5; Page 141; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
```

```
CC bases from G at position 127 to C at position 175 of AAQ64913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
XX Sequence 24 BP; 2 A; 4 C; 15 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 24;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGGGUCCTGGAG 12
XX 9 GGGGTCTGGAG 20
Db
XX
XX RESULT 175
XX AAQ65118
XX ID AAQ65118 standard; DNA; 24 BP.
XX
XX AAQ65118;
XX
XX 21-DEC-1994 (first entry)
XX
XX Antisense oligonucleotide complementary to Hepatitis C Virus genome.
DE
XX Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX inhibition; viral protein precursor; ss.
XX
XX Synthetic.
XX
XX CA2104649-A.
XX
XX 26-FEB-1994.
XX
XX 23-AUG-1993; 93CA-02104649.
XX
XX 25-AUG-1992; 92JP-00248796.
PR 03-MAR-1993; 93JP-00042736.
XX
XX (SEKI/) SEKI M.
XX
XX Seki M, Honda Y, Yamada E;
XX
XX WPI; 1994-151836/19.
XX
XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
PT genome - are useful as antiviral agents.
XX
XX
XX Claim 5; Page 153; 262pp; English.
XX
XX This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AAQ64913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
XX Sequence 24 BP; 2 A; 6 C; 14 G; 2 T; 0 U; 0 Other;
SQ
XX
XX Query Match 66.7%; Score 12; DB 2; Length 24;
XX Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGGGUCCTGGAG 12
XX 11 GGGGTCTGGAG 22
Db
XX
XX RESULT 176
XX AAQ65049
XX ID AAQ65049 standard; DNA; 24 BP.
XX
```

```

AC AA065049;
XX
DT 20-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-02104649.
XX
PR 25-AUG-1992; 92JP-00248796.
XX 03-MAR-1993; 93JP-00042736.
XX
PA (SEKI/) SEKI M.
XX
PI Seki M, Honda Y, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX
PS Claim 5; Page 123; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
SQ Sequence 24 BP; 3 A; 5 C; 13 G; 3 T; 0 U; 0 Other;
XX
QY 1 GGGGUCCTGGAG 12
   |||||:|||||
   5 GGGGTCTCTGGAG 16
XX
Db
XX
RESULT 177
AA065068
ID AA065068 standard; DNA; 24 BP.
XX
AC AA065068;
XX
DT 20-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-02104649.
XX
PR 25-AUG-1992; 92JP-00248796.
XX 03-MAR-1993; 93JP-00042736.
XX

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```

PA (SEKI/) SEKI M.
XX
PI Seki M, Honda Y, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX
PS Claim 5; Page 131; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
SQ Sequence 24 BP; 3 A; 4 C; 14 G; 3 T; 0 U; 0 Other;
XX
QY 1 GGGGUCCTGGAG 12
   |||||:|||||
   7 GGGGTCTCTGGAG 18
XX
Db
XX
RESULT 178
AA065149
ID AA065149 standard; DNA; 24 BP.
XX
AC AA065149;
XX
DT 21-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;
XX inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-02104649.
XX
PR 25-AUG-1992; 92JP-00248796.
XX 03-MAR-1993; 93JP-00042736.
XX
PA (SEKI/) SEKI M.
XX
PI Seki M, Honda Y, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX genome - are useful as antiviral agents.
XX
PS Claim 5; Page 167; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e.
CC it has a base sequence of 15-30 bases which is included within the 49
CC bases from G at position 127 to C at position 175 of AA064913 and which
CC contains at least 7 bases from C at position 147 to C at position 153.
CC The antisense oligonucleotide is useful for inhibiting translation of HCV
CC genes
XX
SQ Sequence 24 BP; 2 A; 6 C; 13 G; 3 T; 0 U; 0 Other;
XX

```

Query Match 66.7%; Score 12; DB 2; Length 24;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 ||||:||||  
 13 GGGGCTCTGGAG 24

Db

RESULT 179  
 AA065058  
 ID AA065058 standard; DNA; 24 BP.  
 AC AA065058;  
 XX  
 DT 20-DEC-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 XX  
 KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KM inhibition; viral protein precursor; ss.  
 XX  
 OS Synthetic.  
 OS  
 PS CA2104649-A.  
 PN  
 XX  
 PD 26-FEB-1994.  
 XX  
 PF 23-AUG-1993; 93CA-02104649.  
 XX  
 PR 25-AUG-1992; 92JP-00248796.  
 PR 03-MAR-1993; 93JP-00042736.  
 XX  
 PA (SEKI/) SEKI M.  
 XX  
 PI Seki M, Honda Y, Yamada E;  
 XX  
 DR WPI; 1994-151836/19.  
 XX  
 PT Antisense oligonucleotide(s) complementary to the hepatitis C virus  
 PT genome - are useful as antiviral agents.  
 XX  
 PS Claim 5; Page 127; 262pp; English.  
 XX  
 CC This oligonucleotide is an example of a preferred antisense compound i.e.  
 CC it has a base sequence of 15-30 bases which is included within the 49  
 CC bases from G at position 127 to C at position 175 of AA064913 and which  
 CC contains at least 7 bases from C at position 147 to C at position 153.  
 CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 CC genes  
 CC  
 SO Sequence 24 BP; 3 A; 5 C; 13 G; 3 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 24;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 ||||:||||  
 6 GGGGCTCTGGAG 17

Db

RESULT 180  
 AA065041  
 ID AA065041 standard; DNA; 24 BP.  
 AC AA065041;  
 XX  
 DT 20-DEC-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 DE Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 XX

KM inhibition; viral protein precursor; ss.  
 XX  
 OS Synthetic.  
 OS  
 PN CA2104649-A.  
 PN  
 XX  
 PD 26-FEB-1994.  
 XX  
 PF 23-AUG-1993; 93CA-02104649.  
 XX  
 PR 25-AUG-1992; 92JP-00248796.  
 PR 03-MAR-1993; 93JP-00042736.  
 XX  
 PA (SEKI/) SEKI M.  
 XX  
 PI Seki M, Honda Y, Yamada E;  
 XX  
 DR WPI; 1994-151836/19.  
 XX  
 PT Antisense oligo:nucleotide(s) complementary to the hepatitis C virus  
 PT genome - are useful as antiviral agents.  
 XX  
 PS Claim 5; Page 120; 262pp; English.  
 XX  
 CC This oligonucleotide is an example of a preferred antisense compound i.e.  
 CC it has a base sequence of 15-30 bases which is included within the 49  
 CC bases from G at position 127 to C at position 175 of AA064913 and which  
 CC contains at least 7 bases from C at position 147 to C at position 153.  
 CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
 CC genes  
 CC  
 SO Sequence 24 BP; 3 A; 5 C; 13 G; 3 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 24;  
 Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 ||||:||||  
 4 GGGGCTCTGGAG 15

Db

RESULT 181  
 AA065079  
 ID AA065079 standard; DNA; 24 BP.  
 AC AA065079;  
 XX  
 DT 20-DEC-1994 (first entry)  
 XX  
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
 DE Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
 KM inhibition; viral protein precursor; ss.  
 OS Synthetic.  
 OS  
 PN CA2104649-A.  
 PN  
 XX  
 PD 26-FEB-1994.  
 XX  
 PF 23-AUG-1993; 93CA-02104649.  
 XX  
 PR 25-AUG-1992; 92JP-00248796.  
 PR 03-MAR-1993; 93JP-00042736.  
 XX  
 PA (SEKI/) SEKI M.  
 XX  
 PI Seki M, Honda Y, Yamada E;  
 XX  
 DR WPI; 1994-151836/19.  
 XX  
 PT Antisense oligo:nucleotide(s) complementary to the hepatitis C virus

PT genome - are useful as antiviral agents.  
XX  
PS Claim 5; Page 136; 262pp; English.  
XX  
CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 15-30 bases which is included within the 49  
CC bases from G at position 127 to C at position 175 of AA064933 and which  
CC contains at least 7 bases from C at position 147 to C at position 153.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 24 BP; 2 A; 4 C; 15 G; 3 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 24;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
DB 8 GGGCTCTGGAG 19  
RESULT 182  
AA064938  
ID AA064938 standard; DNA; 24 BP.  
XX  
AC AA064938;  
XX  
DT 19-DEC-1994 (first entry)  
XX  
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.  
XX  
KM Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy;  
XX inhibition; viral protein precursor; ss.  
XX  
OS Synthetic.  
XX  
PN CA2104649-A.  
XX  
PD 26-FEB-1994.  
XX  
PF 23-AUG-1993; 93CA-02104649.  
XX  
PR 25-AUG-1992; 92JP-00248796.  
PR 03-MAR-1993; 93JP-00042736.  
XX  
PA (SEKI/) SEKI M.  
XX  
PI Seki M, Honda Y, Yamada E;  
XX  
DR WPI, 1994-151836/19.  
XX  
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus  
PT genome - are useful as antiviral agents.  
XX  
PS Claim 5; Page 75; 262pp; English.  
XX  
CC This oligonucleotide is an example of a preferred antisense compound i.e.  
CC it has a base sequence of 16-24 bases which is included within the 24  
CC bases from G at position 127 to C at position 150 of AA064913 and which  
CC contains at least 16 bases from C at position 131 to A at position 146.  
CC The antisense oligonucleotide is useful for inhibiting translation of HCV  
CC genes  
XX  
SQ Sequence 24 BP; 4 A; 7 C; 10 G; 3 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 24;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
DB 1 GGGCTCTGGAG 12

RESULT 183  
AAT1277/C  
ID AAT1277 standard; RNA; 24 BP.  
XX  
AC AAT1277;  
XX  
DT 26-JUN-1996 (first entry)  
XX  
DE Hepatitis C virus 5'-UTR PCR primer AS33.  
XX  
KM Antisense; therapy; complementary; HCV; 5'-untranslated region;  
KM Hepatitis C virus; inhibition; infection; treatment; stem-loop;  
KM clone 2-1; ss.  
XX  
OS Synthetic.  
XX  
PN JP07303485-A.  
XX  
PD 21-NOV-1995.  
XX  
PF 13-MAY-1994; 94JP-00124609.  
XX  
PR 13-MAY-1994; 94JP-00124609.  
XX  
PA (TOFU) TONEN CORP.  
XX  
DR WPI; 1996-035187/04.  
XX  
PT Hepatitis C virus (HCV) anti:sense RNA - inhibits HCV structural gene  
PT expression in vivo for treatment of HCV infection.  
XX  
PS Example 1; Page 4; 12pp; Japanese.  
XX  
CC The present sequence is that of amplification primer AS33 which was used  
CC for amplifying partial 5'-UTR sequences from the HCV genome. Clone 2-1  
CC (Journal of Virology: 66, 1476-1483 (1992)) was used as the template for  
CC PCR. The amplified fragments were transcribed to produce antisense RNA  
CC which is useful for inhibiting expression of HCV structural genes and  
CC thereby inhibiting viral replication in vivo. The antisense therapy can  
CC be used in addition to conventional interferon treatment of HCV  
CC infections  
XX  
SQ Sequence 24 BP; 5 A; 10 C; 5 G; 4 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 24;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
DB 23 GGGCTCTGGAG 12  
RESULT 184  
AAT80269  
ID AAT80269 standard; DNA; 24 BP.  
XX  
AC AAT80269;  
XX  
DT 15-OCT-1997 (first entry)  
XX  
DE Oligo HCV104, targeted to HCV region -3 to +9.  
XX  
KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KM inhibition; replication; expression; detection; chronic hepatitis;  
KM acute hepatitis; hepatocarcinoma; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..24

```

FT      /*tag= a
XX      /note= "Phosphorothioate linkages"
XX
XX      WO9639500-A2.
XX
XX      12-DEC-1996.
XX
XX      04-JUN-1996; 96WO-EP002427.
XX
XX      06-JUN-1995; 95US-00471968.
XX
XX      (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX      (HYBR-) HYBRIDON INC.
XX
XX      Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
XX      Roberts PC, Walthers DM, Wolfe JL;
XX      WPI; 1997-043122/04.
XX
XX      Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX      the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX      carcinoma.
XX
XX      Claim 19; Page 32; 100pp; English.
XX
XX      The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX      which are complementary to a portion of the 5' untranslated region (UTR)
XX      of hepatitis C virus (HCV). These sequences may be used in a
XX      pharmaceutical composition for the control or prevention of HCV
XX      infection. They may be used to inhibit replication or expression of HCV
XX      or for detecting the presence of HCV in a sample. They may be used to
XX      inhibit HCV replication in a cell and are therefore useful in the
XX      treatment of HCV infections such as chronic and acute hepatitis and
XX      hepatocarcinoma. This oligo was used in a luciferase assay to determine
XX      whether it binds successfully to its target.
XX
XX      Sequence 24 BP; 2 A; 5 C; 11 G; 6 T; 0 U; 0 Other;
XX
XX      Query Match 66.7%; Score 12; DB 2; Length 24;
XX      Best Local Similarity 83.3%; Pred. No. 3.4e+03;
XX      Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY 1 GGGGUCCTCGAG 12
XX      13 GGGGTCCTCGAG 24
XX
XX      Db
XX
XX      RESULT 185
XX      AAT80359
XX      ID AAT80359 standard; DNA; 24 BP.
XX
XX      AC AAT80359;
XX
XX      DT 16-OCT-1997 (first entry)
XX
XX      DE Oligo HCV-199, tripartite non-contiguous HCV targeting oligomer.
XX      KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX      inhibition; replication; expression; detection; chronic hepatitis;
XX      acute hepatitis; hepatocarcinoma; ss.
XX      OS Synthetic.
XX
XX      Key Location/Qualifiers
XX      modified_base 1..6
XX      /*tag= b
XX      /note= "Comprises phosphorothioate linkages"
XX      modified_base 7..24
XX      /*tag= a
XX      /note= "2'-OME RNA"
XX
XX      WO9639500-A2.
XX

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```

PD      12-DEC-1996.
XX
XX      04-JUN-1996; 96WO-EP002427.
XX
XX      06-JUN-1995; 95US-00471968.
XX
XX      (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX      (HYBR-) HYBRIDON INC.
XX
XX      Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
XX      Roberts PC, Walthers DM, Wolfe JL;
XX      WPI; 1997-043122/04.
XX
XX      Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX      the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX      carcinoma.
XX
XX      Claim 21; Page 21; 100pp; English.
XX
XX      The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX      which are complementary to a portion of the 5' untranslated region (UTR)
XX      of hepatitis C virus (HCV). These sequences may be used in a
XX      pharmaceutical composition for the control or prevention of HCV
XX      infection. They may be used to inhibit replication or expression of HCV
XX      or for detecting the presence of HCV in a sample. They may be used to
XX      inhibit HCV replication in a cell and are therefore useful in the
XX      treatment of HCV infections such as chronic and acute hepatitis and
XX      hepatocarcinoma. This sequence binds to three non-contiguous regions of
XX      the HCV genome. This sequence is targeted to the 5' target region, +10
XX      to +15, the internal sequence target, -230 to -219 and the 3' target
XX      region, +1 to +6
XX
XX      Sequence 24 BP; 4 A; 4 C; 10 G; 2 T; 4 U; 0 Other;
XX
XX      Query Match 66.7%; Score 12; DB 2; Length 24;
XX      Best Local Similarity 100.0%; Pred. No. 3.4e+03;
XX      Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY 1 GGGGUCCTCGAG 12
XX      7 GGGGUCCTCGAG 18
XX
XX      Db
XX
XX      RESULT 186
XX      AAT80363
XX      ID AAT80363 standard; DNA; 24 BP.
XX
XX      AC AAT80363;
XX
XX      DT 16-OCT-1997 (first entry)
XX
XX      DE Oligo HCV-207, tripartite non-contiguous HCV targeting oligomer.
XX      KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX      inhibition; replication; expression; detection; chronic hepatitis;
XX      acute hepatitis; hepatocarcinoma; ss.
XX      OS Synthetic.
XX
XX      Key Location/Qualifiers
XX      modified_base 1..6
XX      /*tag= b
XX      /note= "Comprises phosphorothioate linkages"
XX      modified_base 7..24
XX      /*tag= a
XX      /note= "2'-OME RNA"
XX
XX      WO9639500-A2.
XX
XX      12-DEC-1996.
XX
XX      04-JUN-1996; 96WO-EP002427.
XX

```

```

XX 06-JUN-1995; 95US-00471968.
PR (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA (HYBR-) HYBRIDON INC.
XX
XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PI Roberts PC, Walther DM, Wolfe JL;
XX WPI; 1997-043122/04.
DR
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT carcinoma.
XX
XX Claim 21; Page 21; 100pp; English.
PS
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC which are complementary to a portion of the 5' untranslated region (UTR)
CC of hepatitis C virus (HCV). These sequences may be used in a
CC pharmaceutical composition for the control or prevention of HCV
CC infection. They may be used to inhibit replication or expression of HCV
CC or for detecting the presence of HCV in a sample. They may be used to
CC inhibit HCV replication in a cell and are therefore useful in the
CC treatment of HCV infections such as chronic and acute hepatitis and
CC hepatocarcinoma. This sequence binds to three non-contiguous regions of
CC the HCV genome. This sequence is targeted to the 5' target region, +20
CC to +25, the internal sequence target, +1 to +6 and the 3' target region,
CC -230 to -219
XX
SQ Sequence 24 BP; 3 A; 4 C; 10 G; 3 T; 4 U; 0 Other;
Query Match 66.7%; Score 12; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
Db 13 GGGGUCCTGGAG 24

```

```

PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA (HYBR-) HYBRIDON INC.
XX
XX Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
PI Roberts PC, Walther DM, Wolfe JL;
XX WPI; 1997-043122/04.
DR
XX Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT carcinoma.
XX
XX Claim 19; Page 32; 100pp; English.
PS
XX The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC which are complementary to a portion of the 5' untranslated region (UTR)
CC of hepatitis C virus (HCV). These sequences may be used in a
CC pharmaceutical composition for the control or prevention of HCV
CC infection. They may be used to inhibit replication or expression of HCV
CC or for detecting the presence of HCV in a sample. They may be used to
CC inhibit HCV replication in a cell and are therefore useful in the
CC treatment of HCV infections such as chronic and acute hepatitis and
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine
CC whether it binds successfully to its target
XX
SQ Sequence 24 BP; 2 A; 5 C; 12 G; 5 T; 0 U; 0 Other;
Query Match 66.7%; Score 12; DB 2; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
Db 1 GGGGCTCTGGAG 12

```

XX	WP1; 1997-043122/04.
DR	
XX	Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT	the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT	carcinoma.
XX	
PS	Claim 21; Page 21; 100pp; English.
XX	
CC	The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC	which are complementary to a portion of the 5' untranslated region (UTR)
CC	of hepatitis C virus (HCV). These sequences may be used in a
CC	pharmaceutical composition for the control or prevention of HCV
CC	infection. They may be used to inhibit replication or expression of HCV
CC	or for detecting the presence of HCV in a sample. They may be used to
CC	inhibit HCV replication in a cell and are therefore useful in the
CC	treatment of HCV infections such as chronic and acute hepatitis and
CC	hepatocarcinoma. This sequence binds to three non-contiguous regions of
CC	the HCV genome. This sequence is targeted to the 5' target region, +1 to
CC	+6, the internal sequence target, -230 to -219 and the 3' target region,
CC	+235 to +240
SO	
XX	Sequence 24 BP; 3 A; 7 C; 10 G; 0 T; 4 U; 0 Other;
QY	
DB	Query Match 66.7%; Score 12; DB 2; Length 24;
	Best Local Similarity 100.0%; Pred. No. 3.4e+03;
	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	1 GGGGCHCUGGAG 12
	7 GGGGUCUGGAG 18
RESULT 189	
ID	AAT80276
XX	AAT80276 standard; DNA; 24 BP.
XX	
XX	AAT80276;
DJT	15-OCT-1997 (first entry)
XX	
DE	Oligo HCV125, targeted to HCV region -4 to -15.
XX	
KW	Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW	inhibition; replication; expression; detection; chronic hepatitis;
XX	acute hepatitis; hepatocarcinoma; ss.
OS	Synthetic.
XX	
FT	Key Location/Qualifiers
FT	modified_base 1..12
FT	/*tag= b
FT	/note= "Optionally phosphorothioate linkages"
FT	modified_base 13..24
FT	/*tag= a
FT	/note= "Optionally 2' OMe modified"
PN	WO9639500-A2.
XX	
PD	12-DEC-1996.
XX	
PF	04-JUN-1996; 96WO-EP002427.
XX	
FR	06-JUN-1995; 95US-00471968.
XX	
PA	(HOFF) HOFFMANN LA ROCHE & CO AG F.
XX	(HYBR-) HYBRIDON INC.
PI	Frank BL, Goodchild J, Hamlin RA, Kiluskie RE, Roberts NA;
PI	Roberts PC, Maltner DM, Wolfe JU;
XX	
RR	WP1; 1997-043122/04.
XX	

PT	Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT	the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT	carcinoma.
PS	Claim 19; Page 32-33; 100pp; English.
XX	
CC	The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC	which are complementary to a portion of the 5' untranslated region (UTR)
CC	of hepatitis C virus (HCV). These sequences may be used in a
CC	pharmaceutical composition for the control or prevention of HCV
CC	infection. They may be used to inhibit replication or expression of HCV
CC	or for detecting the presence of HCV in a sample. They may be used to
CC	inhibit HCV replication in a cell and are therefore useful in the
CC	treatment of HCV infections such as chronic and acute hepatitis and
CC	hepatocarcinoma. This oligo was used in a luciferase assay to determine
CC	whether it binds successfully to its target
SQ	
	Sequence 24 BP, 3 A; 6 C; 11 G; 4 T; 0 U; 0 Other;
Qy	Query Match                  66.7%; Score 12; DB 2; Length 24;
	Best Local Similarity      83.3%; Pred. No. 3.4e+03;
Matches	10; Conservative        2; Mismatches     0; Indels     0; Gaps     0
Db	
	1 GGGGUCUUGAG 12
	:
	1 GGGGTCTTGAG 12
RESULT 190	
AAT80358	
ID	AAT80358 standard; DNA; 24 BP.
AC	
AA	AAT80358;
D7	
DE	16-OCT-1997 (first entry)
OLIGO	HCV-198, tripartite non-contiguous HCV targeting oligomer.
KW	Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW	inhibition; replication; expression; detection; chronic hepatitis;
KW	acute hepatitis; hepatocarcinoma; ss.
OS	Synthetic.
FH	Key
FT	modified_base
FT	Location/Qualifiers
FT	1..6
FT	/*tag= b
FT	/note= "Comprises phosphorothioate linkages"
FT	7..24
FT	/*tag= a
FT	/note= "2'-OME RNA"
FN	
WO	WO9639500-A2.
PD	
PD	12-DEC-1996.
PJ	
PF	04-JUN-1996; 96WO-BP002427.
PR	
PR	06-JUN-1995; 95US-00471968.
PA	(HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA	(HYBR-) HYBRIDON INC.
PI	
PI	Frank BL, Goodchild J, Hamlin HA, Kilhuskie RE, Roberts NA;
PI	Roberts PC, Walther DM, Wolte JL;
DR	
WI	WPI; 1997-043122/04.
OLIGO	nucleotide(s) complementary to HCV 5' untranslated region - used in
PT	the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT	carcinoma.
XX	
XX	Claim 21; Page 21; 100pp; English.



XX The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This sequence binds to three non-contiguous regions of  
CC the HCV genome. This sequence is targeted to the 5' target region, -18  
CC to -13, the internal sequence target, -230 to -219 and the 3' target  
CC region, +1 to +6  
XX  
SQ Sequence 24 BP; 5 A; 5 C; 10 G; 0 T; 4 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGCGAG 12  
|||||  
7 GGGGUCGCGAG 18  
Db  
RESULT 191  
AAT80265  
ID AAT80265 standard; DNA; 24 BP.  
XX  
AC AAT80265;  
XX  
DT 15-OCT-1997 (first entry)  
XX  
DE Oligo HCV99, targeted to HCV region +4 to +15.  
XX  
KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KM inhibition; replication; expression; detection; chronic hepatitis;  
KM acute hepatitis; hepatocarcinoma; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..24  
FT /\*tag= a  
FT /note= "Phosphorothioate linkages"  
XX  
XX WO9639500-A2.  
XX  
PD 12-DEC-1996.  
XX  
PF 04-JUN-1996; 96WO-EP002427.  
XX  
PR 06-JUN-1995; 95US-00471968.  
XX  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
PA (HYBR-) HYBRIDON INC.  
XX  
PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
PI Roberts PC, Walther DM, Wolfe JL;  
XX  
DR WPI; 1997-043122/04.  
XX  
PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
PS Claim 19; Page 32; 100pp; English.  
XX  
CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This sequence binds to three non-contiguous regions of  
CC the HCV genome. This sequence is targeted to the 5' target region, -18  
CC to -13, the internal sequence target, -230 to -219 and the 3' target  
CC region, +1 to +6  
XX

CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine  
CC whether it binds successfully to its target  
XX  
SQ Sequence 24 BP; 3 A; 4 C; 11 G; 6 T; 0 U; 0 Other;  
Query Match 66.7%; Score 12; DB 2; Length 24;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGCGAG 12  
|||||  
1 GGGGUCGCGAG 12  
Db  
RESULT 192  
AAT80271  
ID AAT80271 standard; DNA; 24 BP.  
XX  
AC AAT80271;  
XX  
DT 15-OCT-1997 (first entry)  
XX  
DE Oligo HCV107 targeted to HCV region +1 to +12.  
XX  
KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KM inhibition; replication; expression; detection; chronic hepatitis;  
KM acute hepatitis; hepatocarcinoma; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..24  
FT /\*tag= a  
FT /note= "Phosphorothioate linkages"  
XX  
XX WO9639500-A2.  
XX  
PD 12-DEC-1996.  
XX  
PF 04-JUN-1996; 96WO-EP002427.  
XX  
PR 06-JUN-1995; 95US-00471968.  
XX  
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
PA (HYBR-) HYBRIDON INC.  
XX  
PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
PI Roberts PC, Walther DM, Wolfe JL;  
XX  
DR WPI; 1997-043122/04.  
XX  
PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
PS Claim 19; Page 32; 100pp; English.  
XX  
CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This oligo was used in a luciferase assay to determine  
CC whether it binds successfully to its target  
XX  
SQ Sequence 24 BP; 3 A; 5 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 24;  
Best Local Similarity 83.3%; Pred. No. 3.4e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
13 GGGGUCCTGGAG 24  
Db

RESULT 193  
AAT80366  
ID AAT80366 standard; DNA; 24 BP.  
XX  
AC AAT80366;  
XX  
DT 16-OCT-1997 (first entry)  
XX  
DE Oligo HCV-214, tripartite non-contiguous HCV targeting oligomer.  
XX  
KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KM inhibition; replication; expression; detection; chronic hepatitis;  
KM acute hepatitis; hepatocarcinoma; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FH modified\_base 1..18  
FT /\*tag= a  
FT /note= "2'-OME RNA"  
FT 19..24  
FT modified\_base  
FT /\*tag= b  
FT /note= "Comprises phosphorothioate linkages"  
XX  
PN WO9639500-A2.  
XX  
PD 12-DEC-1996.  
XX  
PF 04-JUN-1996; 96WO-EP002427.  
XX  
PR 06-JUN-1995; 95US-00471968.  
XX  
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
PA (HYBR-) HYBRIDON INC.  
XX  
PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
PI Roberts PC, Walther DM, Wolfe JL;  
XX  
DR WPI; 1997-043122/04.  
XX  
PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
PS Claim 21; Page 21; 100pp; English.  
XX  
CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This sequence binds to three non-contiguous regions of  
CC the HCV genome. This sequence is targeted to the 5' target region, +1 to  
CC +6, the internal sequence target, -230 to -219 and the 3' target region,  
CC +230 to +235  
XX  
SQ Sequence 24 BP; 3 A; 4 C; 12 G; 1 T; 4 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
7 GGGGUCCTGGAG 18  
Db

RESULT 194  
AAT80368  
ID AAT80368 standard; DNA; 24 BP.  
XX  
AC AAT80368;  
XX  
DT 16-OCT-1997 (first entry)  
XX  
DE Oligo HCV-220, tripartite non-contiguous HCV targeting oligomer.  
XX  
KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KM inhibition; replication; expression; detection; chronic hepatitis;  
KM acute hepatitis; hepatocarcinoma; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FH modified\_base 1..18  
FT /\*tag= a  
FT /note= "2'-OME RNA"  
FT 19..24  
FT modified\_base  
FT /\*tag= b  
FT /note= "Comprises phosphorothioate linkages"  
XX  
PN WO9639500-A2.  
XX  
PD 12-DEC-1996.  
XX  
PF 04-JUN-1996; 96WO-EP002427.  
XX  
PR 06-JUN-1995; 95US-00471968.  
XX  
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
PA (HYBR-) HYBRIDON INC.  
XX  
PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;  
PI Roberts PC, Walther DM, Wolfe JL;  
XX  
DR WPI; 1997-043122/04.  
XX  
PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
PS Claim 21; Page 21; 100pp; English.  
XX  
CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This sequence binds to three non-contiguous regions of  
CC the HCV genome. This sequence is targeted to the 5' target region, +1 to  
CC +6, the internal sequence target, -230 to -219 and the 3' target region,  
CC +240 to +245  
XX  
SQ Sequence 24 BP; 4 A; 4 C; 11 G; 1 T; 4 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
|||||

Db 7 GGGGUCUGAG 18

# RESULT 195

AA780274 ID AAT80274 standard; DNA; 24 BP.

AA780274;

15-OCT-1997 (first entry)

Oligo HCV112, targeted to HCV region -6 to +6.

Complementary: 5' untranslated region; UTR; hepatitis C virus; HCV; inhibition; replication; expression; detection; chronic hepatitis; acute hepatitis; hepatocarcinoma; ss.

Synthetic.

Key Location/Qualifiers

modified\_base 1..12 /tag= a /note= "Optionally 2' Ome modified"

modified\_base 13..24 /tag= b /note= "Phosphorothioate linkages"

WO9639500-A2.

12-DEC-1996.

04-JUN-1996; 96WO-EP002427.

06-JUN-1995; 95US-00471968.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

(HYBR-) HYBRIDON INC.

Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;

Roberts PC, Walthers DM, Wolfe JL;

WPI; 1997-043122/04.

Oligo: nucleotide(s) complementary to HCV 5' untranslated region - used in the treatment and detection of HCV infection, esp. hepatitis and hepatocarcinoma.

Claim 19; Page 32; 100pp; English.

The sequences given in AAT80211-382 represent synthetic oligonucleotides which are complementary to a portion of the 5' untranslated region (UTR) of hepatitis C virus (HCV). These sequences may be used in a pharmaceutical composition for the control or prevention of HCV infection. They may be used to inhibit replication or expression of HCV or for detecting the presence of HCV in a sample. They may be used to inhibit HCV replication in a cell and are therefore useful in the treatment of HCV infections such as chronic and acute hepatitis and hepatocarcinoma. This oligo was used in a luciferase assay to determine whether it binds successfully to its target

Sequence 24 BP; 3 A; 5 C; 11 G; 3 T; 2 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 24;

Best Local Similarity 100.0%; Pred. No. 3.4e+03; Mismatches 0; Indels 0; Gaps 0;

1 GGGGUCUGAG 12

1 GGGGUCUGAG 12

# RESULT 196

AAT80267

ID AAT80267 standard; DNA; 24 BP.

AA780267;

15-OCT-1997 (first entry)

Oligo HCV102, targeted to HCV region -9 to +3.

Complementary: 5' untranslated region; UTR; hepatitis C virus; HCV; inhibition; replication; expression; detection; chronic hepatitis; acute hepatitis; hepatocarcinoma; ss.

Synthetic.

Key Location/Qualifiers

modified\_base 1..24 /tag= a /note= "Phosphorothioate linkages"

WO9639500-A2.

12-DEC-1996.

04-JUN-1996; 96WO-EP002427.

06-JUN-1995; 95US-00471968.

(HOFF) HOFFMANN LA ROCHE & CO AG F.

(HYBR-) HYBRIDON INC.

Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;

Roberts PC, Walthers DM, Wolfe JL;

WPI; 1997-043122/04.

Oligo: nucleotide(s) complementary to HCV 5' untranslated region - used in the treatment and detection of HCV infection, esp. hepatitis and hepatocarcinoma.

Claim 19; Page 32; 100pp; English.

The sequences given in AAT80211-382 represent synthetic oligonucleotides which are complementary to a portion of the 5' untranslated region (UTR) of hepatitis C virus (HCV). These sequences may be used in a pharmaceutical composition for the control or prevention of HCV infection. They may be used to inhibit replication or expression of HCV or for detecting the presence of HCV in a sample. They may be used to inhibit HCV replication in a cell and are therefore useful in the treatment of HCV infections such as chronic and acute hepatitis and hepatocarcinoma. This oligo was used in a luciferase assay to determine whether it binds successfully to its target

Sequence 24 BP; 3 A; 5 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 24;

Best Local Similarity 83.3%; Pred. No. 3.4e+03; Mismatches 2; Indels 0; Gaps 0;

1 GGGGUCUGAG 12

13 GGGGUCUGAG 24

# RESULT 197

AA780270 ID AAT80270 standard; DNA; 24 BP.

AA780270;

15-OCT-1997 (first entry)

Oligo HCV106, targeted to HCV region +1 to +12.

KM	Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;	
KM	inhibition; replication; expression; detection; chronic hepatitis;	
KM	acute hepatitis; hepatocarcinoma; ss.	
XX		
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	modified_base	1..24
FT		/*tag= a
FT		/note= "Phosphorothioate linkages"
PN	W09639500-A2.	
XX		
PD	12-DEC-1996.	
XX		
PF	04-JUN-1996;	96MO-EP002427.
XX		
PR	06-JUN-1995;	95US-00471968.
XX		
PA	(HOPF) HOFFMANN LA ROCHE & CO AG F.	
XX	(HYBR-) HYBRIDON LA.	
PI	Frank BL, Goodchild J, Hamlin HA, Kiluskie RE, Roberts NA;	
PI	Roberts PC, Walthers DM, Wolfe JL;	
XX		
DR	WPI; 1997-043122/04.	
XX		
PT	Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in	
PT	the treatment and detection of HCV infection, esp. hepatitis and hepato-	
PT	carcinoma.	
XX		
PS	Claim 19; Page 32; 100pp; English.	
XX		
CC	The sequences given in AAT80211-382 represent synthetic oligonucleotides	
CC	which are complementary to a portion of the 5' untranslated region (UTR)	
CC	of hepatitis C virus (HCV). These sequences may be used in a	
CC	pharmaceutical composition for the control or prevention of HCV	
CC	infection. They may be used to inhibit replication or expression of HCV	
CC	or for detecting the presence of HCV in a sample. They may be used to	
CC	inhibit HCV replication in a cell and are therefore useful in the	
CC	treatment of HCV infection such as chronic and acute hepatitis and	
CC	hepatocarcinoma. This oligo was used in a luciferase assay to determine	
CC	whether it binds successfully to its target	
XX		
XX	Sequence 24 BP; 3 A; 5 C; 9 G; 7 T; 0 U; 0 Other;	
SO		
	Query Match	66.7%; Score 12; DB 2; Length 24;
	Best Local Similarity	83.3%; Pred. No. 3.4e+03;
	Matches 10; Conservative	2; Mismatches 0; Indels 0; Gaps 0;
OY	1 GGGGCTCCGAG 12	
	:	
DB	1 GGGGCTCCGAG 12	
	RESULT 198	
	AAT80275	
	ID AAT80275 standard; DNA; 24 BP.	
XX	AAT80275;	
AC		
XX	15-OCT-1997 (first entry)	
DT		
XX		
DE	Oligo HCV113, targeted to HCV region -6 to +6.	
XX		
KM	Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;	
KM	inhibition; replication; expression; detection; chronic hepatitis;	
KM	acute hepatitis; hepatocarcinoma; ss.	
XX		
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	modified_base	1..12

FT	/*tag= b
FT	/note= "Phosphorothioate linkages"
FT	modified_base 13..24
FT	/*tag= a
FT	/note= "Optionally 2'-Ome modified"
PN	WO9639500-A2.
PN	12-DEC-1996.
PD	
XX	
XX	04-JUN-1996; 96WO-EP002427.
XX	
XX	06-JUN-1995; 95US-00471968.
PA	(HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA	(HYBR ) HYBRIDON INC.
XX	
XX	Frank BL, Goodchild J, Hamlin HA, Kilbuckie RE, Roberts NA,
PI	Roberts PC, Walther DM, Wolfe JL,
DR	WPL, 1997-043122/04.
XX	
XX	Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
PT	the treatment and detection of HCV infection, esp. hepatitis and hepato-
PT	carcinoma.
XX	
XX	Claim 19; Page 32; 100pp; English.
PS	
XX	
CC	The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC	which are complementary to a portion of the 5' untranslated region (UTR)
CC	of hepatitis C virus (HCV). These sequences may be used in a
CC	pharmaceutical composition for the control or prevention of HCV
CC	infection. They may be used to inhibit replication or expression of HCV
CC	or for detecting the presence of HCV in a sample. They may be used to
CC	inhibit HCV replication in a cell and are therefore useful in the
CC	treatment of HCV infections such as chronic and acute hepatitis and
CC	hepatocarcinoma. This oligo was used in a luciferase assay to determine
CC	whether it binds successfully to its target
XX	
SO	Sequence 24 BP; 3 A; 5 C; 11 G; 3 T; 2 U; 0 Other;
	Query Match 66.7%; Score 12; DB 2; Length 24;
	Best Local Similarity 100.0%; Pred. No. 3.4e+03;
	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY	1 GGGGUCGUGAG 12
	13 GGGGUCGUGAG 24
Db	
RESULT 199	
AAT80365	
ID	AAT80365 standard; DNA; 24 BP.
XX	
XX	AAT80365;
XX	
DT	16-OCT-1997 (first entry)
XX	
XX	Oligo HCV-211, tripartite non-continuous HCV targeting oligomer.
XX	
KW	Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW	inhibition; replication; expression; detection; chronic hepatitis;
KW	acute hepatitis; hepatocarcinoma; sr.
XX	
OS	Synthetic.
XX	
XX	
XX	Key Location/Qualifiers
FT	modified_base 1..6
FT	/*tag= b
FT	/note= "Comprises phosphorothioate linkages"
FT	modified_base 7..24
FT	/*tag= a
FT	/note= "2'-Ome RNA"
FT	

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XX PN M09639500-A2.
XX XX 12-DEC-1996.
XX PD 04-JUN-1996; 96WO-EP002427.
XX PF 06-JUN-1995; 95US-00471968.
XX PR (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PA (HYBR-) HYBRIDON INC.
XX PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
XX PI Roberts PC, Walther DM, Wolfe JL;
XX DR WPI; 1997-043122/04.
XX PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX PT carcinoma.
XX PS Claim 21; Page 21; 100pp; English.
XX SS The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX CC which are complementary to a portion of the 5' untranslated region (UTR)
XX CC of hepatitis C virus (HCV). These sequences may be used in a
XX CC pharmaceutical composition for the control or prevention of HCV
XX CC infection. They may be used to inhibit replication or expression of HCV
XX CC or for detecting the presence of HCV in a sample. They may be used to
XX CC inhibit HCV replication in a cell and are therefore useful in the
XX CC treatment of HCV infections such as chronic and acute hepatitis and
XX CC hepatocarcinoma. This sequence binds to three non-contiguous regions of
XX CC the HCV genome. This sequence is targeted to the 5' target region, +25
XX CC to +30, the internal sequence target, +1 to +6 and the 3' target region,
XX CC -230 to -219
XX SQ Sequence 24 BP; 2 A; 5 C; 8 G; 5 T; 4 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGCGAG 12
   |||||
Db 13 GGGGUCGCGAG 24

RESULT 200
AAT80258
ID AAT80258 standard; DNA; 24 BP.
XX AC AAT80258;
XX DT 15-OCT-1997 (first entry)
XX DE Oligo HCV88, targeted to HCV -9 to +3.
XX KM Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
XX KM inhibition; replication; expression; detection; chronic hepatitis;
XX KM acute hepatitis; hepatocarcinoma; ss.
XX OS Synthetic.
XX PH Key
XX PH modified_base 1..24
XX FT /*tag= a
XX FT /note= "Comprises phosphorothioate linkages"
XX PN M09639500-A2.
XX PD 12-DEC-1996.
XX PF 04-JUN-1996; 96WO-EP002427.

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XX PR 06-JUN-1995; 95US-00471968.
XX XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PA (HYBR-) HYBRIDON INC.
XX XX
XX PI Frank BL, Goodchild J, Hamlin HA, Kilkuskie RE, Roberts NA;
XX PI Roberts PC, Walther DM, Wolfe JL;
XX DR WPI; 1997-043122/04.
XX DR
XX PT Oligo:nucleotide(s) complementary to HCV 5' untranslated region - used in
XX PT the treatment and detection of HCV infection, esp. hepatitis and hepato-
XX PT carcinoma.
XX PS Claim 19; Page 31; 100pp; English.
XX SS The sequences given in AAT80211-382 represent synthetic oligonucleotides
XX CC which are complementary to a portion of the 5' untranslated region (UTR)
XX CC of hepatitis C virus (HCV). These sequences may be used in a
XX CC pharmaceutical composition for the control or prevention of HCV
XX CC infection. They may be used to inhibit replication or expression of HCV
XX CC or for detecting the presence of HCV in a sample. They may be used to
XX CC inhibit HCV replication in a cell and are therefore useful in the
XX CC treatment of HCV infections such as chronic and acute hepatitis and
XX CC hepatocarcinoma. This oligo was used in a luciferase assay to determine
XX CC whether it binds successfully to its target
XX SQ Sequence 24 BP; 3 A; 5 C; 12 G; 4 T; 0 U; 0 Other;

Query Match 66.7%; Score 12; DB 2; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.4e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGCGAG 12
   |||||
Db 1 GGGGUCGCGAG 12

Search completed: April 25, 2005, 13:45:37
Job time : 233.053 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 25, 2005, 13:09:46 ; Search time 1731.32 Seconds  
(without alignments)  
395.743 Million cell updates/sec

Title: US-08-887-505B-38

Perfect score: 18

Sequence: 1 GGGGUCUGAGNNNNNN 18

Scoring table: OLIGO\_NUC

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

EST: \*  
1: gb\_esc1: \*  
2: gb\_esc2: \*  
3: gb\_hmc: \*  
4: gb\_esc3: \*  
5: gb\_esc4: \*  
6: gb\_esc5: \*  
7: gb\_esc6: \*  
8: gb\_g881: \*  
9: gb\_g882: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88.9	807	9	CL656406	PR10126C
2	83.3	298	7	CN046841	VL_P8_J15
3	83.3	646	3	AY110482	Zea mays
4	83.3	2267	3	AY110086	Zea mays
5	83.3	2334	9	AY406052	Mus muscu
6	83.3	3643	9	AY406378	Pan trogl
7	77.8	295	9	CL605849	CH240_183
8	77.8	306	9	CL607685	CH240_173
9	77.8	350	6	CB781043	AMGNNUC:S
10	77.8	410	6	CB803895	AMGNNUC:Y
11	77.8	446	4	CG466788	CH240_136
12	77.8	447	4	BG275153	NXSI_140
13	77.8	451	9	CG981750	CH240_167
14	77.8	503	9	CG608913	OST28585
15	77.8	593	6	CB584419	AMGNNUC:N
16	77.8	715	9	CL683372	PR10136C
17	77.8	745	9	CC923806	CO71108ba
18	77.8	764	9	CC918669	CO09611ba
19	77.8	785	9	CL677391	PR10120a
20	77.8	789	6	CB897169	trico10xa
21	77.8	809	6	CB900187	trico21xe
22	77.8	1392	9	AY413964	Homo sapi
23	77.8	1392	9	AY413965	Pan trogl
24	77.8	1527	9	AY411600	Homo sapi

25	14	77.8	1527	9	AY411601	AY411601 Pan trogl
26	14	77.8	2907	3	AY18641	Homo sapi
27	14	77.8	5308	9	AY109382	AY109382 Zea mays
28	13	72.2	91	9	CG976547	CH240_166
29	13	72.2	122	2	BE242665	TCAP1E17
30	13	72.2	166	9	CG918380	CH240_144
31	13	72.2	211	9	CG979398	CH240_171
32	13	72.2	212	9	CL609827	CH240_177
33	13	72.2	221	9	CG986238	CH240_156
34	13	72.2	224	9	CL603268	CH240_178
35	13	72.2	226	9	CC467061	CH240_136
36	13	72.2	250	9	CG989067	CH240_146
37	13	72.2	256	9	CG982763	CH240_164
38	13	72.2	327	9	CG983959	CH240_153
39	13	72.2	332	9	CC470613	CH240_144
40	13	72.2	377	9	CL211616	W13C04 G
41	13	72.2	392	6	CB774359	AMGNNUC:N
42	13	72.2	393	9	CG989457	CH240_146
43	13	72.2	412	9	CG980948	CH240_161
44	13	72.2	424	9	CG984052	CH240_153
45	13	72.2	424	9	CL604436	CH240_180
46	13	72.2	431	8	BZ759976	622_3L4_E
47	13	72.2	433	8	BZ759980	622_3L4_F
48	13	72.2	466	9	CL604951	CH240_181
49	13	72.2	484	4	BM492637	NXRV_027
50	13	72.2	484	9	CG982237	CG982237
51	13	72.2	487	9	CC467322	CH240_137
52	13	72.2	503	8	AQ597630	HS_2065_B
53	13	72.2	504	9	CG986681	CH240_157
54	13	72.2	506	9	CL608092	CH240_174
55	13	72.2	509	9	CG983697	CH240_165
56	13	72.2	526	9	CL608426	CH240_175
57	13	72.2	536	9	CG986355	CH240_157
58	13	72.2	533	4	CG985260	CH240_155
59	13	72.2	533	9	BG713519	pg11n.pk0
60	13	72.2	601	9	CG989575	CH240_147
61	13	72.2	604	9	CG978763	CH240_170
62	13	72.2	606	9	CG992853	CH240_152
63	13	72.2	614	6	CA754085	BR0400100
64	13	72.2	615	9	CG985739	CH240_155
65	13	72.2	618	9	AY417454	Pan trogl
66	13	72.2	619	8	BZ922485	CH240_121
67	13	72.2	625	8	BH760082	Mc_H2M02
68	13	72.2	638	9	CG976913	CH240_167
69	13	72.2	655	9	CG978073	CH240_169
70	13	72.2	674	3	AY111821	Zea mays
71	13	72.2	679	8	BZ912643	CH240_111
72	13	72.2	684	4	BM251975	BOTL01000
73	13	72.2	701	9	CG992790	CH240_152
74	13	72.2	716	5	CN035898	nm_11_g12
75	13	72.2	756	5	BQ438636	607145436
76	13	72.2	783	7	CN042530	vi1_p42_o
77	13	72.2	802	3	AY111174	Zea mays
78	13	72.2	825	9	AY405397	Pan trogl
79	13	72.2	835	5	BQ948650	AGENCOURT
80	13	72.2	858	5	CG921276	CO47002ba
81	13	72.2	873	5	BQ957217	AGENCOURT
82	13	72.2	895	5	AY110949	AGENCOURT
83	13	72.2	895	3	AY110949	Zea mays
84	13	72.2	903	3	AY110206	AGENCOURT
85	13	72.2	928	3	BO927240	AGENCOURT
86	13	72.2	980	5	BQ620039	AGENCOURT
87	13	72.2	1000	5	BQ062584	AGENCOURT
88	13	72.2	1073	5	BQ062584	AGENCOURT
89	13	72.2	1124	9	AY410559	Homo sapi
90	13	72.2	1170	9	AY410559	Homo sapi
91	13	72.2	1170	9	AY410560	Pan trogl
92	13	72.2	1170	9	AY410561	Mus muscu
93	13	72.2	1247	9	AY409438	Pan trogl
94	13	72.2	1271	9	AY409437	Homo sapi
95	13	72.2	1613	9	AY421522	Pan trogl
96	13	72.2	1920	9	AY409605	Homo sapi
97	13	72.2	1920	9	AY409606	Pan trogl

C 98	13	72.2	2001	9	AY402163	AY402163	Pan tlogl	171	12	66.7	195	7	D45320	D45320	HUMHG5144 H
C 99	13	72.2	2036	9	AY405709	AY405709	Pan tlogl	172	12	66.7	196	2	AM836385	AM836385	PW0-LT003
C 100	13	72.2	2073	9	AY417388	AY417388	Pan tlogl	173	12	66.7	197	7	CF162671	CF162671	B0715A10-
C 101	13	72.2	2075	9	AY417387	AY417387	Homo sapi	174	12	66.7	200	1	AA337180	AA337180	ESTJ1873
C 102	13	72.2	2075	9	AY417389	AY417389	Mus muscu	175	12	66.7	200	2	BE398334	BE398334	WHE0010.E
C 103	13	72.2	2257	9	AY413512	AY413512	Pan tlogl	176	12	66.7	200	2	BI047779	BI047779	MR4-ST024
C 104	13	72.2	2772	9	AY410786	AY410786	Mus muscu	177	12	66.7	201	8	AZ791991	AZ791991	2M0043H07
C 105	13	72.2	3129	9	AY405708	AY405708	Homo sapi	178	12	66.7	203	1	AI503108	AI503108	vm92a11.x
C 106	13	72.2	3878	9	AY420125	AY420125	Mus muscu	179	12	66.7	203	2	AM204396	AM204396	UT-H-B11-
C 107	12	66.7	69	9	CG918361	CG918361	CH240.143	180	12	66.7	203	2	BM246707	BM246707	BB246707
C 108	12	66.7	73	8	AF219075	AF219075	AF219075	181	12	66.7	204	2	BM523008	BM523008	BB523008
C 109	12	66.7	94	1	AA929340	AA929340	vz41a10.r	182	12	66.7	205	6	CB935773	CB935773	BB523008
C 110	12	66.7	100	2	BF374161	BF374161	MR0-SN004	183	12	66.7	206	2	AM353129	AM353129	BB523008
C 111	12	66.7	101	7	CP537121	CP537121	UT-M-FT0-	184	12	66.7	207	7	NB4369	NB4369	BB523008
C 112	12	66.7	102	7	CK87998	CK87998	L0923G09-	185	12	66.7	208	2	AM353798	AM353798	BB523008
C 113	12	66.7	105	5	BO809065	BO809065	1030008H1	186	12	66.7	208	4	BI017022	BI017022	BB523008
C 114	12	66.7	107	1	AA915600	AA915600	vz32f08.r	187	12	66.7	208	7	CF614056	CF614056	BB523008
C 115	12	66.7	110	8	AZ557012	AZ557012	RPCT-23-1	188	12	66.7	208	9	CE743112	CE743112	BB523008
C 116	12	66.7	116	2	AM326734	AM326734	19665 MAR	189	12	66.7	209	1	AI594283	AI594283	BB523008
C 117	12	66.7	121	7	CO549288	CO549288	LYST6835	190	12	66.7	209	1	CV337093	CV337093	BB523008
C 118	12	66.7	123	6	CD286354	CD286354	11_K23.ab	191	12	66.7	209	9	CL603743	CL603743	BB523008
C 119	12	66.7	128	2	AM480318	AM480318	PM1-HT045	192	12	66.7	210	2	BO802813	BO802813	BB523008
C 120	12	66.7	133	2	AM385180	AM385180	PM1-HT045	193	12	66.7	210	9	AL764056	AL764056	BB523008
C 121	12	66.7	134	1	AI280744	AI280744	QW07c10.x	194	12	66.7	210	9	CG988556	CG988556	BB523008
C 122	12	66.7	134	2	AM358302	AM358302	42366 MAR	195	12	66.7	211	1	AA607115	AA607115	BB523008
C 123	12	66.7	135	6	CA378150	CA378150	656898 NC	196	12	66.7	211	4	BM705448	BM705448	BB523008
C 124	12	66.7	141	2	CI965510	CI965510	OB1-FCC039	197	12	66.7	211	4	CV494873	CV494873	BB523008
C 125	12	66.7	143	2	BB606528	BB606528	BB606528	198	12	66.7	211	1	AV152436	AV152436	BB523008
C 126	12	66.7	146	7	CO544031	CO544031	LYEST1172	199	12	66.7	212	4	BM756685	BM756685	BB523008
C 127	12	66.7	147	9	CG918274	CG918274	CH240.142	200	12	66.7	212	4	CE204335	CE204335	BB523008
C 128	12	66.7	150	9	CG918034	CG918034	CH240.136	201	12	66.7	214	2	AM832847	AM832847	BB523008
C 129	12	66.7	151	8	BZ280016	BZ280016	CH230-480	202	12	66.7	215	2	AM832847	AM832847	BB523008
C 130	12	66.7	151	9	CE594318	CE594318	11gr-g8s-	203	12	66.7	215	2	AM832847	AM832847	BB523008
C 131	12	66.7	152	6	CB482045	CB482045	11gr-g8s-	204	12	66.7	216	6	CB298482	CB298482	BB523008
C 132	12	66.7	155	9	CG677253	CG677253	11gr-g8s-	205	12	66.7	217	2	BF902433	BF902433	BB523008
C 133	12	66.7	155	9	CL303190	CL303190	11gr-g8s-	206	12	66.7	218	2	BI172301	BI172301	BB523008
C 134	12	66.7	158	9	CL607849	CL607849	CH240.174	207	12	66.7	218	2	BF083384	BF083384	BB523008
C 135	12	66.7	160	2	CR081247	CR081247	Reverese MA	208	12	66.7	218	7	RS9325	RS9325	BB523008
C 136	12	66.7	161	2	BF651925	BF651925	275345 MA	209	12	66.7	218	7	CE469148	CE469148	BB523008
C 137	12	66.7	163	2	AM848479	AM848479	113-CT021	210	12	66.7	219	5	BQ088625	BQ088625	BB523008
C 138	12	66.7	168	2	BB569306	BB569306	BB569306	211	12	66.7	219	5	BQ088625	BQ088625	BB523008
C 139	12	66.7	171	6	CAB50537	CAB50537	D03A06.se	212	12	66.7	219	5	BQ088625	BQ088625	BB523008
C 140	12	66.7	171	6	CE350113	CE350113	11gr-g8s-	213	12	66.7	220	2	BE175932	BE175932	BB523008
C 141	12	66.7	172	6	CD557019	CD557019	AGENCOURT	214	12	66.7	221	1	AA381335	AA381335	BB523008
C 142	12	66.7	173	6	CD519554	CD519554	AGENCOURT	215	12	66.7	221	2	BI118547	BI118547	BB523008
C 143	12	66.7	174	1	AV275702	AV275702	AGENCOURT	216	12	66.7	221	2	BE118547	BE118547	BB523008
C 144	12	66.7	174	5	BO326528	BO326528	PM1-CN015	217	12	66.7	222	4	BE118547	BE118547	BB523008
C 145	12	66.7	175	2	CL303253	CL303253	P005A07 G	218	12	66.7	222	8	AZ677747	AZ677747	BB523008
C 146	12	66.7	175	2	BE926972	BE926972	RCO-CN002	219	12	66.7	223	1	AV277410	AV277410	BB523008
C 147	12	66.7	176	9	BQ348169	BQ348169	RCO-Heart	220	12	66.7	224	2	BB605546	BB605546	BB523008
C 148	12	66.7	176	5	CE745681	CE745681	11gr-g8s-	221	12	66.7	224	4	BB332881	BB332881	BB523008
C 149	12	66.7	179	9	CE745681	CE745681	11gr-g8s-	222	12	66.7	224	8	B99227	B99227	BB523008
C 150	12	66.7	180	1	AJ463066	AJ463066	11gr-g8s-	223	12	66.7	227	1	AA612447	AA612447	BB523008
C 151	12	66.7	182	4	BG062863	BG062863	L0958H12-	224	12	66.7	227	2	BF851905	BF851905	BB523008
C 152	12	66.7	182	5	BM183955	BM183955	BM183955	225	12	66.7	227	2	BI152101	BI152101	BB523008
C 153	12	66.7	185	1	AA500916	AA500916	V903408.r	226	12	66.7	228	2	BI102477	BI102477	BB523008
C 154	12	66.7	185	7	F31582	F31582	HSPD2786 H	227	12	66.7	228	9	BK9997135	BK9997135	BB523008
C 155	12	66.7	185	7	H39042	H39042	YP65B04.r1	228	12	66.7	229	2	BF752144	BF752144	BB523008
C 156	12	66.7	186	2	BB281821	BB281821	BB281821	229	12	66.7	229	2	BF777206	BF777206	BB523008
C 157	12	66.7	188	6	CE739078	CE739078	11gr-g8s-	230	12	66.7	229	5	BK523660	BK523660	BB523008
C 158	12	66.7	189	6	CD016191	CD016191	NXCI_029	231	12	66.7	230	1	CL603506	CL603506	BB523008
C 159	12	66.7	190	6	CD612432	CD612432	56086375H	232	12	66.7	230	1	AV048448	AV048448	BB523008
C 160	12	66.7	190	6	CE683453	CE683453	11gr-g8s-	233	12	66.7	230	1	BB016133	BB016133	BB523008
C 161	12	66.7	191	6	BF832234	BF832234	PM3-HT092	234	12	66.7	230	7	CE272878	CE272878	BB523008
C 162	12	66.7	191	6	CD612233	CD612233	56086375H	235	12	66.7	230	7	Z41293	Z41293	BB523008
C 163	12	66.7	191	6	CD612233	CD612233	56086375H	236	12	66.7	230	7	AM820590	AM820590	BB523008
C 164	12	66.7	192	7	CP613742	CP613742	EST887248	237	12	66.7	232	2	CG492926	CG492926	BB523008
C 165	12	66.7	192	9	CG987201	CG987201	CH240.158	238	12	66.7	233	2	BF759712	BF759712	BB523008
C 166	12	66.7	193	4	CE424526	CE424526	11gr-g8s-	239	12	66.7	233	9	CE704990	CE704990	BB523008
C 167	12	66.7	194	4	BM238031	BM238031	K051B01-	240	12	66.7	234	2	AM563031	AM563031	BB523008
C 168	12	66.7	195	4	BB017291	BB017291	BB017291	241	12	66.7	234	2	BE754085	BE754085	BB523008
C 169	12	66.7	195	4	BI047499	BI047499	MR4-ST024	242	12	66.7	234	4	BI704456	BI704456	BB523008
C 170	12	66.7	195	7	CV025592	CV025592	3313_Full	243	12	66.7	234	7	CR582000	CR582000	BB523008



244	12	66.7	235	2	BF542973	UI-R-Y0-a	317	12	66.7	265	7	CK227224
C 245	12	66.7	235	2	BB017167	BB017167	318	12	66.7	265	7	CO945287
C 246	12	66.7	235	2	BB328750	BB328750	319	12	66.7	266	7	D45315
C 247	12	66.7	235	9	CG516844	CG516844 OST76404	320	12	66.7	267	2	AM884379
C 248	12	66.7	236	1	AV254473	AV254473	321	12	66.7	267	2	BE837043
C 249	12	66.7	236	1	AV289026	AV289026	322	12	66.7	267	2	BE077731
C 250	12	66.7	236	4	BG146822	BG146822 mab93h01.	323	12	66.7	267	7	CN439133
C 251	12	66.7	236	4	BM740588	K-EST0011	324	12	66.7	268	2	BE370631
C 252	12	66.7	237	1	AI845958	UI-M-AKI-	325	12	66.7	268	2	BE510384
C 253	12	66.7	237	1	AV253155	AV253155	326	12	66.7	268	2	BE510384
C 254	12	66.7	237	5	BQ528062	BQ528062 1091054A0	327	12	66.7	268	4	BI774348
C 255	12	66.7	237	1	CC469406	CC469406 CH240.142	328	12	66.7	268	7	CO577136
C 256	12	66.7	238	1	AA963688	AA963688 UI-R-El-9	329	12	66.7	268	9	CG543981
C 257	12	66.7	238	6	AI851860	UI-M-BHO-	330	12	66.7	269	2	BE837040
C 258	12	66.7	239	6	CE831455	CE831455 743976 MA	331	12	66.7	269	5	BI362301
C 259	12	66.7	239	9	CE722972	CE722972 UI-R-g88-	332	12	66.7	269	7	BI362301
C 260	12	66.7	240	2	AM495593	AM495593 UI-M-BH41	333	12	66.7	270	1	AA851971
C 261	12	66.7	241	2	BF752142	BF752142 RC0-BN041	334	12	66.7	270	1	AA978123
C 262	12	66.7	242	1	AV127381	AV127381 AV127381	335	12	66.7	270	2	BF765024
C 263	12	66.7	243	1	AV234199	AV234199 AV234199	336	12	66.7	270	7	CG342995
C 264	12	66.7	243	1	AV242455	AV242455	337	12	66.7	270	7	N81856
C 265	12	66.7	243	2	BI771141	BI771141	338	12	66.7	270	8	A2956865
C 266	12	66.7	243	2	BB392742	BB392742	339	12	66.7	271	8	AM479994
C 267	12	66.7	243	4	BM446164	BM446164 11L4C9.ab	340	12	66.7	271	2	BE551073
C 268	12	66.7	244	9	CE679091	CE679091 UI-R-g88-	341	12	66.7	271	2	BE517563
C 269	12	66.7	245	1	AA326703	AA326703 EST29938	342	12	66.7	271	8	BE878816
C 270	12	66.7	245	1	AA357582	AA357582 EST66330	343	12	66.7	272	2	BE216174
C 271	12	66.7	245	2	BB022056	BB022056	344	12	66.7	272	6	CD542099
C 272	12	66.7	246	2	BF202156	BF202156 WHE1778 C	345	12	66.7	273	8	A2077912
C 273	12	66.7	247	1	AV205320	AV205320	346	12	66.7	273	8	A2077912
C 274	12	66.7	247	2	BB516760	BB516760	347	12	66.7	274	1	CK227223
C 275	12	66.7	247	6	CD620963	CD620963 56038392J	348	12	66.7	274	1	CK227223
C 276	12	66.7	247	7	CK227219	CK227219 701032654	349	12	66.7	275	1	AA253386
C 277	12	66.7	247	9	CL335852	CL335852 RPCI4.4.25	350	12	66.7	275	1	AA261297
C 278	12	66.7	248	2	BF560803	BF560803 UI-R-CO-h	351	12	66.7	275	1	AA226091
C 279	12	66.7	248	2	BF929783	BF929783 QV3-NT021	352	12	66.7	275	2	BF370621
C 280	12	66.7	249	9	BF353862	BF353862 IL5-HT070	353	12	66.7	275	2	BE723048
C 281	12	66.7	249	9	CE124814	CE124814 UI-R-g88-	354	12	66.7	275	7	TT22771
C 282	12	66.7	251	7	BB606888	BB606888	355	12	66.7	276	2	BE836978
C 283	12	66.7	251	7	CN315060	CN315060 170004179	356	12	66.7	276	4	BM115144
C 284	12	66.7	253	7	H31872	H31872 EST106388 R	357	12	66.7	276	9	CC574544
C 285	12	66.7	254	1	AA237458	AA237458 mw95908.r	358	12	66.7	277	2	BB008264
C 286	12	66.7	254	2	BF752143	BF752143 RC0-BN041	359	12	66.7	277	2	BB196872
C 287	12	66.7	254	6	CA013872	CA013872 RTO9L18r	360	12	66.7	277	5	BM059750
C 288	12	66.7	254	7	CK227222	CK227222 700774271	361	12	66.7	277	6	CD681152
C 289	12	66.7	255	2	BB091609	BB091609	362	12	66.7	278	2	AM431474
C 290	12	66.7	255	2	AB077246	AB077246	363	12	66.7	279	2	BB033250
C 291	12	66.7	256	2	BB020321	BB020321	364	12	66.7	279	2	BB327685
C 292	12	66.7	257	2	BB345500	BB345500	365	12	66.7	279	2	BB498881
C 293	12	66.7	257	7	CO191359	CO191359 EC30753.5	366	12	66.7	279	2	BE599902
C 294	12	66.7	258	1	AV209463	AV209463	367	12	66.7	279	7	CV465909
C 295	12	66.7	258	9	CE858911	CE858911 UI-R-g88-	368	12	66.7	280	1	AA978208
C 296	12	66.7	260	1	AV123252	AV123252	369	12	66.7	280	2	AM417210
C 297	12	66.7	260	1	AV263940	AV263940	370	12	66.7	280	2	AM418234
C 298	12	66.7	260	2	BB577765	BB577765	371	12	66.7	280	2	BB176724
C 299	12	66.7	260	5	BP103065	BP103065	372	12	66.7	280	2	BE836994
C 300	12	66.7	260	7	CE272628	CE272628 14ETL--01	373	12	66.7	280	8	AQ069839
C 301	12	66.7	261	7	CN415331	CN415331 170005122	374	12	66.7	280	8	AZ381336
C 302	12	66.7	261	4	BE837035	BE837035 RC6-FN008	375	12	66.7	280	8	BH092106
C 303	12	66.7	261	4	BG982648	BG982648 IL5-CN006	376	12	66.7	281	1	AV075818
C 304	12	66.7	261	7	CNS76464	CNS76464 rc65C06.x	377	12	66.7	281	1	AV137880
C 305	12	66.7	261	7	CE317310	CE317310 UI-R-g88-	378	12	66.7	281	2	BB081511
C 306	12	66.7	262	1	AV442031	AV442031	379	12	66.7	282	1	AA355247
C 307	12	66.7	263	2	BF412757	BF412757 UI-R-BT10	380	12	66.7	282	2	BF371084
C 308	12	66.7	263	2	BF759646	BF759646 CM1-CT060	381	12	66.7	282	2	BB310977
C 309	12	66.7	263	9	CG560120	CG560120 OST180067	382	12	66.7	282	9	CG977185
C 310	12	66.7	264	1	AV268669	AV268669	383	12	66.7	282	9	CG977185
C 311	12	66.7	264	9	CG188511	CG188511 PUFSD12TD	384	12	66.7	282	9	CG977185
C 312	12	66.7	265	1	AI608577	AI608577 v41Gc11.x	385	12	66.7	283	2	BF817082
C 313	12	66.7	265	1	AV019951	AV019951	386	12	66.7	283	2	AM833996
C 314	12	66.7	265	2	BF588625	BF588625 7120A06.x	387	12	66.7	283	2	BI126874
C 315	12	66.7	265	2	BB605782	BB605782	388	12	66.7	283	4	BI154663
C 316	12	66.7	265	2	BB605782	BB605782	389	12	66.7	283	4	BG071262

C 390	12	66.7	283	7	CN372754	170006001	C 463	12	302	2	BB269914
C 391	12	66.7	284	2	BB438340	BB438340	C 464	12	302	2	BB295403
C 392	12	66.7	284	8	CC355492	PUMPT39TB	C 465	12	302	2	BB532636
C 393	12	66.7	285	2	AM673477	AM673477 bas4e04.y	C 466	12	302	7	NA4912
C 394	12	66.7	285	2	BB158442	BB158442	C 467	12	303	1	AA683100
C 395	12	66.7	285	2	BB259178	BB259178	C 468	12	303	2	BB175587
C 396	12	66.7	285	2	BB279579	BB279579	C 469	12	303	2	BB254629
C 397	12	66.7	285	5	BM059057	BM059057	C 470	12	303	2	BB543513
C 398	12	66.7	286	2	BB194136	BB194136	C 471	12	303	7	CK376764
C 399	12	66.7	286	2	BB31626	BB31626	C 472	12	304	1	AA954464
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C 401	12	66.7	286	4	BF10987	BF10987	C 474	12	304	2	BE476820
C 402	12	66.7	286	4	BI036185	BI036185	C 475	12	305	1	AV137546
C 403	12	66.7	286	9	CG589169	CG589169	C 476	12	305	1	AV146284
C 404	12	66.7	287	2	BF049319	BF049319	C 477	12	305	2	BB085899
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C 406	12	66.7	287	7	CO947765	CO947765	C 479	12	305	2	BB175392
C 407	12	66.7	287	8	AZ562354	AZ562354	C 480	12	306	7	AI1414363
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C 410	12	66.7	288	5	BB338809	BB338809	C 483	12	308	2	AM719928
C 411	12	66.7	288	8	AZ807087	AZ807087	C 484	12	308	5	BY056713
C 412	12	66.7	288	8	CL962179	CL962179	C 485	12	309	2	BB270278
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C 416	12	66.7	289	9	CG624510	CG624510	C 489	12	309	5	BY292648
C 417	12	66.7	290	5	BY007660	BY007660	C 490	12	309	7	CK730332
C 418	12	66.7	291	1	AA356674	AA356674	C 491	12	309	9	CG990143
C 419	12	66.7	291	1	BF456561	BF456561	C 492	12	309	9	CL125230
C 420	12	66.7	292	1	AA886697	AA886697	C 493	12	310	1	AV047111
C 421	12	66.7	292	1	AI073183	AI073183	C 494	12	310	1	AV138059
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C 423	12	66.7	292	2	BB179308	BB179308	C 496	12	310	2	BF333568
C 424	12	66.7	292	2	BB295757	BB295757	C 497	12	310	2	AM660090
C 425	12	66.7	292	4	BB516254	BB516254	C 498	12	310	2	BB120099
C 426	12	66.7	292	4	BB946527	BB946527	C 499	12	310	9	CG188509
C 427	12	66.7	292	6	CG2320	CG2320	C 500	12	311	2	BB400673
C 428	12	66.7	293	2	AI659006	AI659006	C 501	12	311	6	CA385323
C 429	12	66.7	293	2	BB476877	BB476877	C 502	12	311	9	CG977401
C 430	12	66.7	293	2	BB509176	BB509176	C 503	12	312	2	AM455580
C 431	12	66.7	293	9	CC468448	CC468448	C 504	12	312	2	AM455580
C 432	12	66.7	295	2	BB388445	BB388445	C 505	12	312	2	BB156954
C 433	12	66.7	295	2	BB517144	BB517144	C 506	12	312	2	BB174777
C 434	12	66.7	295	4	BM427908	BM427908	C 507	12	312	2	BB502019
C 435	12	66.7	296	1	AA754707	AA754707	C 508	12	312	2	BB560962
C 436	12	66.7	296	1	AI556225	AI556225	C 509	12	312	5	CD552541
C 437	12	66.7	296	2	CG589846	CG589846	C 510	12	312	6	CD552541
C 438	12	66.7	297	2	BB162381	BB162381	C 511	12	312	6	CD553320
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C 441	12	66.7	298	5	AA227041	AA227041	C 514	12	313	7	CF928827
C 442	12	66.7	298	5	BY126409	BY126409	C 515	12	313	7	CF928827
C 443	12	66.7	298	7	CO261062	CO261062	C 516	12	313	7	CF928827
C 444	12	66.7	299	1	AV168610	AV168610	C 517	12	313	8	AA090361
C 445	12	66.7	299	2	AM109755	AM109755	C 518	12	314	1	AA090361
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C 447	12	66.7	299	2	BB401045	BB401045	C 520	12	314	1	AA090361
C 448	12	66.7	299	2	BF150583	BF150583	C 521	12	314	1	AA090361
C 449	12	66.7	299	2	AG266328	AG266328	C 522	12	315	6	CD553450
C 450	12	66.7	299	2	CG989511	CG989511	C 523	12	315	9	CL608641
C 451	12	66.7	300	2	BB463304	BB463304	C 524	12	316	2	BB542407
C 452	12	66.7	300	2	BB509370	BB509370	C 525	12	316	2	BB542407
C 453	12	66.7	300	9	BF012723	BF012723	C 526	12	316	2	BF108857
C 454	12	66.7	301	1	AA996342	AA996342	C 527	12	316	4	BSMC33C4
C 455	12	66.7	301	1	AA996342	AA996342	C 528	12	316	9	BSMC33C4
C 456	12	66.7	301	2	BB260439	BB260439	C 529	12	317	9	BSMC33C4
C 457	12	66.7	301	2	BB387319	BB387319	C 530	12	317	5	BB476362
C 458	12	66.7	301	2	BB387319	BB387319	C 531	12	317	5	BB476362
C 459	12	66.7	301	9	CE824217	CE824217	C 532	12	317	5	BB476362
C 460	12	66.7	302	2	BB082384	BB082384	C 533	12	318	8	BB221059
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## ALIGNMENTS

RESULT 1  
 LOCUS CL656406  
 DEFINITION PRI0126C.B11 - PRI0126C.B21 (807) Mixed stage fosmid library of P. survey Sequence.

ACCESSION CL656406  
 VERSION CL656406.1 GI:50136810  
 SOURCE GSS.

ORGANISM Pristionchus pacificus  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasteridae; Nematodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 807)  
 Striyyasan, V., Otto, G. W., Kahlow, U., Geisler, R. and Sommer, R. J.  
 Appad: an AcceB database for the nematode satellite organism  
 Pristionchus pacificus  
 Nucleic Acids Res. 32 (1), D421-D422 (2004)  
 CONTACT: Sommer RJ  
 JOURNAL  
 COMMENT Evolutionary Biology  
 Max-Planck-Institute for Developmental Biology  
 Spemannstr. 37-39, Tuebingen D-72076, Germany  
 Tel: 00497071601371  
 Fax: 00497071601498  
 Email: ralf.sommer@tuebingen.mpg.de  
 This library was generated at Caltech, Pasadena, USA and end  
 sequenced at Vancouver, Canada.  
 Seq primer: T7  
 Class: Fosmid ends.

## FEATURES

source  
 1..807  
 Location/Qualifiers  
 /organism="Pristionchus pacificus"  
 /mol\_type="genomic DNA"  
 /strain="California"  
 /db\_xref="taxon:54126"  
 /clone\_lib="Mixed stage fosmid library of P. pacificus var. California"  
 /note="Vector: pB1fos-5 Fosmid vector"

Query Match

88.9%; Score 16; DB 9; Length 807;

Best Local Similarity 87.5%; Pred. No. 1.3e+02;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGUCCUGAGNNNNNN 18  
 DB 608 GGUCCUGAGNNNNNN 623

RESULT 2  
 LOCUS CN046841 296 bp mRNA linear EST 25-MAR-2004  
 DEFINITION v1\_p8\_j19-triplexid\_v1 Ambystoma mexicanum cDNA, mRNA sequence.

ACCESSION CN046841  
 VERSION CN046841.1 GI:45817206  
 KEYWORDS EST.  
 SOURCE Ambystoma mexicanum (axolotl)  
 ORGANISM Ambystoma mexicanum

REFERENCE 1 (bases 1 to 298)  
 Ambystoma.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae; Ambystoma.

AUTHORS Putta, S., Smith, J. J., Walker, J. A., Ronder, M., Weisrock, D., Monaghan, J., Samuels, A. K., Kump, K., King, D. C., Maness, N. J., Habermann, B., Tanaka, E., Bryant, S. V., Gardiner, D. M., Parichy, D. M. and Voss, S. R.  
 From biomedicine to natural history research: EST resources for Ambystomatid salamanders  
 BMC Genomics 5 (1), 54 (2004)  
 CONTACT: SR Voss  
 JOURNAL Department of Biology  
 COMMENT University of Kentucky  
 TH Morgan Building, Lexington, KY 40506, USA  
 Tel: 859 257 9888  
 Fax: 859 257 1717  
 Email: srvoos@uky.edu  
 The EST is quality trimmed at the ends with a 20 base window and quality threshold of 15 (phred quality score). Please visit <http://salamander.uky.edu> for any information (trace, quality files etc) regarding this EST.

## FEATURES

source  
 1..298  
 /organism="Ambystoma mexicanum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8296"  
 /issue\_type="Tail Blastema adn Proximal Tail Tissue"  
 /clone\_lib="V1"

## ORIGIN

Query Match 83.3%; Score 15; DB 7; Length 298;  
 Best Local Similarity 86.7%; Pred. No. 4.9e+02;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GUCCUGAGNNNNNN 18  
 DB 1 GUCCUGAGNNNNNN 15

RESULT 3  
 LOCUS AY110482 646 bp mRNA linear HTC 17-OCT-2002  
 DEFINITION Zea mays CL34196\_1 mRNA sequence.  
 ACCESSION AY110482  
 VERSION AY110482.1 GI:21214891  
 KEYWORDS HTC.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE Hainey, C. F., Dolan, M., Miao, G. H., Vogel, J. M., Whitsitt, M. S., Arthur, L. W., Hanafey, M., Morante, M. and Tingey, S. V.  
 Maize Mapping Project/Dupont Consensus Sequences for Design of

**JOURNAL** Overgo Probes  
**REFERENCE** Unpublished (2002)  
**AUTHORS** 2 (bases 1 to 646)  
**TITLE** Coe,E.H.  
**JOURNAL** Direct Submission  
**COMMENT** Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA  
 If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.  
 Location/Qualifiers  
 source  
 1..646  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /db\_xref="MaizEDB:631545"  
 /db\_xref="taxon:4577"  
 /clone\_lib="Maize Mapping Project/DuPont Cornsensus Library"  
 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"  
**ORIGIN**  
 Query Match 83.3%; Score 15; DB 3; Length 646;  
 Best Local Similarity 86.7%; Pred. No. 4.6e+02;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4 GUUCUGAGAGNNNNNN 18  
 |||||  
 115 GTCTCGAGNNNNNN 129  
**RESULT 4**  
**LOCUS** AY110086/c  
**DEFINITION** Zea mays CL1418\_1 mRNA sequence.  
**ACCESSION** AY110086  
**VERSION** AY110086.1 GI:21214173  
**KEYWORDS** HTC.  
**SOURCE** Zea mays  
**ORGANISM** Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.  
**REFERENCE** Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes  
**TITLE** Unpublished (2002)  
**REFERENCE** 2 (bases 1 to 2267)  
**AUTHORS** Coe,E.H.  
**JOURNAL** Direct Submission  
**REFERENCE** Submitted (23-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA  
**TITLE** If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.  
**COMMENT** location/Qualifiers  
 1..2267  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
**FEATURES**  
**SOURCE**

		/db_xref="MaizeDB:630280"	
		/clone_lib="Maize Mapping Project/Dupont Cornsensus Library"	
		/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont configs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACS in conjunction with the Maize Mapping Project"	
ORIGIN			
Query Match	83.3%;	Score 15;	DB 3; Length 2267;
Best Local Similarity	86.7%;	Pred. NO. 4.1e+02;	
Matches 13;	Conservative 2;	Mismatches 0;	Indels 0; Gaps 0;
OY	4	GUCCUGAGANNNNNN 18	
DB	339	GTCTCGAGANNNNNN 325	
RESULT 5			
AY406052		2334 bp	DNA linear GSS 15-DEC-2003
LOCUS			
DEFINITION	Mus musculus ABLIM1 gene, VIRTUAL TRANSCRIPT, partial sequence,		
ACCESSION	AY406052		
VERSION	AY406052.1	GI:39762026	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 2334)		
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.		
	Interfering nonneutral evolution from human-chimp-mouse orthologous gene trios		
TITLE	Science 302 (5652), 1960-1963 (2003)		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCES	2 (bases 1 to 2334)		
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.		
	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
FEATURES			
Source	Location/Qualifiers		
	1..2334		
	/organism="Mus musculus"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:10090"		
	<1..>2334		
	/gene="ABLIM1"		
	/locus_tag="HCM2428"		
ORIGIN			
Query Match	83.3%;	Score 15;	DB 9; Length 2334;
Best Local Similarity	86.7%;	Pred. NO. 4.1e+02;	
Matches 13;	Conservative 2;	Mismatches 0;	Indels 0; Gaps 0;
OY	4	GUCCUGAGANNNNNN 18	
DB	886	GTCTCGAGANNNNNN 900	
RESULT 6			
AY406378			

LOCUS AY406378 3643 bp DNA linear GSS 12-DEC-2003  
 DEFINITION Pan troglodytes HCM2537 gene, VIRtual TRANSCRIPT, partial sequence.  
 ACCESSION AY406378  
 VERSION AY406378.1 GI:39762352  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 1 (bases 1 to 3643)  
 Clark, A.G., Gianowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
 Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering them based on alignment.  
 Location/Qualifiers  
 1. 3643  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 <1..>3643  
 /locus\_tag="HCM2537"

ORIGIN  
 gene  
 Query Match 83.3%; Score 15; DB 9; Length 3643;  
 Best Local Similarity 86.7%; Pred. No. 3.9e+02;  
 Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GUCCUGAGANNNNN 18  
 ||:|||||  
 DB 85 GTCCTGGAGNNNNN 99

RESULT 7  
 LOCUS CL605849 295 bp DNA linear GSS 17-JUN-2004  
 DEFINITION CH240\_183G18.TJ CHORI-240 Bos taurus genomic clone CH240\_183G18, genomic survey sequence.  
 ACCESSION CL605849  
 VERSION CL605849.1 GI:48873881  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 295)  
 Costa, J.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)  
 Other GSSs: CH240\_183G18.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Email: acaetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have phred quality value equal to or higher than 20.  
 For BAC library availability, please contact Pieter de Jong  
 (pdejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources  
 (<http://www.chori.org/bacpac/ordering/information.htm>).  
 This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia with financing from Conselho Nacional de Desenvolvimento Cientifico e tecnologico (CNPq), Brazil  
 Plate: 183 row: G column: 18  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence strop: 295.  
 Location/Qualifiers  
 1. 295  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_183G18"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

ORIGIN  
 Query Match 77.8%; Score 14; DB 9; Length 295;  
 Best Local Similarity 85.7%; Pred. No. 1.7e+03;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGANNNNN 18  
 ||:|||||  
 DB 165 TCCTGGAGNNNNN 178

RESULT 8  
 LOCUS CL607685 306 bp DNA linear GSS 17-JUN-2004  
 DEFINITION CH240\_173D24.TJ CHORI-240 Bos taurus genomic clone CH240\_173D24, genomic survey sequence.  
 ACCESSION CL607685  
 VERSION CL607685.1 GI:48875717  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 306)  
 Costa, J.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)  
 Other GSSs: CH240\_173D24.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acaetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have phred quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT



(pdejong@mail.cbo.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering\_information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil

Plate: 173 row: D column: 24  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 306.  
Location/Qualifiers

FEATURES  
source  
1..306  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="Breed: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_173D24"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pTARBAcl.3, Site\_1: MboI, Site\_2: MboI;  
Hereford bull l1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 77.8%; Score 14; DB 9; Length 306;  
Best Local Similarity 85.7%; Pred. No. 1.7e+03;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 5 UCCUGAGGNNNNN 18  
Db 172 TCCTGGAGNNNNN 159

RESULT 9  
CB781043 350 bp mRNA linear EST 16-MAY-2003  
LOCUS  
DEFINITION  
AMGNNUC:SRPB2-00120-G1-A srpb2 (10220) Rattus norvegicus cDNA clone

CB781043  
VERSION  
CB781043.1 GI:29869434  
KEYWORDS  
EST.  
SOURCE  
Rattus norvegicus (Norway rat)

ORGANISM  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE  
1 (bases 1 to 350)  
AUTHORS  
Amgen EST Program.  
JOURNAL  
Amgen Rat EST Program  
Unpublished (2003)  
COMMENT  
Contact: Dan Fitzpatrick  
Amgen, Inc  
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00120 row: 9 column: 1.  
Location/Qualifiers

FEATURES  
source  
1..350  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="srpb2-00120-g1"  
/issue\_type="prostate tissue"  
/clone\_lib="srpb2 (10220)"  
/note="Vector: pSPOR1, Site 1: SalI; Site 2: NotI; rat  
prostate normalized double selected poly(A+) mRNA size  
fraction > 1 kb"

## ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 350;  
Best Local Similarity 85.7%; Pred. No. 1.7e+03;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 5 UCCUGAGGNNNNN 18  
Db 220 TCCTGGAGNNNNN 233

RESULT 10  
CB803895 410 bp mRNA linear EST 16-MAY-2003  
LOCUS  
DEFINITION  
AMGNNUC:YRAPB2-00001-B1-A Plap-b hypothalamus (10617) Rattus  
norvegicus cDNA clone yrapb2-00001-b1 5', mRNA sequence.

CB803895  
ACCESSION  
CB803895  
VERSION  
CB803895.1 GI:29919524  
KEYWORDS  
EST.  
SOURCE  
Rattus norvegicus (Norway rat)

ORGANISM  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE  
1 (bases 1 to 410)  
AUTHORS  
Amgen EST Program.  
JOURNAL  
Amgen Rat EST Program  
Unpublished (2003)  
COMMENT  
Contact: Dan Fitzpatrick  
Amgen, Inc  
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00001 row: b column: 1.  
Location/Qualifiers

FEATURES  
source  
1..410  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="Yrapb2-00001-b1"  
/issue\_type="hypothalamus normal"  
/clone\_lib="Plap-b hypothalamus (10617)"  
/note="Vector: pCDNA3.1(-)/Plap-5a, Site\_1: XbaI; Site\_2:  
NotI"

## ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 410;  
Best Local Similarity 85.7%; Pred. No. 1.7e+03;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 5 UCCUGAGGNNNNN 18  
Db 244 TCCTGGAGNNNNN 257

RESULT 11  
CC466788 446 bp DNA linear GSS 12-JUN-2003  
LOCUS  
DEFINITION  
CH240\_136M10.TV CHORI-240 Bos taurus genomic clone CH240\_136M10,  
genomic survey sequence.

CC466788  
ACCESSION  
CC466788.1 GI:31653020  
KEYWORDS  
GSS.  
SOURCE  
Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.

REFERENCE  
1 (bases 1 to 446)  
AUTHORS  
Costa, J.N., Mota, M. and Caetano, A.R.  
JOURNAL  
Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240  
Unpublished (2003)  
COMMENT  
Other\_GSSs: CH240\_136M10.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasilia

Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: [acaetano@cenargen.embrapa.br](mailto:acaetano@cenargen.embrapa.br)  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>). Bases shown have phred  
 quality value equal to or higher than 20. Bases with quality value  
 below 20 were masked with 'N'. For BAC library availability, please  
 contact Pieter de Jong ([pdejong@mail.cho.org](mailto:pdejong@mail.cho.org)). Clones may be  
 purchased from BACPAC Resources  
 ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)). This work  
 was undertaken as part of the International Bovine BAC Mapping  
 Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia  
 with financing from Conselho Nacional de Desenvolvimento Cientifico  
 e Tecnol6gico (CNPq), Brazil  
 Plate: 136 row: M column: 10  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 446.  
 Location/Qualifiers  
 1..446  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_136M10"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_1ib="CHORI-240"  
 /note="Vector: pIRBAC1.3; Site\_1: MboI; Site\_2: MboI;  
 Hereford bull l1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 77.8%; Score 14; DB 9; Length 446;  
 Best Local Similarity 85.7%; Pred. No. 1.7e+03;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 UCCUGAGAGNNNNNN 18  
 :||:|||||||  
 Db 134 TCCTGAGAGNNNNN 147

RESULT 12  
 BG275153 447 bp mRNA linear EST 07-MAY-2003  
 LOCUS NXSI 140 D03 F NXSI (Nef Xylem Side wood inclined) Pinus taeda cDNA  
 Definition A5502960 unknown protein see  
<http://mips.gsf.de/proj/thal/db/index.html>, mRNA sequence.  
 BG275153  
 BG275153.1 GI:13068180  
 EST.  
 Pinus taeda (loblolly pine)  
 SOURCE  
 ORGANISM  
 Pinus taeda  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
 1 (bases 1 to 447)  
 Sederoff, R.  
 Molecular Basis of Wood Formation in the Pine Megagenome  
 Unpublished (2000)  
 Contact: Sederoff, Ron  
 Forest Biotechnology  
 North Carolina State University  
 840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,  
 NC 27695, USA  
 Tel: 919 515 7800  
 Fax: 919 515 7801  
 Email: [ron.sederoff@ncsu.edu](mailto:ron.sederoff@ncsu.edu), [jerry\\_johnson@ncsu.edu](mailto:jerry_johnson@ncsu.edu)  
 Please see <http://web.ahc.umn.edu/biodata/nsfpine/> for further  
 information.  
 Seq primer: T3.  
 Location/Qualifiers  
 1..447

## ORIGIN

Query Match 77.8%; Score 14; DB 4; Length 447;  
 Best Local Similarity 85.7%; Pred. No. 1.6e+03;  
 Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 UCCUGAGAGNNNNNN 18  
 :||:|||||||  
 Db 425 TCCTGAGAGNNNNN 438

/organism="Pinus taeda"  
 /mol\_type="mRNA"  
 /strain="Coastal plain loblolly pine from North Carolina"  
 /db\_xref="taxon:3352"  
 /clone="NXSI 140 D03"  
 /tissue\_type="Xylem"  
 /cell\_type="Side"  
 /dev\_stage="juvenile"  
 /lab\_host="XLI-Blue"  
 /clone\_1ib="NXSI (Nef Xylem Side wood Inclined)"  
 /note="Vector: Bluescript SK; Site\_1: Eco RI; Site\_2:  
 XhoI; The library is from early (spring) wood, taken from  
 three six-year old trees (three different genotypes), in  
 the juvenile phase. These trees were induced to form side  
 wood by bending to a 45 degree angle and tying them to the  
 ground. Differentiating xylem was harvested from the sides  
 of the inclined stems, and a mixture of all three  
 genotypes was used for the library. oligo-dT primed cDNA  
 was directionally cloned into the EcoRI-XhoI Bluescript SK  
 vector arms. NOTE: The sequences contain a 'cDNA adapter'  
 between the EcoRI site and the start of the EST. The  
 adapter sequence is 'ATTTCGACGACG'."

RESULT 13  
 CG981750 451 bp DNA linear GSS 15-DEC-2003  
 LOCUS CH240 162B19 TV CHORI-240 Bos taurus genomic clone CH240\_162B19,  
 Definition genomic survey sequence.  
 CG981750  
 CG981750.1 GI:39907529  
 GSS.  
 Bos taurus (cow)  
 SOURCE  
 ORGANISM  
 Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Kumlantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 451)  
 Costa, V.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)  
 Other\_GSSs: CH240\_162B19.TV  
 Contact: Caetano, AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estraco Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372 70770-900 Brasilia  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: [acaetano@cenargen.embrapa.br](mailto:acaetano@cenargen.embrapa.br)  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have Phred quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 ([pdejong@mail.cho.org](mailto:pdejong@mail.cho.org)).  
 Clones may be purchased from BACPAC Resources  
 ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Cientifico e Tecnol6gico (CNPq), Brazil  
 Plate: 162 row: B column: 19

Seq primer: SP6  
Class: BAC ends  
High quality sequence, stop: 451.  
Location/Qualifiers

# FEATURES

Source

1..451  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_162B19"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_1ib="CHORI-240"  
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull Li Domino 993/5; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

# ORIGIN

Query Match 77.8%; Score 14; DB 9; Length 451;  
Best Local Similarity 85.7%; Pred. No. 1.6e+03;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNN 18  
:|||||  
Db 227 TCTGTGAGNNNNN 240

RESULT 14  
CG608913 503 bp mRNA linear GSS 02-OCT-2003  
LOCUS CG608913/c  
DEFINITION OST89585 Mus musculus 129SV/Ev Mus musculus cDNA clone OST89585,  
mRNA sequence.

ACCESSION CG608913.1 GI:37432762  
VERSION GSS.  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 503)  
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Zambrowicz, B.P., Abuln, A., Ramirez-Solis, R., Richter, L.D.,  
Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,  
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,  
Key, B.W. Jr., Klipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,  
Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,  
Spark, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,  
Zhu, Q., Person, C. and Sands, A.T.  
Mnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
screen to identify potential targets for therapeutic intervention  
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

TITLE Contact: Zambrowicz BP  
JOURNAL OmilBank  
COMMENT Lexicon Genetics Incorporated  
4000 Research Forest Drive, The Woodlands, TX 77381, USA  
Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)  
Class: Gene Trap.

# FEATURES

Source

1..503  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129SV/Ev"  
/db\_xref="taxon:10090"  
/clone="OST89585"  
/cell\_type="embryonic stem cell"  
/clone\_1ib="Mus musculus 129SV/Ev"

# ORIGIN

Query Match 77.8%; Score 14; DB 9; Length 503;  
Best Local Similarity 85.7%; Pred. No. 1.6e+03;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGUCUGAGAGNNN 15  
:|||||  
Db 495 GGTCCTGAGAGNN 482

RESULT 15  
CB584419 593 bp mRNA linear EST 03-APR-2003  
LOCUS AMGNNUC:NRH5-00282-F9-A W Rat hypothalamus (10471) Rattus  
DEFINITION norvegicus cDNA clone nrh5-00282-f9 5', mRNA sequence.  
CB584419  
ACCESSION CB584419.1 GI:29527870  
VERSION EST.  
KEYWORDS Rattus norvegicus (Norway rat)  
SOURCE Rattus norvegicus  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 593)  
AUTHORS Amgen EST Program.  
TITLE Amgen Rat EST Program  
JOURNAL Unpublished (2003)  
COMMENT Contact: Dan Fitzpatrick  
Amgen, Inc  
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00282 row: f column: 9.

FEATURES  
Source  
1..593  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="nrh5-00282-f9"  
/clone\_1ib="W Rat hypothalamus (10471)"  
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; W Rat  
hypothalamus adult female Wistar rat avg. Insert size 2.3  
kb fraction 6 and 7"

# ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 593;  
Best Local Similarity 85.7%; Pred. No. 1.6e+03;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNN 18  
:|||||  
Db 105 TCTGTGAGAGNNNNN 118

RESULT 16  
CL683372 715 bp DNA linear GSS 09-JUL-2004  
LOCUS PRI0136C\_G09\_2 - PRI0136C.BR (715) Mixed stage fosmid library of P.  
DEFINITION pacificus var. California Pristionchus pacificus genomic, genomic  
survey sequence.

ACCESSION CL683372.1 GI:50191062  
VERSION GSS.  
KEYWORDS Pristionchus pacificus  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus

REFERENCE 1 (bases 1 to 715)  
AUTHORS Strinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.  
TITLE AppADB: an Acedb database for the nematode satellite organism  
Pristionchus pacificus  
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)  
COMMENT Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de

This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.

Seq primer: T7

Class: fosmid ends.

FEATURES  
source Location/Qualifiers

1..715

/organism="Pristionchus pacificus"

/mol\_type="genomic DNA"

/strain="California"

/db\_xref="taxon:54126"

/clone\_lib="Mixed stage fosmid library of P. pacificus  
var. California"

/note="Vector: pBplfos-5 Fosmid vector"

ORIGIN

Query Match 77.8%; Score 14; DB 9; Length 715;

Best Local Similarity 85.7%; Pred. No. 1.6e+03;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNNN 18

DB 282 TCCTGAGAGNNNNNN 269

RESULT 17.

CC923806/c

LOCUS t071108ba.f1 TAMB7 Bos taurus genomic clone t071108ba, genomic

DEFINITION Survey sequence.

ACCESSION CC923806

VERSION CC923806.1 GI:33559145

KEYWORDS GSS.

SOURCE Bos taurus

ORGANISM Bos taurus (cow)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovinae; Bos.

1 (bases 1 to 745)

Lin.S., Najjar,F.Z., Adelson,D., Gill,C.A. and Roe,B.A.

Bovine BAC End Sequences from Library TAMB7

Unpublished (2003)

Contact: Bruce A. Roe

Advanced Center for Genome Technology

University of Oklahoma Department of Chemistry and Biochemistry

620 Parrington Oval, Room 208, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

Class: BAC ends

High quality sequence stop: 659.

Location/Qualifiers

1..745

/organism="Bos taurus"

/mol\_type="genomic DNA"

/strain="Angus bull T A M U Shoshone Y6 11519666"

/db\_xref="taxon:9913"

/clone="t071108ba"

/sex="Male"

/cell\_type="Blood"

/clone\_lib="TAMB7"

/note="Vector: pBelobAC11; Site\_1: HindIII; Site\_2:

HindIII; TAMB7 Bovine BAC library (Male) produced by Texas

A&M University, Department of Animal Science."

ORIGIN

Query Match 77.8%; Score 14; DB 9; Length 745;

Best Local Similarity 85.7%; Pred. No. 1.6e+03;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNNN 18

DB 38 TCCTGAGAGNNNNNN 25

RESULT 18

CC918669/c

LOCUS t009e11ba.f1 TAMB7 Bos taurus genomic clone t009e11ba, genomic

DEFINITION Survey sequence.

ACCESSION CC918669

VERSION CC918669.1 GI:33549379

KEYWORDS GSS.

SOURCE Bos taurus

ORGANISM Bos taurus (cow)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovinae; Bos.

1 (bases 1 to 764)

Lin.S., Najjar,F.Z., Adelson,D., Gill,C.A. and Roe,B.A.

Bovine BAC End Sequences from Library TAMB7

Unpublished (2003)

Contact: Bruce A. Roe

Advanced Center for Genome Technology

University of Oklahoma Department of Chemistry and Biochemistry

620 Parrington Oval, Room 208, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

Class: BAC ends

High quality sequence stop: 6

High quality sequence stop: 457.

Location/Qualifiers

1..764

/organism="Bos taurus"

/mol\_type="genomic DNA"

/strain="Angus bull T A M U Shoshone Y6 11519666"

/db\_xref="taxon:9913"

/clone="t009e11ba"

/sex="Male"

/cell\_type="Blood"

/clone\_lib="TAMB7"

/note="Vector: pBelobAC11; Site\_1: HindIII; Site\_2:

HindIII; TAMB7 Bovine BAC library (Male) produced by Texas

A&M University, Department of Animal Science."

ORIGIN

Query Match 77.8%; Score 14; DB 9; Length 764;

Best Local Similarity 85.7%; Pred. No. 1.6e+03;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGAGNNNNNN 18

DB 32 TCCTGAGAGNNNNNN 19

RESULT 19

CL677391

LOCUS PRI0120a.G09.2 - PRI0120a.BR (785) Mixed stage fosmid library of P.

pacificus var. California Pristionchus pacificus genomic, genomic

DEFINITION Survey sequence.

ACCESSION CL677391

VERSION CL677391.1 GI:50183399

KEYWORDS GSS.

SOURCE Pristionchus pacificus

ORGANISM Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;

Neodiplogasteridae; Pristionchus.

1 (bases 1 to 785)

Srinivasan,U., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.U.

Apadbi: an Acedb database for the nematode satellite organism

Pristionchus pacificus

Nucleic Acids Res. 32 (1), D421-D422 (2004)

Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
This library was generated at Caltech, Pasadena, USA and end  
sequenced at Vancouver, Canada.

Seq primer: T7  
Class: fosmid ends.

# FEATURES

## source

Location/Qualifiers  
1..785  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Mixed stage fosmid library of P. pacificus  
var. California"  
/note="Vector: pGP1fos-5 Fosmid vector"

## ORIGIN

Query Match 77.8%; Score 14; DB 9; Length 785;

Best Local Similarity 85.7%; Pred. No. 1.6e+03;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGGNNNNN 18

Db 369 TCCTGAGGNNNNN 362

## RESULT 20

CB897169 789 bp mRNA linear EST 02-JUL-2003

LOCUS tric010x18 T.reesei mycelial culture, Version 3 april Hypocrea  
jecorina cDNA clone tric010x18, mRNA sequence.

ACCESSION CB897169

VERSION CB897169.1 GI:30111827

## KEYWORDS

EST.

ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)

REFERENCE Hypocrea jecorina

1 (bases 1 to 789)

Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,

Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J.,

Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,

Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.

Transcriptional regulation of biomass-degrading enzymes in the

filamentous fungus Trichoderma reesei

J. Biol. Chem. 278 (34), 31988-31997 (2003)

JOURNAL MEDLINE

PUBMED 12788920

COMMENT Contact: Pamela K. Foreman

Genencor Intl.

925 Page Mill Road, Palo Alto, CA 94304, USA

Tel: (650) 846-7635

Fax: (650) 621-7817

Email: Pforeman@genencor.com

Seq primer: LT-F1 primer.

Location/Qualifiers

1..789

/organism="Hypocrea jecorina"

/mol\_type="mRNA"

/strain="QM6a"

/db\_xref="taxon:51453"

/clone="tric010x18"

/dev\_stage="mycelia"

/clone\_lib="T.reesei mycelial culture, Version 3 april"

/note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial

culture grown from 24 hrs to 6 days with varying Carbon

## ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 789;

Best Local Similarity 85.7%; Pred. No. 1.6e+03;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGGNNNNN 18

Db 67 TCCTGAGGNNNNN 54

## RESULT 21

CB900187 809 bp mRNA linear EST 02-JUL-2003

LOCUS tric021xe04 T.reesei mycelial culture, Version 3 april Hypocrea

jecorina cDNA clone tric021xe04, mRNA sequence.

ACCESSION CB900187

VERSION CB900187.1 GI:30114845

## KEYWORDS

## SOURCE

ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)

Hypocrea jecorina

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

1 (bases 1 to 809)

Foreman, P.K., Brown, D.E., Dankmeyer, L., Dean, R., Diener, S.,

Dunn-Coleman, N.S., Goedegebuur, F., Houfek, T.D., England, G.J.,

Kelley, A.S., Meerman, H.J., Mitchell, T., Mitchinson, C.,

Olivares, H.A., Teunissen, P.J., Yao, J., and Ward, M.

Transcriptional regulation of biomass-degrading enzymes in the

filamentous fungus Trichoderma reesei

J. Biol. Chem. 278 (34), 31988-31997 (2003)

JOURNAL MEDLINE

PUBMED 12788920

COMMENT Contact: Pamela K. Foreman

Genencor Intl.

925 Page Mill Road, Palo Alto, CA 94304, USA

Tel: (650) 846-7635

Fax: (650) 621-7817

Email: Pforeman@genencor.com

Seq primer: LT-F1 primer.

Location/Qualifiers

1..809

/organism="Hypocrea jecorina"

/mol\_type="mRNA"

/strain="QM6a"

/db\_xref="taxon:51453"

/clone="tric021xe04"

/dev\_stage="mycelia"

/clone\_lib="T.reesei mycelial culture, Version 3 april"

/note="Vector: pREP3Y; Site 1: Not I/Sal I; Mycelial

culture grown from 24 hrs to 6 days with varying Carbon

and Nitrogen sources and concentrations."

## ORIGIN

Query Match 77.8%; Score 14; DB 6; Length 809;

Best Local Similarity 85.7%; Pred. No. 1.6e+03;

Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 UCCUGAGGNNNNN 18

Db 61 TCCTGAGGNNNNN 48

## RESULT 22

AY413964 1392 bp DNA linear GSS 17-DEC-2003

LOCUS Homo sapiens PML gene, VIRTUAL TRANSCRIPT, partial, sequence,

genomic survey sequence.

ACCESSION AY413964

VERSION AY413964.1 GI:39769926

## KEYWORDS

## SOURCE

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 1392)

Clark, A.G., Glanowski, S., Nielsen, R., Thomas, P., Kejariwal, A.,

```

/locus_tag="HCM5066"
/gene="FMNL"

ORIGIN
Query Match          77.8%; Score 14; DB 9; Length 1392;
Best Local Similarity 85.7%; Pred. No. 1.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0

QY
5 UCCUGAGAGNNNNN 18
:|:|:|:|:|:|:|:|:|
Db          587 TCCTGAGAGNNNNN 600

RESULT 24
AY411601/c
LOCUS
DEFINITION
Hom sapiens HCM4278 gene, VIRUTAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY411600.1 GI:39767568
VERSION
GSS.
KEYWORDS
Homo sapiens (human)
SOURCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1527)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tenebaum,D.M., Clivello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Interfering nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 1527)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tenebaum,D.M., Clivello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submision
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
TITLE
JOURNAL
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1. 1527
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..1527
/locus_tag="HCM4278"
ORIGIN
Query Match          77.8%; Score 14; DB 9; Length 1527;
Best Local Similarity 85.7%; Pred. NO. 1.5e+03;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY
5 UCCUGAGAGNNNNN 18
:|:|:|:|:|:|:|:|:|
Db          420 TCCTGAGAGNNNNN 407

RESULT 25
AY411601/c
LOCUS
DEFINITION
Pan troglodytes HCM4278 gene, VIRUTAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY411601.1 GI:39767569
VERSION
GSS.
KEYWORDS
Pan troglodytes (chimpanzee)
SOURCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE 1 (bases 1 to 1527)  
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1527)  
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment  
FEATURES  
SOURCE Location/Qualifiers  
1..1527  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
1..>1527  
/locus\_tag="HCM4278"  
ORIGIN  
Query Match 77.8%; Score 14; DB 9; Length 1527;  
Best Local Similarity 85.7%; Pred. No. 1.5e+03;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 5 UCCUGAGAGNNNNN 18  
Db 420 TCCTGGAGNNNNN 407  
RESULT 26  
AY18641 2907 bp DNA linear GSS 17-DEC-2003  
LOCUS Homo sapiens NFKB1 gene, VIRUAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AY18641  
VERSION AY18641.1 GI:39774601  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 2907)  
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 2907)  
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT These sequences were made by sequencing genomic exons and ordering them based on alignment  
FEATURES  
SOURCE Location/Qualifiers  
1..2907  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"

gene  
/db\_xref="taxon:9606"  
1..>2907  
/gene="NFKB1"  
/locus\_tag="HCM6625"  
ORIGIN  
Query Match 77.8%; Score 14; DB 9; Length 2907;  
Best Local Similarity 85.7%; Pred. No. 1.4e+03;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 5 UCCUGAGAGNNNNN 18  
Db 2114 TCCTGGAGNNNNN 2127  
RESULT 27  
AY109382 5308 bp mRNA linear HTC 17-OCT-2002  
LOCUS Zea mays CL2032\_1 mRNA sequence.  
DEFINITION AY109382  
ACCESSION AY109382  
VERSION AY109382.1 GI:21213087  
KEYWORDS HTC.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 5308)  
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.  
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes  
JOURNAL Unpublished (2002)  
AUTHORS 2 (bases 1 to 5308)  
Coe,E.H.  
TITLE Direct Submission  
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA  
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSU, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Malbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.  
FEATURES  
SOURCE Location/Qualifiers  
1..5308  
/organism="Zea mays"  
/mol\_type="mRNA"  
/db\_xref="maizedb:630758"  
/db\_xref="taxon:4577"  
/clone\_id="Maize Mapping Project/DuPont Consensus Library"  
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"  
ORIGIN  
Query Match 77.8%; Score 14; DB 3; Length 5308;  
Best Local Similarity 85.7%; Pred. No. 1.3e+03;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 5 UCCUGAGAGNNNNN 18  
Db 4002 TCCTGGAGNNNNN 3989  
RESULT 28  
CG976547/c 91 bp DNA linear GSS 15-DEC-2003  
LOCUS CG976547

DEFINITION CH240.166D21.TV CHORI-240 Bos taurus genomic clone CH240.166D21.  
 genomic survey sequence.  
 ACCESSION CG976547  
 VERSION CG976547.1 GI:39902326  
 KEYWORDS  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 91)  
 Costa, J.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)  
 Other\_GSSs: CH240.166D21.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel.: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm).  
 Bases shown have Phred quality value equal to or higher than 20.  
 For BAC library availability, please contact Pieter de Jong  
 (pdejong@mail.cbo.org).  
 Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering/information.htm).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Cientifico e Tecnol6gico (CNPq), Brazil  
 Plate: 166 row: D column: 21  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 91.  
 Location/Qualifiers  
 1..91  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_166D21"  
 /sex="male"  
 /cell\_type="Blood"  
 /clone\_id="CHORI-240"  
 /note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 Hereford bull 11 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

ORIGIN  
 Query Match 72.2%; Score 13; DB 9; Length 91;  
 Best Local Similarity 92.3%; Pred. No. 6.6e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
 ||:|||||||  
 25 CCTGAGAGNNNNNN 13

RESULT 29  
 BE242665 122 bp mRNA linear EST 03-OCT-2001  
 LOCUS TCAAP1711 Pediatric acute myelogenous leukemia cell (FAB M1)  
 DEFINITION Baylor-HSC project-TCAA Homo sapiens CDNA clone TCAAP1711, mRNA  
 sequence.  
 BE242665  
 VERSION BE242665.1 GI:9094395  
 KEYWORDS EST.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 122)  
 Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman Jr., F.R.,  
 Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.  
 Pediatric Leukemia cDNA Sequencing Project  
 Unpublished (2000)  
 Contact: Dr. Judith F. Margolin  
 Texas Children's Cancer Center and Human Genome Sequencing Center  
 at Baylor College of Medicine  
 1102 Bates, MC3-3320 Houston, TX 77030, USA  
 Tel: 832-824-4536  
 Fax: 832-825-4038  
 Email: clones@ccc.org  
 Citation: Carninci, P. and Hayashizaki, Y. High efficiency  
 full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
 Seq primer: M13 primer.  
 Location/Qualifiers  
 1..122  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="TCAAP1711"  
 /sex="male"  
 /tissue\_type="leukocytes"  
 /cell\_type="myeloid cell"  
 /dev\_stage="pediatric 6 years"  
 /lab\_host="DH10B"  
 /clone\_id="Pediatric acute myelogenous leukemia cell (FAB  
 M1) Baylor-HSC project-TCAA"  
 /note="Vector: lambda PSB; Site 1: BamHI; Site 2: EcoRI;  
 first strand cDNA was primed with an anchored  
 XhoI-0190(dT) primer [5'GGAGGACTCGAGCGCGCGAGGAG(T)VN  
 3'; V=A,C,G; N=A,C,G,T] and then dg tailed. Second strand  
 was primed with a BamHI-dC primer  
 [5'AGAGAGCTGCGATCCGCGCGCCCAATATATAT(C) 3'].  
 Double-stranded cDNA was then digested with BamHI and XhoI  
 and directionally cloned into the BamHI and SalI sites of  
 lambda PSB vector. Library went through one round of  
 normalization. Library was constructed by Wei Yu at RIKEN  
 of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,  
 Itoh M, Nagasaki S, Sasaki N, Okazaki Y, Muramatsu M,  
 Schneider C, Hayashizaki Y, High efficiency selection of  
 full-length cDNA by improved biotinylated cap trapper.  
 DNA Res 4: 1, 61-6, Feb 28, 1997")

ORIGIN  
 Query Match 72.2%; Score 13; DB 2; Length 122;  
 Best Local Similarity 84.6%; Pred. NO. 6.5e+03;  
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAGN 13  
 |||:|||||  
 93 GGGGTCTCTGGAGN 105

RESULT 30  
 CG918380 166 bp DNA linear GSS 12-DEC-2003  
 LOCUS CH240.144J23.TV CHORI-240 Bos taurus genomic clone CH240.144J23,  
 genomic survey sequence.  
 ACCESSION CG918380  
 VERSION CG918380.1 GI:39778063  
 KEYWORDS  
 SOURCE GSS.  
 ORGANISM Bos taurus (cow)  
 Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 166)  
 Costa, J.N., Mota, M. and Caetano, A.R.



**TITLE** Brazil's Contribution to End-Sequencing the Bovine BAC Library  
**JOURNAL** CHORI-240  
**COMMENT** Unpublished (2003)  
Other\_GSSs: CH240\_144J23.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetano@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have phred quality value equal to or higher than 20.  
Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering\_information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 144 row: J column: 23  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 166.  
Location/Qualifiers  
1. 166  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="breed: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_144J23"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pTARBA1.3; Site\_1: MboI; Site\_2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

**ORIGIN**  
Query Match 72.2%; Score 13; DB 9; Length 166;  
Best Local Similarity 92.3%; Pred. No. 6.3e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

**QY** 6 CCUGAGANNNNNN 18  
||:|||||||  
Db 134 CCTGGAGNNNNNN 146

**RESULT 31**  
CG979398/c 211 bp DNA linear GSS 15-DEC-2003  
**LOCUS** CH240\_171D16.TV CHORI-240 Bos taurus genomic clone CH240\_171D16,  
genomic survey sequence.  
**ACCESSION** CG979398  
**VERSION** CG979398.1 GI:39905177  
**KEYWORDS** GSS.  
**SOURCE** Bos taurus (cow)  
**ORGANISM** Bos taurus (cow)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 211)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240  
Unpublished (2003)  
Other GSSs: CH240\_171D16.TV  
Contact: Caetano AR  
Department of Biotechnology

**REFERENCE**  
**AUTHORS**  
**TITLE**  
**JOURNAL**  
**COMMENT**

Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetano@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have phred quality value equal to or higher than 20.  
Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering\_information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 171 row: D column: 16  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 211.  
Location/Qualifiers  
1. 211  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="breed: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_171D16"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pTARBA1.3; Site\_1: MboI; Site\_2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

**ORIGIN**  
Query Match 72.2%; Score 13; DB 9; Length 211;  
Best Local Similarity 92.3%; Pred. No. 6.2e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

**QY** 6 CCUGAGANNNNNN 18  
||:|||||||  
Db 54 CCTGGAGNNNNNN 42

**RESULT 32**  
CL609827/c 212 bp DNA linear GSS 17-JUN-2004  
**LOCUS** CH240\_177J19.TV CHORI-240 Bos taurus genomic clone CH240\_177J19,  
genomic survey sequence.  
**ACCESSION** CL609827  
**VERSION** CL609827.1 GI:4887859  
**KEYWORDS** GSS.  
**SOURCE** Bos taurus (cow)  
**ORGANISM** Bos taurus (cow)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 212)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240  
Unpublished (2003)  
Other GSSs: CH240\_177J19.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetano@cenargen.embrapa.br

**REFERENCE**  
**AUTHORS**  
**TITLE**  
**JOURNAL**  
**COMMENT**

Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have phred quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 ([pdjong@mail.cho.org](mailto:pdjong@mail.cho.org)).  
 Clones may be purchased from BACPAC Resources  
 (<http://www.chori.org/bacpac/ordering/information.htm>).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBMC) by Embrapa Recursos Genéticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Científico e Tecnológico (CNPq), Brazil  
 Plate: 177 row: J column: 19  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 212.  
 Location/Qualifiers  
 1..212  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_177019"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 Hereford bull U1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 212;  
 Best Local Similarity 92.3%; Pred. No. 6.2e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
 ||:|||||||  
 125 CCTGGAGNNNNNN 113

RESULT 33  
 CG986238 231 bp DNA linear GSS 15-DEC-2003  
 DEFINITION CH240\_156L04.TV CHORI-240 Bos taurus genomic clone CH240\_156L04,  
 genomic survey sequence.  
 ACCESSION CG986238  
 VERSION CG986238.1 GI:39912008  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 231)  
 Costa, J.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)  
 Other GSSs: CH240\_156L04.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Genéticos e Biotecnologia  
 Parque Estação Biológica, Final Av. W/5 Norte, Brasília-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: [acaetano@cenargen.embrapa.br](mailto:acaetano@cenargen.embrapa.br)  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have phred quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 ([pdjong@mail.cho.org](mailto:pdjong@mail.cho.org)).

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Clones may be purchased from BACPAC Resources  
 (<http://www.chori.org/bacpac/ordering/information.htm>).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBMC) by Embrapa Recursos Genéticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Científico e Tecnológico (CNPq), Brazil  
 Plate: 156 row: L column: 04  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 231.  
 Location/Qualifiers  
 1..231  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_156L04"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 Hereford bull U1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 231;  
 Best Local Similarity 92.3%; Pred. No. 6.1e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
 ||:|||||||  
 155 CCTGGAGNNNNNN 167

RESULT 34  
 CL603268 234 bp DNA linear GSS 17-JUN-2004  
 DEFINITION CH240\_178I01.TV CHORI-240 Bos taurus genomic clone CH240\_178I01,  
 genomic survey sequence.  
 ACCESSION CL603268  
 VERSION CL603268.1 GI:48871300  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 234)  
 Costa, J.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)  
 Other GSSs: CH240\_178I01.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Genéticos e Biotecnologia  
 Parque Estação Biológica, Final Av. W/5 Norte, Brasília-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: [acaetano@cenargen.embrapa.br](mailto:acaetano@cenargen.embrapa.br)  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have phred quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 ([pdjong@mail.cho.org](mailto:pdjong@mail.cho.org)).  
 Clones may be purchased from BACPAC Resources  
 (<http://www.chori.org/bacpac/ordering/information.htm>).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBMC) by Embrapa Recursos Genéticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Científico e Tecnológico (CNPq), Brazil

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Plate: 178 row: 1 column: 01  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 234.  
Location/Qualifiers  
1..234

FEATURES  
source  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_178101"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 234;  
Best Local Similarity 92.3%; Pred. No. 6.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGAGNNNNNN 18  
||:|||||||  
Db 60 CCTGGAGAGNNNNNN 48

## RESULT 35

LOCUS CC467061 236 bp DNA linear GSS 12-JUN-2003  
DEFINITION CH240\_136F14.TJ CHORI-240 Bos taurus genomic clone CH240\_136F14,  
genomic survey sequence.

ACCESSION CC467061  
VERSION CC467061.1 GI:31653293  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 236)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library

## REFERENCE

AUTHORS CHORI-240  
TITLE Unpublished (2003)  
COMMENT Other GSSs: CH240\_136F14.TV

JOURNAL  
COMMENT Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658

Email: acetano@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm). Bases shown have Phred  
quality value equal to or higher than 20. Bases with quality value  
below 20 were masked with 'N'. For BAC library availability, please  
contact Pieter de Jong (pdejong@mail.cho.org). Clones may be  
purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm). This work  
was undertaken as part of the International Bovine BAC Mapping  
Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia  
with financing from Conselho Nacional de Desenvolvimento Cientifico  
e Tecnol6gico (CNPq), Brazil.  
Plate: 136 row: F column: 14  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 236.  
Location/Qualifiers  
1..236  
/organism="Bos taurus"

/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_136F14"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 236;  
Best Local Similarity 92.3%; Pred. No. 6.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGAGNNNNNN 18  
||:|||||||  
Db 25 CCTGGAGAGNNNNNN 37

## RESULT 36

LOCUS CG989067 250 bp DNA linear GSS 15-DEC-2003  
DEFINITION CH240\_146O19.TJ CHORI-240 Bos taurus genomic clone CH240\_146O19,  
genomic survey sequence.

ACCESSION CG989067  
VERSION CG989067.1 GI:39914846  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 250)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library

## REFERENCE

AUTHORS CHORI-240  
TITLE Unpublished (2003)  
COMMENT Other GSSs: CH240\_146O19.TV

JOURNAL  
COMMENT Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658

Email: acetano@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm). Bases shown have Phred  
quality value equal to or higher than 20. Bases with quality value  
below 20 were masked with 'N'. For BAC library availability, please  
contact Pieter de Jong (pdejong@mail.cho.org). Clones may be  
purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm). This work  
was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnol6gico (CNPq), Brazil  
Plate: 146 row: O column: 19  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 250.  
Location/Qualifiers  
1..250  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_146O19"  
/sex="Male"  
/cell\_type="Blood"

## FEATURES

## source

1..236  
/organism="Bos taurus"

## ORIGIN

/clone.lib="CHORI-240"  
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

Query Match 72.2%; Score 13; DB 9; Length 250;  
Best Local Similarity 92.3%; Pred. No. 6.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGANNNNNN 18  
Db 83 CCTGAGANNNNNN 95

RESULT 37  
CG982763 266 bp DNA linear GSS 15-DEC-2003  
LOCUS CH240\_164102.TJ CHORI-240 Bos taurus genomic clone CH240\_164102,  
DEFINITION genomic survey sequence.

ACCESSION CG982763.1 GI:39908542  
VERSION  
KEYWORDS  
SOURCE

ORGANISM  
Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos

REFERENCE  
AUTHORS  
TITLE  
1 (bases 1 to 266)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240

JOURNAL  
COMMENT  
Unpublished (2003)  
Other GSSs: CH240\_164102.TJ

Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetano@cenargen.embrapa.br

Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have phred quality value equal to or higher than 20.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil

Plate: 164 row: I column: 02  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 266.  
Location/Qualifiers  
1..266

## FEATURES

## source

/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_164102"  
/sex="Male"  
/cell\_type="Blood"  
/clone.lib="CHORI-240"  
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 266;  
Best Local Similarity 92.3%; Pred. No. 6e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGANNNNNN 18  
Db 37 CCTGAGANNNNNN 25

RESULT 38  
CG983959 327 bp DNA linear GSS 15-DEC-2003  
LOCUS CH240\_153005.TJ CHORI-240 Bos taurus genomic clone CH240\_153005,  
DEFINITION genomic survey sequence.

ACCESSION CG983959  
VERSION CG983959.1 GI:39909738  
KEYWORDS  
SOURCE  
ORGANISM

Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos

REFERENCE  
AUTHORS  
TITLE  
1 (bases 1 to 327)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240

JOURNAL  
COMMENT  
Unpublished (2003)  
Other GSSs: CH240\_153005.TJ

Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetano@cenargen.embrapa.br

Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have phred quality value equal to or higher than 20.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil

Plate: 153 row: O column: 05  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 327.  
Location/Qualifiers  
1..327

## FEATURES

## source

/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_153005"  
/sex="Male"  
/cell\_type="Blood"  
/clone.lib="CHORI-240"  
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 327;  
Best Local Similarity 92.3%; Pred. No. 5.9e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGANNNNNN 18  
||:|||||

Db 209 CCTGGAGNNNNNN 221

RESULT 39  
LOCUS CC470613  
DEFINITION CH240\_144J13\_TV CHORI-240 Bos taurus genomic clone CH240\_144J13,  
genomic survey sequence.  
ACCESSION CC470613  
VERSION CC470613.1 GI:31656845  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
REFERENCE 1 (bases 1 to 332)  
Coستا,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240  
COMMENT Unpublished (2003)  
Other\_GSSs: CH240\_144J13\_TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372-70770-900 Brasilia  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetano@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm). Bases shown have Phred  
quality value equal to or higher than 20. Bases with quality value  
below 20 were masked with 'N'. For BAC library availability, please  
contact Pletier de Jong (pdejong@mail.cho.org). Clones may be  
(http://www.chori.org/bacpac/ordering/information.htm). This work  
was undertaken as part of the International Bovine BAC Mapping  
Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia  
with financing from Conselho Nacional de Desenvolvimento Cientifico  
e Tecnol6gico (CNPq), Brazil.  
Plate: 144 row: J column: 13  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 332.  
Location/Qualifiers  
1..332  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_144J13"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99373; CHORI-240 Bovine BAC  
library (Male) produced by Pletier de Jong"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 332;  
Best Local Similarity 92.3%; Pred. No. 5.9e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNNN 18  
||:|||||||  
||:|||||||

Db 144 CCTGGAGNNNNNN 156

RESULT 40  
LOCUS CL211616/c  
DEFINITION W173C04 GGTG Gene Trap Library GV04C04 Mus musculus cDNA clone

W173C04, mRNA sequence.  
CL211616  
VERSION CL211616.1 GI:40728517  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 377)  
Hansen,J., Flores,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F.,  
Arnold,H.H., Schutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P.  
A large-scale, gene-driven mutagenesis approach for the functional  
analysis of the mouse genome  
Proc Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)  
22810117  
12904583  
JOURNAL MEDLINE  
PUBMED  
COMMENT Contact: GGTG  
German Genetrap Consortium (GGTC)  
Email: info@genetrap.de  
Roabdetageo gene trap. Sequence tag generated by 5'RACE. Additional  
sequence information can be found at:  
'http://genetrap.gsf.de/project/web\_new/database/result\_clone.html?clone\_id=W173C04' ES cell line harboring insertion mutation of  
target gene is available at:  
'http://genetrap.gsf.de/project/web\_new/order\_clones/howtoorder.htm'  
1' Inhouse Sequence Identifier: 10363  
Class: Gene Trap.  
Location/Qualifiers  
1..377  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129 Sv"  
/db\_xref="taxon:10090"  
/clone="W173C04"  
/sex="Male"  
/cell\_type="Embryonic stem cell"  
/clone\_lib="ES cells 129S2 (formerly 129/SvPas)"  
/clone\_lib="GGTC Gene Trap Library GV04C04"  
/note="Vector: ROSAbetageo"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 377;  
Best Local Similarity 92.3%; Pred. No. 5.9e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNNN 18  
||:|||||||  
||:|||||||

Db 129 CCTGGAGNNNNNN 117

RESULT 41  
LOCUS CB774359/c  
DEFINITION CB774359 392 bp mRNA linear EST 16-MAY-2003  
ANGNNNC:NRPI3-00052-D2-A W Rat pituitary (10477) Rattus norvegicus  
cDNA clone nrp13-00052-d2 5', mRNA sequence.  
CB774359  
VERSION CB774359.1 GI:29862750  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 392)  
Amgen EST Program.  
Amgen Rat EST Program  
Unpublished (2003)  
Contact: Dan Fitzpatrick  
Amgen, Inc  
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00052 row: d column: 2.  
Location/Qualifiers

FEATURES

```

ORIGIN
Query Match
Best Local Similarity 72.2%; Score 13; DB 9; Length 393;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18
||:|||||
12 CCTGGAGNNNNNN 24

RESULT 43
CG980948/c
LOCUS
DEFINITION
CG980948 412 bp DNA linear GSS 15-DEC-2003
CH240_161C05.TV CHORI-240 Bos taurus genomic clone CH240_161C05,
genomic survey sequence.
CG980948
CG980948.1 GI:3906727
GSS.
Bos taurus (cow)
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 412)
Costa, J.N., Mora, M. and Caetano, A.R.
Brazil's Contribution to End-Sequencing the Bovine BAC Library
CHORI-240
Unpublished (2003)
Other GSSs: CH240_161C05.TV
Contact: Caetano AR
Department of Biotechnology
Embrapa Recursos Geneticos e Biotecnologia
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.
02372, 70770-900 Brasil
Tel: 55 61 448 4778
Fax: 55 61 340 3658
Email: acacetano@cena.gen.embrapa.br
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm).
Bases shown have Phred quality value equal to or higher than 20.
Bases with quality value below 20 were masked with 'N'.
For BAC library availability, please contact Pieter de Jong
(pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm).
This work was undertaken as part of the International Bovine BAC
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e
Biotecnologia with financing from Conselho Nacional de
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil
Plate: 161 row: C column: 05
Seq primer: T7
Class: BAC ends
High quality sequence step: 412.
Location/Qualifiers
1. 412
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_161C05"
/sex="Male"
/cell_type="Blood"
/clone_1b="CHORI-240"
/notes="Vector: pTARhAC1.3; Site 1: Mbol; Site 2: Mbol;
Hereford bull L1 Domingo 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN
Query Match
Best Local Similarity 72.2%; Score 13; DB 9; Length 412;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18
||:|||||
12 CCTGGAGNNNNNN 24

RESULT 43
CG980948/c
LOCUS
DEFINITION
CG980948 412 bp DNA linear GSS 15-DEC-2003
CH240_161C05.TV CHORI-240 Bos taurus genomic clone CH240_161C05,
genomic survey sequence.
CG980948
CG980948.1 GI:3906727
GSS.
Bos taurus (cow)
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 412)
Costa, J.N., Mora, M. and Caetano, A.R.
Brazil's Contribution to End-Sequencing the Bovine BAC Library
CHORI-240
Unpublished (2003)
Other GSSs: CH240_161C05.TV
Contact: Caetano AR
Department of Biotechnology
Embrapa Recursos Geneticos e Biotecnologia
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.
02372, 70770-900 Brasil
Tel: 55 61 448 4778
Fax: 55 61 340 3658
Email: acacetano@cena.gen.embrapa.br
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm).
Bases shown have Phred quality value equal to or higher than 20.
Bases with quality value below 20 were masked with 'N'.
For BAC library availability, please contact Pieter de Jong
(pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm).
This work was undertaken as part of the International Bovine BAC
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e
Biotecnologia with financing from Conselho Nacional de
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil
Plate: 161 row: C column: 05
Seq primer: T7
Class: BAC ends
High quality sequence step: 412.
Location/Qualifiers
1. 412
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_161C05"
/sex="Male"
/cell_type="Blood"
/clone_1b="CHORI-240"
/notes="Vector: pTARhAC1.3; Site 1: Mbol; Site 2: Mbol;
Hereford bull L1 Domingo 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN
Query Match
Best Local Similarity 72.2%; Score 13; DB 9; Length 412;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18
||:|||||
12 CCTGGAGNNNNNN 24

RESULT 43
CG980948/c
LOCUS
DEFINITION
CG980948 412 bp DNA linear GSS 15-DEC-2003
CH240_161C05.TV CHORI-240 Bos taurus genomic clone CH240_161C05,
genomic survey sequence.
CG980948
CG980948.1 GI:3906727
GSS.
Bos taurus (cow)
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 412)
Costa, J.N., Mora, M. and Caetano, A.R.
Brazil's Contribution to End-Sequencing the Bovine BAC Library
CHORI-240
Unpublished (2003)
Other GSSs: CH240_161C05.TV
Contact: Caetano AR
Department of Biotechnology
Embrapa Recursos Geneticos e Biotecnologia
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.
02372, 70770-900 Brasil
Tel: 55 61 448 4778
Fax: 55 61 340 3658
Email: acacetano@cena.gen.embrapa.br
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm).
Bases shown have Phred quality value equal to or higher than 20.
Bases with quality value below 20 were masked with 'N'.
For BAC library availability, please contact Pieter de Jong
(pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm).
This work was undertaken as part of the International Bovine BAC
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e
Biotecnologia with financing from Conselho Nacional de
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil
Plate: 161 row: C column: 05
Seq primer: T7
Class: BAC ends
High quality sequence step: 412.
Location/Qualifiers
1. 412
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_161C05"
/sex="Male"
/cell_type="Blood"
/clone_1b="CHORI-240"
/notes="Vector: pTARhAC1.3; Site 1: Mbol; Site 2: Mbol;
Hereford bull L1 Domingo 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN
Query Match
Best Local Similarity 72.2%; Score 13; DB 9; Length 412;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18
||:|||||
12 CCTGGAGNNNNNN 24

RESULT 43
CG980948/c
LOCUS
DEFINITION
CG980948 412 bp DNA linear GSS 15-DEC-2003
CH240_161C05.TV CHORI-240 Bos taurus genomic clone CH240_161C05,
genomic survey sequence.
CG980948
CG980948.1 GI:3906727
GSS.
Bos taurus (cow)
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 412)
Costa, J.N., Mora, M. and Caetano, A.R.
Brazil's Contribution to End-Sequencing the Bovine BAC Library
CHORI-240
Unpublished (2003)
Other GSSs: CH240_161C05.TV
Contact: Caetano AR
Department of Biotechnology
Embrapa Recursos Geneticos e Biotecnologia
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.
02372, 70770-900 Brasil
Tel: 55 61 448 4778
Fax: 55 61 340 3658
Email: acacetano@cena.gen.embrapa.br
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm).
Bases shown have Phred quality value equal to or higher than 20.
Bases with quality value below 20 were masked with 'N'.
For BAC library availability, please contact Pieter de Jong
(pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm).
This work was undertaken as part of the International Bovine BAC
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e
Biotecnologia with financing from Conselho Nacional de
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil
Plate: 161 row: C column: 05
Seq primer: T7
Class: BAC ends
High quality sequence step: 412.
Location/Qualifiers
1. 412
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_161C05"
/sex="Male"
/cell_type="Blood"
/clone_1b="CHORI-240"
/notes="Vector: pTARhAC1.3; Site 1: Mbol; Site 2: Mbol;
Hereford bull L1 Domingo 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN
Query Match
Best Local Similarity 72.2%; Score 13; DB 9; Length 412;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18
||:|||||
12 CCTGGAGNNNNNN 24

RESULT 43
CG980948/c
LOCUS
DEFINITION
CG980948 412 bp DNA linear GSS 15-DEC-2003
CH240_161C05.TV CHORI-240 Bos taurus genomic clone CH240_161C05,
genomic survey sequence.
CG980948
CG980948.1 GI:3906727
GSS.
Bos taurus (cow)
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 412)
Costa, J.N., Mora, M. and Caetano, A.R.
Brazil's Contribution to End-Sequencing the Bovine BAC Library
CHORI-240
Unpublished (2003)
Other GSSs: CH240_161C05.TV
Contact: Caetano AR
Department of Biotechnology
Embrapa Recursos Geneticos e Biotecnologia
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.
02372, 70770-900 Brasil
Tel: 55 61 448 4778
Fax: 55 61 340 3658
Email: acacetano@cena.gen.embrapa.br
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm).
Bases shown have Phred quality value equal to or higher than 20.
Bases with quality value below 20 were masked with 'N'.
For BAC library availability, please contact Pieter de Jong
(pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm).
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Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e
Biotecnologia with financing from Conselho Nacional de
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil
Plate: 161 row: C column: 05
Seq primer
```

Best Local Similarity 92.3%; Pred. No. 5.8e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNN 18  
Db 402 CCTGGAGNNNNN 390

RESULT 44  
CG984052/c 424 bp DNA linear GSS 15-DEC-2003  
LOCUS CH240\_153A12.TV CHORI-240 Bos taurus genomic clone CH240\_153A12,  
DEFINITION genomic survey sequence.

ACCESSION CG984052  
VERSION CG984052.1 GI:39909831  
KEYWORDS GSS.

SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.

REFERENCE 1 (bases 1 to 424)  
AUTHORS Costa,J.N., Mota,M. and Caetano,A.R.  
TITLE Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240

JOURNAL Unpublished (2003)  
COMMENT Other\_GSSs: CH240\_153A12.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658

Email: acetano@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have phased quality value equal to or higher than 20.  
Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pieter de Jong  
(pjejong@mail.cho.org).

Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 153 row: A column: 12  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 424.

FEATURES  
source Location/Qualifiers

1..424  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_153A12"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pTRABAC1.3; Site\_1: MboI; Site\_2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 424;  
Best Local Similarity 92.3%; Pred. No. 5.8e+03;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNN 18  
Db 35 CCTGGAGNNNNN 23

RESULT 45

CL604436 424 bp DNA linear GSS 17-JUN-2004  
LOCUS CH240\_180K02.TV CHORI-240 Bos taurus genomic clone CH240\_180K02,  
DEFINITION genomic survey sequence.

ACCESSION CL604436  
VERSION CL604436 GI:48872468  
KEYWORDS GSS.

SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.

REFERENCE 1 (bases 1 to 424)  
AUTHORS Costa,J.N., Mota,M. and Caetano,A.R.  
TITLE Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240

JOURNAL Unpublished (2003)  
COMMENT Other\_GSSs: CH240\_180K02.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658

Email: acetano@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have phased quality value equal to or higher than 20.  
Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pieter de Jong  
(pjejong@mail.cho.org).

Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 180 row: K column: 02  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 424.

FEATURES  
source Location/Qualifiers

1..424  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_180K02"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pTRABAC1.3; Site\_1: MboI; Site\_2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 424;  
Best Local Similarity 92.3%; Pred. No. 5.8e+03;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNN 18  
Db 384 CCTGGAGNNNNN 396

RESULT 46  
B2759976/c 431 bp DNA linear GSS 12-MAR-2003  
LOCUS 622\_3L4\_E10\_BAC\_081 RPT-86 Male Felis catus genomic,  
DEFINITION

genomic survey sequence.

ACCESSION BZ759976  
 VERSION BZ759976.1 GI:28929399  
 KEYWORDS GSS.  
 SOURCE Felis catus (cat)  
 ORGANISM Felis catus

REFERENCE  
 AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; 1 (bases 1 to 431)  
 Title Banerji,N., Lilienel,M., Li,X., Zhang,Q., Dwan,C., Retzel,E., Yuhki,N., O'Brien,S., Kapur,V. and Kanjilal,S.  
 Title Felis catus BAC-end sequencing project  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Kanjilal, S.  
 Comparative Cancer Genomics  
 University of Minnesota  
 1971 Commonwealth Ave. St. Paul, MN 55108, USA  
 Tel: 612-624-3248  
 Fax: 612-625-5203  
 Email: kanjilal@umn.edu

End sequencing of clones from the Felis catus RPCI-86 Male Feline BAC library was performed at the Laboratory of Comparative Cancer Genomics at the University of Minnesota. Clone plates 620 through 624 of the RPCI-86 BAC library (prepared at the Children's Hospital Oakland Research Institute) were provided by the Laboratory of Genomic Diversity, National Cancer Institute. All sequencing reactions were run at the Advanced Genetic Analysis Center (<http://www.agac.umn.edu>) and the results processed through an automated pipeline 'biodata' at the Center for Computational Genomics and Bioinformatics at the University of Minnesota. Vector sequences were screened and the BAC-end sequences were trimmed to phred quality scores above 20 as described (<http://web.ahc.umn.edu/biodata/catbac/>). Vector and quality screened sequences > 150 nt in length are submitted.

Plate: 622\_3 row: E column: 10  
 Class: BAC ends.

FEATURES  
 source Location/Qualifiers  
 1..431  
 /organism="Felis catus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9685"  
 /clone\_lib="RPCI-86 Male Feline BAC"  
 /note="Vector: PTARBAC2; Site\_1: EcoRI"

ORIGIN

Query Match 72.2%; Score 13; DB 8; Length 431;  
 Best Local Similarity 92.3%; Pred. No. 5.8e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNN 18  
 ||:|||||||  
 Db 200 CCTGGAGNNNNN 188

RESULT 47  
 BZ759980  
 LOCUS 622 314 F02 BAC 025 RPCI-86 Male Feline BAC Felis catus genomic.  
 DEFINITION genomic survey sequence.  
 ACCESSION BZ759980  
 VERSION BZ759980.1 GI:28929403  
 KEYWORDS GSS.  
 SOURCE Felis catus (cat)  
 ORGANISM Felis catus

REFERENCE  
 AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; 1 (bases 1 to 433)  
 Title Banerji,N., Lilienel,M., Li,X., Zhang,Q., Dwan,C., Retzel,E., Yuhki,N., O'Brien,S., Kapur,V. and Kanjilal,S.  
 Title Felis catus BAC-end sequencing project  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Kanjilal, S.  
 Comparative Cancer Genomics

University of Minnesota  
 1971 Commonwealth Ave. St. Paul, MN 55108, USA  
 Tel: 612-624-3248  
 Fax: 612-625-5203  
 Email: kanjilal@umn.edu

End sequencing of clones from the Felis catus RPCI-86 Male Feline BAC library was performed at the Laboratory of Comparative Cancer Genomics at the University of Minnesota. Clone plates 620 through 624 of the RPCI-86 BAC library (prepared at the Children's Hospital Oakland Research Institute) were provided by the Laboratory of Genomic Diversity, National Cancer Institute. All sequencing reactions were run at the Advanced Genetic Analysis Center (<http://www.agac.umn.edu>) and the results processed through an automated pipeline 'biodata' at the Center for Computational Genomics and Bioinformatics at the University of Minnesota. Vector sequences were screened and the BAC-end sequences were trimmed to phred quality scores above 20 as described (<http://web.ahc.umn.edu/biodata/catbac/>). Vector and quality screened sequences > 150 nt in length are submitted.

Plate: 622\_3 row: F column: 02  
 Class: BAC ends.

FEATURES  
 source Location/Qualifiers  
 1..433  
 /organism="Felis catus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9685"  
 /clone\_lib="RPCI-86 Male Feline BAC"  
 /note="Vector: PTARBAC2; Site\_1: EcoRI"

ORIGIN

Query Match 72.2%; Score 13; DB 8; Length 433;  
 Best Local Similarity 92.3%; Pred. No. 5.8e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNN 18  
 ||:|||||||  
 Db 243 CCTGGAGNNNNN 255

RESULT 48  
 CL604951/c  
 LOCUS CH240\_181A02.TV CHORI-240 Bos taurus genomic clone CH240\_181A02.  
 DEFINITION genomic survey sequence.  
 ACCESSION CL604951  
 VERSION CL604951.1 GI:48872983  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 Title 1 (bases 1 to 466)  
 Title Costa,J.N., Mota,M. and Caetano,A.R.  
 Title Brazil's Contribution to End-sequencing the Bovine BAC library  
 JOURNAL CHORI-240  
 COMMENT Unpublished (2003)  
 Other\_GSSes: CH240\_181A02.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estrada Biologica, Final Av. W/S Norte, Brasilia-DF C.P. 02372, 70770-900 Brasilia  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetanoc@embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have phred quality value equal to or higher than 20. Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources



(http://www.chori.org/bacpac/ordering/information.htm).

This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by Embrapa Recursos Genéticos e Biotecnologia with financing from Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Brazil

Plate: 181 row: A column: 02  
Seq primer: T7  
Class: BAC ends

High quality sequence stop: 466.

Location/Qualifiers

1. .466

/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"

/db\_xref="taxon:9913"

/clone="CH240\_181A02"

/sex="Male"

/cell\_type="Blood"

/clone\_1ib="CHORI-240"

/note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

#### ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 466;  
Best Local Similarity 92.3%; Pred. No. 5.8e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGNNNNNN 18  
||:|||||||  
46 CCTGAGNNNNNN 34

Db 46 CCTGAGNNNNNN 34

#### RESULT 49

BM492637 484 bp mRNA linear EST 07-MAY-2003  
LOCUS NXRV\_027\_F08\_F NXRV (Nsf Xylem Root wood Vertical) Pinus taeda cDNA  
DEFINITION clone NXRV\_027\_F08 5', mRNA sequence.  
ACCESSION BM492637  
VERSION BM492637.1 GI:18613568  
KEYWORDS EST.  
SOURCE Pinus taeda (loblolly pine)  
ORGANISM Pinus taeda

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
REFERENCE 1 (bases 1 to 484)  
AUTHORS Sederoff, R.

TITLE Molecular Basis of Wood Formation in the Pine Megagenome  
JOURNAL Unpublished (2000)  
COMMENT Contact: Sederoff, Ron

Forest Biotechnology  
North Carolina State University  
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,  
NC 27695, USA  
Tel: 919 515 7800  
Fax: 919 515 7801

Email: ron\_sederoff@ncsu.edu, jerri\_johnson@ncsu.edu  
Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further  
information.

Seq primer: T3.

High quality sequence stop: 466.

Location/Qualifiers

1. .484

/organism="Pinus taeda"

/mol\_type="mRNA"

/strain="Coastal plain loblolly pine from North Carolina"

/db\_xref="taxon:3352"

/clone="NXRV\_027\_F08"

/tissue\_type="Xylem"

/cell\_type="Root (primary)"

/dev\_stage="Transitional"

/lab\_host="XL1-Blue"

/clone\_1ib="NXRV (Nsf Xylem Root wood Vertical)"

/note="Vector: pBluescript SK-, Site\_1: Eco RI; Site\_2:

#### ORIGIN

Query Match 72.2%; Score 13; DB 4; Length 484;  
Best Local Similarity 92.3%; Pred. No. 5.8e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGNNNNNN 18  
||:|||||||  
442 CCTGAGNNNNNN 454

Db 442 CCTGAGNNNNNN 454

#### RESULT 50

CG982237 494 bp DNA linear GSS 15-DEC-2003  
LOCUS CH240\_163C16.TV CHORI-240 Bos taurus genomic clone CH240\_163C16,  
DEFINITION genomic survey sequence.  
ACCESSION CG982237  
VERSION CG982237.1 GI:3908016  
KEYWORDS GSS.

SOURCE Bos taurus (cow)  
ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.

REFERENCE 1 (bases 1 to 494)  
AUTHORS Coستا, J.N., Mota, M. and Caetano, A.R.

TITLE Brazil's Contribution to End-Sequencing the Bovine BAC Library  
JOURNAL CHORI-240

Unpublished (2003)  
Other GSSs: CH240\_163C16.TV  
Contact: Caetano AR

Department of Biotechnology  
Embrapa Recursos Genéticos e Biotecnologia  
Parque Estação Biológica, Final Av. W/5 Norte, Brasília-DF C.P.

02372, 70770-900 Bras11  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658

Email: acaetano@embrapa.br

Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).

Bases shown have Phred quality value equal to or higher than 20.

Bases with quality value below 20 were masked with 'N'.

For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cno.org).

Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm).

This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by Embrapa Recursos Genéticos e Biotecnologia with financing from Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Brazil

Plate: 163 row: C column: 16  
Seq primer: T7

Class: BAC ends

High quality sequence stop: 494.

Location/Qualifiers

1. .494

/organism="Bos taurus"

/mol\_type="genomic DNA"

/strain="bred: Hereford"

/db\_xref="taxon:9913"

/clone="CH240\_163C16"

/sex="Male"

/cell\_type="Blood"

/clone\_1ib="CHORI-240"

/note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 494;  
 Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
 ||:|||||  
 Db 207 CCTGAGNNNNNN 195

RESULT 51  
 CC467322/c 497 bp DNA linear GSS 12-JUN-2003  
 LOCUS CH240\_137M17.TV CHORI-240 Bos taurus genomic clone CH240\_137M17,  
 DEFINITION genomic survey sequence.

ACCESSION CC467322  
 VERSION CC467322.1 GI:31653554  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 497)  
 TITLE Costa, J.N., Mota, M. and Caetano, A.R.  
 AUTHORS Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 JOURNAL CHORI-240  
 COMMENT Unpublished (2003)  
 Other\_GSSs: CH240\_137M17.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658

Email: acetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm). Bases shown have Phred  
 quality value equal to or higher than 20. Bases with quality value  
 below 20 were masked with 'N'. For BAC library availability, please  
 contact Pieter de Jong (pdejong@mail.cho.org). Clones may be  
 purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering/information.htm). This work  
 was undertaken as part of the International Bovine BAC Mapping  
 Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia  
 with financing from Conselho Nacional de Desenvolvimento Cientifico  
 e Tecnologico (CNPq), Brazil.  
 Plate: 137 row: M column: 17  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 497.

FEATURES  
 source location/Qualifiers  
 1..497

/organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="Breed: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_137M17"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: PTARBAC1.3; Site 1: Mbol; Site 2: Mbol;  
 Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 497;  
 Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18

Db 119 CCTGAGNNNNNN 107  
 ||:|||||

RESULT 52  
 A0597630/c 503 bp DNA linear GSS 08-JUN-1999  
 LOCUS HS 2065 B2 H08 MR CIT Approved Human Genomic Sperm Library D Homo  
 DEFINITION sapiens genomic clone Plate=2065 Col=16 Row=F, genomic survey  
 sequence.

ACCESSION A0597630  
 VERSION A0597630.1 GI:5028842  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 503)  
 TITLE Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,  
 Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,  
 Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and  
 Hood, L.

Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome  
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
 JOURNAL MEDLINE  
 PUBMED 99380589  
 CONTACT: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887

Email: jwallace@u.washington.edu  
 Clones may be purchased from Research Genetics (info@resgen.com).  
 BAC end Web Server: http://www.htec.washington.edu  
 Plate: 2065 row: P column: 16  
 Seq primer: M13 Reverse  
 Class: BAC ends  
 High quality sequence stop: 503.

FEATURES  
 source location/Qualifiers  
 1..503

/organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9605"  
 /clone="Plate=2065 Col=16 Row=P"  
 /sex="male"  
 /clone\_lib="CIT Approved Human Genomic Sperm Library D"  
 /note="Organ: sperm; Vector: pBelOBAC11; BAC clones in  
 E-Coli DH10B"

## ORIGIN

Query Match 72.2%; Score 13; DB 8; Length 503;  
 Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
 ||:|||||  
 Db 62 CCTGAGNNNNNN 50

RESULT 53  
 CG986681/c 504 bp DNA linear GSS 15-DEC-2003  
 LOCUS CH240\_157H05.TV CHORI-240 Bos taurus genomic clone CH240\_157H05,  
 DEFINITION genomic survey sequence.

ACCESSION CG986681  
 VERSION CG986681.1 GI:39912460  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.

REFERENCE 1 (bases 1 to 504)  
AUTHORS Costa,J.N., Mota,M. and Caetano,A.R.  
TITLE Brazil's Contribution to End-Sequencing the Bovine BAC Library  
JOURNAL CHORI-240  
COMMENT Unpublished (2003)  
Other GSSs: CH240\_157H05.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetanoc@embrapa.br  
Clones are derived from the Bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have phred quality value equal to or higher than 20.  
Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering\_information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 157 Row: H Column: 05  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 504.  
Location/Qualifiers  
1..504  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_157H05"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 504;  
Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCGGAGNNNNNN 18  
||:|||||||  
Db 41 CCTGGAGNNNNNN 29

RESULT 54  
LOCUS CL608092 506 bp DNA linear GSS 17-JUN-2004  
DEFINITION CH240\_174M24.TV CHORI-240 Bos taurus genomic clone CH240\_174M24,  
genomic survey sequence.  
ACCESSION CL608092  
VERSION CL608092.1 GI:48876124  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 506)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240  
Unpublished (2003)  
Other\_GSSs: CH240\_174M24.TV

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetanoc@embrapa.br  
Clones are derived from the Bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have phred quality value equal to or higher than 20.  
Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering\_information.htm).  
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Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 174 Row: M Column: 24  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 506.  
Location/Qualifiers  
1..506  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_174M24"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 506;  
Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCGGAGNNNNNN 18  
||:|||||||  
Db 14 CCTGGAGNNNNNN 26

RESULT 55  
LOCUS CG983697 509 bp DNA linear GSS 15-DEC-2003  
DEFINITION CH240\_165H06.TV CHORI-240 Bos taurus genomic clone CH240\_165H06,  
genomic survey sequence.  
ACCESSION CG983697  
VERSION CG983697.1 GI:39909476  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 509)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240  
Unpublished (2003)  
Other\_GSSs: CH240\_165H06.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Fax: 55 61 340 3658  
 Email: [acaetano@cenargen.embrapa.br](mailto:acaetano@cenargen.embrapa.br)  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have phased quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 ([pdjong@mail.choi.org](mailto:pdjong@mail.choi.org)).  
 Clones may be purchased from BACPAC Resources  
 ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBBMC) by Embrapa Recursos Genéticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Científico e Tecnológico (CNPq), Brazil  
 Plate: 165 row: H column: 06  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 509.  
 Location/Qualifiers  
 1..509  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_165H06"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 509;  
 Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
 ||:|||||||  
 Db 432 CCTGAGNNNNNN 444

RESULT 56  
 CL608426 526 bp DNA linear GSS 17-JUN-2004  
 LOCUS CH240\_175007.TJ CHORI-240 Bos taurus genomic clone CH240\_175007,  
 DEFINITION genomic survey sequence.  
 ACCESSION CL608426  
 VERSION CL608426.1 GI:48976458  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 526)  
 Costa, J.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 JOURNAL Unpublished (2003)  
 COMMENT Other GSSs: CH240\_175007.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Genéticos e Biotecnologia  
 Parque Estação Biológica, Final Av. W/5 Norte, Brasília-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: [acaetano@cenargen.embrapa.br](mailto:acaetano@cenargen.embrapa.br)  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have phased quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.

For BAC library availability, please contact Pieter de Jong  
 ([pdjong@mail.choi.org](mailto:pdjong@mail.choi.org)).  
 Clones may be purchased from BACPAC Resources  
 ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBBMC) by Embrapa Recursos Genéticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Científico e Tecnológico (CNPq), Brazil  
 Plate: 175 row: O column: 07  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 526.  
 Location/Qualifiers  
 1..526  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_175007"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 526;  
 Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCTGAGNNNNNN 18  
 ||:|||||||  
 Db 15 CCTGAGNNNNNN 27

RESULT 57  
 CG986353/c 536 bp DNA linear GSS 15-DEC-2003  
 LOCUS CH240\_157E15.TV CHORI-240 Bos taurus genomic clone CH240\_157E15,  
 DEFINITION genomic survey sequence.  
 ACCESSION CG986353  
 VERSION CG986353.1 GI:39912132  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 536)  
 Costa, J.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 JOURNAL Unpublished (2003)  
 COMMENT Other GSSs: CH240\_157E15.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Genéticos e Biotecnologia  
 Parque Estação Biológica, Final Av. W/5 Norte, Brasília-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: [acaetano@cenargen.embrapa.br](mailto:acaetano@cenargen.embrapa.br)  
 Clones are derived from the bovine BAC library CHORI-240  
 (<http://www.chori.org/bacpac/bovine240.htm>).  
 Bases shown have phased quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 ([pdjong@mail.choi.org](mailto:pdjong@mail.choi.org)).  
 Clones may be purchased from BACPAC Resources  
 ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBBMC) by Embrapa Recursos Genéticos e

Biotechnology with financing from Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Brazil  
 Plate: 157 Row: E Column: 15  
 Seq primer: T7  
 Class: BAC ends

High quality sequence stop: 536.

FEATURES  
 source Location/Qualifiers

1. 536  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_157B15"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_id="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 536;  
 Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGNNNNN 18  
 ||:|||||||  
 DB 533 CCTGGAGNNNNN 521

## RESULT 58

LOCUS CG985260 573 bp DNA linear GSS 15-DEC-2003  
 DEFINITION CH240\_155K17\_TV CHORI-240 Bos taurus genomic clone CH240\_155K17,  
 genomic survey sequence.

ACCESSION CG985260  
 VERSION CG985260.1 GI:39911039  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 573)  
 AUTHORS Costa,J.N., Mota,M. and Caetano,A.R.  
 TITLE Brazil's Contribution to End-Sequencing the Bovine BAC library  
 JOURNAL CHORI-240  
 COMMENT Unpublished (2003)  
 OTHER GSSes: CH240\_155K17\_TV  
 CONTACT: Caetano AR  
 DEPARTMENT OF Biotechnology  
 EMBRAPA Recursos Genéticos e Biotecnologia  
 Parque Estação Biológica, Final Av. W/5 Norte, Brasília-DF C.P.  
 02372, 70770-900 Brasil  
 TEL: 55 61 448 4778  
 FAX: 55 61 340 3658  
 EMAIL: acaetano@embrapa.br

Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm).  
 Bases shown have phased quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 (pdejong@mail.choi.org).

Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering/information.htm).

This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBBMC) by Embrapa Recursos Genéticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Científico e Tecnológico (CNPq), Brazil  
 Plate: 155 Row: K Column: 17  
 Seq primer: T7  
 Class: BAC ends

High quality sequence stop: 573.

FEATURES  
 source Location/Qualifiers

1. 573  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_155K17"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_id="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 573;  
 Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGNNNNN 18  
 ||:|||||||  
 DB 14 CCTGGAGNNNNN 26

## RESULT 59

LOCUS BG713519 593 bp mRNA linear EST 08-MAY-2001  
 DEFINITION pgl1n.pk007.024 Normalized Liver Library Gallus gallus cDNA clone  
 pgl1n.pk007.024 5' similar to p1r[S57631/S57631 translation  
 elongation factor eEF-1 delta-2 chain - African clawed frog  
 p1r[S55483 translation elongation factor eEF-1 delta chain (version  
 2) - African clawed frog emb[CNA59420.1] (X85096) elongation  
 factor-1 delta [X, mRNA sequence].

ACCESSION BG713519 GI:14007469  
 VERSION BG713519  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 593)  
 AUTHORS Burnside,J., Morgan,R.W. and Cogburn,L.A.  
 TITLE Chicken ESTs from a normalized liver library  
 JOURNAL Unpublished (2001)  
 CONTACT: Joan Burnside  
 DEPARTMENT Molecular Endocrinology  
 UNIVERSITY OF Delaware  
 40 Townsend Hall, Newark, DE 19717, USA  
 TEL: 302 831-1345  
 FAX: 302 831-3411  
 EMAIL: joan@udel.edu, www.chickest.udel.edu.

FEATURES  
 source Location/Qualifiers

1. 593  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9031"  
 /clone="pgl1n.pk007.024"  
 /sex="Male and Female"  
 /tissue\_type="liver"  
 /lab\_host="E.coli EMDH10B"  
 /clone\_id="Normalized Liver Library"  
 /note="Vector: pCMVSPORT 6"

## ORIGIN

Query Match 72.2%; Score 13; DB 4; Length 593;  
 Best Local Similarity 84.6%; Pred. No. 5.7e+03;  
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 UCCUGAGNNNNN 17  
 ||:|||||||  
 DB 485 TCCUGAGNNNNN 497

RESULT 60  
CG989575  
LOCUS  
DEFINITION CH240\_147M19.TU CHORI-240 Bos taurus genomic clone CH240\_147M19,  
genomic survey sequence.  
ACCESSION CG989575  
VERSION CG989575.1 GI:39915354  
KEYWORDS  
SOURCE  
ORGANISM Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 601)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240  
Unpublished (2003)  
Other GSSs: CH240\_147M19.TU  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasilia  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetano@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have Phred quality value equal to or higher than 20.  
Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 147 row: M column: 19  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 601.  
Location/Qualifiers  
1..601  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="breed: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_147M19"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pPARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

ORIGIN  
Query Match 72.2% Score 13; DB 9; Length 601;  
Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCTGGAGNNNNNN 18.  
||:|||||  
Db 525 CCTGGAGNNNNNN 537

RESULT 61  
CG978763  
LOCUS  
DEFINITION CH240\_170G16.TU CHORI-240 Bos taurus genomic clone CH240\_170G16,  
genomic survey sequence.

ACCESSION CG978763  
VERSION CG978763.1 GI:39904542  
KEYWORDS  
SOURCE  
ORGANISM Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 604)  
Costa,J.N., Mota,M. and Caetano,A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240  
Unpublished (2003)  
Other GSSs: CH240\_170G16.TU  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasilia  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetano@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have Phred quality value equal to or higher than 20.  
Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 170 row: G column: 16  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 604.  
Location/Qualifiers  
1..604  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="breed: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_170G16"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pPARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

ORIGIN  
Query Match 72.2% Score 13; DB 9; Length 604;  
Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCTGGAGNNNNNN 18  
||:|||||  
Db 93 CCTGGAGNNNNNN 105

RESULT 62  
CG992853  
LOCUS  
DEFINITION CH240\_152H24.TU CHORI-240 Bos taurus genomic clone CH240\_152H24,  
genomic survey sequence.  
ACCESSION CG992853  
VERSION CG992853.1 GI:39918632  
KEYWORDS  
SOURCE  
ORGANISM Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 606)  
 Costa, J.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library CHORI-240  
 Unpublished (2003)  
 Other GSSs: CH240\_152H24.TV  
 Contact: Caetano, A.R.  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P. 02372, 70770-900 Brasilia  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm).  
 Bases shown have phred quality value equal to or higher than 20. Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pletier de Jong (pdejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering/information.htm).  
 This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia with financing from Conselho Nacional de Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
 Plate: 152 row: H column: 24  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 606.  
 Location/Qualifiers  
 1..606  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_152H24"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site 1: Mbol; Site 2: Mbol; Hereford bull L1 Domingo 99375; CHORI-240 Bovine BAC library (Male) produced by Pletier de Jong"

ORIGIN  
 Query Match 72.2%; Score 13; DB 9; Length 606;  
 Best Local Similarity 92.3%; Pred. No. 5.7e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNN 18  
 ||:|||||||  
 40 CCTGAGAGNNNNN 52

Db

RESULT 63  
 CA754085/c 614 bp mRNA linear EST 27-NOV-2002  
 BR040010000 PLATE\_D07\_52\_060.ab1 OA Oryza sativa (japonica cultivar-group) cDNA clone BR040010000\_PLATE\_D07\_52\_060.ab1 similar to No protein alignment, mRNA sequence.  
 CA754085 GI:25798188  
 EST.  
 Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 614)  
 Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferreira, H., Kawaeski, S., McColough, A., Michalowski, C.B.,

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Palacio, C., Scara, G., Wheeler, M. and Zepeda, G.R.  
 Functional Genomics of Plant Stress Tolerance  
 Unpublished (2000)  
 Contact: Mark Fredricksen  
 Department of Plant Biology  
 University of Illinois  
 1201 W. Gregory Dr., Urbana, IL 61801, USA  
 Tel: 2172655473  
 Email: bohnertlab@life.uiuc.edu.  
 Location/Qualifiers  
 1..614  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nipponbare"  
 /db\_xref="taxon:3947"  
 /clone="BR040010000\_PLATE\_D07\_52\_060.ab1"  
 /tissue\_type="roots"  
 /dev\_stage="3-4 weeks"  
 /clone\_lib="OA"  
 /note="19 h 200mM NaCl"

FEATURES  
 source

ORIGIN  
 Query Match 72.2%; Score 13; DB 6; Length 614;  
 Best Local Similarity 92.3%; Pred. No. 5.6e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNN 18  
 ||:|||||||  
 424 CCTGAGAGNNNNN 412

Db

RESULT 64  
 CG985739 615 bp DNA linear GSS 15-DEC-2003  
 CH240\_155N02.TV CHORI-240 Bos taurus genomic clone CH240\_155N02, genomic survey sequence.  
 CG985739  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Bos taurus (cow)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 615)  
 Costa, J.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library CHORI-240  
 Unpublished (2003)  
 Other GSSs: CH240\_155N02.TV  
 Contact: Caetano, A.R.  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P. 02372, 70770-900 Brasilia  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240 (http://www.chori.org/bacpac/bovine240.htm).  
 Bases shown have phred quality value equal to or higher than 20. Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pletier de Jong (pdejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering/information.htm).  
 This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia with financing from Conselho Nacional de Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
 Plate: 155 row: N column: 02  
 Seq primer: T7  
 Class: BAC ends

High quality sequence stop: 615.  
Location/Qualifiers  
1. 615  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_155N02"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pTARBA1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 615;  
Best Local Similarity 92.3%; Pred. No. 5.6e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNN 18  
||:|||||||  
45 CCTGAGANNNNN 57

Db 46 CCTGAGANNNNN 58

RESULT 65  
AY417454 618 bp DNA linear GSS 12-DEC-2003  
LOCUS AY417454  
DEFINITION Pan troglodytes HCM6229 gene, VIRUTAL TRANSCRIPT, partial sequence, genomic survey sequence.  
VERSION AY417454.1 GI:39773414  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
REFERENCE 1 (bases 1 to 618)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferritera,S., Wang,G., Zheng,X.H., White,T.J., Sainsky,J.J., Adams,M.D. and Cargill,M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
Science 302 (5652), 1960-1963 (2003)  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 618)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferritera,S., Wang,G., Zheng,X.H., White,T.J., Sainsky,J.J., Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering them based on alignment.  
Location/Qualifiers  
1. 618  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
<1\_>618  
/locus\_tag="HCM6229"

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 618;  
Best Local Similarity 92.3%; Pred. No. 5.6e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNN 18  
||:|||||||  
45 CCTGAGANNNNN 57

Db 45 CCTGAGANNNNN 57

RESULT 66  
B2922485 619 bp DNA linear GSS 12-JUN-2003  
LOCUS B2922485  
DEFINITION CH240\_121E17.TV CHORI-240 Bos taurus genomic clone CH240\_121E17, genomic survey sequence.  
B2922485  
ACCESSION B2922485.1 GI:31647871  
VERSION B2922485.1 GI:31647871  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 619)  
Larkin,D.M., Everts-van der Wind,A., Rebelz,M., Schweitzer,P., Bachman,S., Green,S., Campos,E.J., Benson,L.D., Edwards,J., Liu,L., Womack,J.E., de Jong,P.J. and Lewin,H.A.  
A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human Genome Sequence  
Unpublished (2003)  
Other GSS: CH240\_121E17.TV  
Contact: Harris Lewin  
Department of Animal Sciences  
University of Illinois at Urbana Champaign  
1201 W. Gregory Dr., Urbana, IL 61801, USA  
Tel: 217 353 5998  
Fax: 217 244 5617  
Email: h-lewin@uiuc.edu  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pjejong@uiuc.edu).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering\_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by the University of Illinois at Urbana Champaign, USA with funds provided by grant No. AG202-34480-11828 from USDA-CSREES and AG99-35205-8534 from USDA/NRI (Livestock Genome Sequencing Initiative)  
Plate: 121 row: E column: 17  
Seq primer: 17  
Class: BAC ends.  
Location/Qualifiers  
1. 619  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_121E17"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pTARBA1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 72.2%; Score 13; DB 8; Length 619;  
Best Local Similarity 84.6%; Pred. No. 5.6e+03;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 UCCUGAGANNNN 17  
||:|||||||  
Db 551 TCCTGAGANNNN 563

RESULT 67  
BH760082 625 bp DNA linear GSS 14-MAR-2002  
LOCUS BH760082/c  
DEFINITION Mc\_H2M02\_021J13 r McH2 Medicago truncatula BAC library Medicago  
truncatula genomic clone Mc\_H2M02\_021J13, genomic survey sequence.  
BH760082  
ACCESSION BH760082.1 GI:19425219



**KEYWORDS**  
**SOURCE** GSS.  
**ORGANISM** Medicago truncatula (barrel medic)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

**REFERENCE**  
 1 (bases 1 to 625)  
 Larsen, D., Mudge, J., Denny, R., Yan, H. and Young, N.D.  
 BAC end sequencing of Medicago truncatula (UMN)  
 Unpublished (2002)  
**JOURNAL**  
 Contact: Young Nevin D  
 Department of Plant Pathology  
 University of Minnesota  
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul MN 55108, USA  
 Tel: 612 625 2225  
 Fax: 612 625 9728  
 Email: nevin@tc.umn.edu  
 For more information, see the Center for Computational Genomics and Bioinformatics biodata web site at:  
<http://web.ahc.umn.edu/biodata/medicagoyoung/>  
 Seq primer: M13R  
 Class: BAC ends.

**FEATURES**  
 source  
 Location/Qualifiers  
 1..625  
 /organism="Medicago truncatula"  
 /mol\_type="genomic DNA"  
 /cultiivar="genotype A17"  
 /db\_xref="taxon:3880"  
 /clone\_lib="Mc H2M02\_021J13"  
 /note="Vector: pBelobAC1; Site\_1: HindIII; Site\_2: HindIII; Cook et al, in preparation"

**ORIGIN**  
 Query Match 72.2%; Score 13; DB 8; Length 625;  
 Best Local Similarity 92.3%; Pred. No. 5.6e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

**QY** 6 CCUGAGAGNNNNN 18  
 ||:|||||||  
 Db 614 CCTGAGAGNNNNN 602

**RESULT 68**  
**LOCUS** CG976913  
**DEFINITION** CH240\_167A15.TV CHORI-240 Bos taurus genomic clone CH240\_167A15, genomic survey sequence.  
**ACCESSION** CG976913  
**VERSION** CG976913.1 GI:39902692  
**KEYWORDS** GSS.  
**SOURCE** Bos taurus (cow)  
**ORGANISM** Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 638)  
 Costa, J.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)  
**JOURNAL**  
 Other\_GSSs: CH240\_167A15.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372-70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
<http://www.chori.org/bacpac/bovine240.htm>.

Bases shown have Phred quality value equal to or higher than 20. Bases with quality value below 20 were masked with 'N'. For BAC library availability, please contact Pieter de Jong (pjejong@mail.cfo.org).

Clones may be purchased from BACPAC Resources ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)).

This work was undertaken as part of The International Bovine BAC Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia with financing from Conselho Nacional de Desenvolvimento Cientifico e Tecnológico (CNPq), Brazil  
 Plate: 167 row: A column: 15  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 638.

**FEATURES**  
 source  
 Location/Qualifiers  
 1..638  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_167A15"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pTARAC1.3; Site\_1: MboI; Site\_2: MboI; Hereford bull Lt Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

**ORIGIN**  
 Query Match 72.2%; Score 13; DB 9; Length 638;  
 Best Local Similarity 92.3%; Pred. No. 5.6e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

**QY** 6 CCUGAGAGNNNNN 18  
 ||:|||||||  
 Db 604 CCTGAGAGNNNNN 616

**RESULT 69**  
**LOCUS** CG978073  
**DEFINITION** CH240\_169C17.TV CHORI-240 Bos taurus genomic clone CH240\_169C17, genomic survey sequence.  
**ACCESSION** CG978073  
**VERSION** CG978073.1 GI:39903852  
**KEYWORDS** GSS.  
**SOURCE** Bos taurus (cow)  
**ORGANISM** Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 655)  
 Costa, J.N., Mota, M. and Caetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)  
**JOURNAL**  
 Other\_GSSs: CH240\_169C17.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372-70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
<http://www.chori.org/bacpac/bovine240.htm>.  
 Bases shown have Phred quality value equal to or higher than 20. Bases with quality value below 20 were masked with 'N'. For BAC library availability, please contact Pieter de Jong (pjejong@mail.cfo.org).  
 Clones may be purchased from BACPAC Resources ([http://www.chori.org/bacpac/ordering\\_information.htm](http://www.chori.org/bacpac/ordering_information.htm)).

assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

1.655

1.655

[illegible]

ORGANISM	LOCALITY
<i>Bos taurus</i>	India
<i>Bos taurus</i>	India
<i>Mammalia; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.</i>	
1 (bases 1 to 679)	
Larkin, D.M., Everts-van der Wind, A., Rebeiz, M., Schwartz, P., Bachtman, S., Green, S., Cannon, F.T., Benson, L.D., Batzli, R., et al.	

11115 Reactlet-human comparative map built with cattle BAC-ends and Human  
Genome Sequence  
Journal Unpublished (2003)  
Other GSSs: CH240, 111E20.TV  
Comment Contact: Harris Lewin  
Department of Animal Sciences  
University of Illinois at Urbana Champaign  
1201 W. Gregory Dr., Urbana, IL 61801, USA  
Tel: 217 333 5998  
Fax: 217 244 5617

```

FEATURES
  source
    (http://www.choiri.org/bacpac/bovine240.htm) . For BAC library
    availability, please contact Pieter de Jong (pdejong@gmail.cho.org) .
    Clones may be purchased from BACpAC Resources
    (http://www.choiri.org/bacpac/ordering/information.htm) . This work
    was undertaken as part of the International Bovine BAC Mapping
    Consortium (IBMC) by the University of Illinois at Urbana
    Champaign, USA with funds provided by grant No. AG202-34480-11828
    from USDA-CGRRES and AG99-35205-8534 from USDA/NRI (Livestock
    Genome Sequencing Initiative)
    Plate: 111 row: E column: 20
    Seq primer: SP6
    Class: BAC ends.
    Location/Qualifiers
      1..679
        /organism="Bos taurus"
        /mol_type="genomic DNA"
        /strain="Breed: Hereford"
        /db_xref="taxon:9913"
        /clone="CH240_111R20"

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ORIGIN
Query Match          72.2% ; Score 13 ; DB 8 ; Length 679 ;
Best Local Similarity 92.3% ; Pred. No. 5.6e+03 ;
Matches 12 ; Conservative 1 ; Mismatches 0 ; Totals 0 ; Gaps 0 ;
/seqname="CH270_111220"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/notes="Vector: pTARHAC1.3 ; Site_1: MboI ; Site_2: MboI ;
Hereford bull L1 Domino 99375 ; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

```

OY 6 CCUGAGNNNNNN 18  
 DB 597 CCTGAGNNNNNN 585

RESULT 72  
 LOCUS BM251975/c  
 DEFINITION BMT010100013\_F04 Normalized Bovine Total Leukocyte cDNA Library (BMTL) Bos taurus cDNA 3', mRNA sequence.

ACCESSION BM251975  
 VERSION BM251975.1 GI:17887603  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 684)  
 YAO, J., BURTON, J.L., SLEPKOVSKY, S. and COUSENS, P.M.  
 TITLE Generation of EST and cDNA microarray resources for the study of bovine immunobiology  
 JOURNAL Acta Vet. Scand. 42 (3), 391-406 (2001)  
 MEDLINE 21885187  
 PUBMED 11887399  
 COMMENT Contact: Jianbo Yao  
 Division of Animal and Veterinary Sciences  
 West Virginia University  
 Morgantown, WV 26506-6108, USA  
 Tel: 303-293-2631  
 Fax: 304-293-2322  
 Email: jianbo.yao@mail.wvu.edu  
 Seq primer: M13 reverse  
 Location/Qualifiers  
 source  
 1..684  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /sex="female"  
 /tissue\_type="Blood"  
 /cell\_type="peripheral blood leukocytes"  
 /dev\_stage="mid-lactation"  
 /lab\_host="DH10B"  
 /clone\_lib="Normalized Bovine Total Leukocyte cDNA Library (BMTL)"  
 /note="vector: pSPORT1; Site\_1: NotI; Site\_2: SalI"

ORIGIN  
 Query Match 72.2%; Score 13; DB 4; Length 684;  
 Best Local Similarity 84.6%; Pred. No. 5.6e+03;  
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAGN 13  
 DB 609 GGGGTCCTGAGN 597

RESULT 73  
 LOCUS CG992790  
 DEFINITION CH240\_152H03\_TV CHORI-240 Bos taurus genomic clone CH240\_152H03, genomic survey sequence.

ACCESSION CG992790  
 VERSION CG992790.1 GI:39918569  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 701)  
 COSTA, J.N., MOTA, M. and CAETANO, A.R.

TITLE Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 JOURNAL Unpublished (2003)  
 COMMENT Other\_GSSs: CH240\_152H03.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estraco Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetanoc@embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm).  
 Bases shown have phased quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 (pjejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering\_information.htm).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
 Plate: 152 row: H column: 03  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 701.  
 Location/Qualifiers  
 source  
 1..701  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="Breed: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_152H03"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="vector: pTRABAC1.3; Site\_1: MboI; Site\_2: MboI;  
 Hereford bull L1 Domingo 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

ORIGIN  
 Query Match 72.2%; Score 13; DB 9; Length 701;  
 Best Local Similarity 92.3%; Pred. No. 5.6e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGNNNNNN 18  
 DB 675 CCTGAGNNNNNN 687

RESULT 74  
 LOCUS CN035898  
 DEFINITION nm\_11912\_t3\_Mach Ambystoma mexicanum cDNA, mRNA sequence.

ACCESSION CN035898  
 VERSION CN035898.1 GI:45806269  
 KEYWORDS EST.  
 SOURCE Ambystoma mexicanum (axolotl)  
 ORGANISM Ambystoma mexicanum  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandridae; Ambystomatidae; Ambystoma.

REFERENCE 1 (bases 1 to 716)  
 PUTTA, S., SMITH, J.J., WALKER, J.A., RONDET, M., WEISROCK, D.,  
 MONAGHAN, J., SAMUELS, A.K., KUMP, K., KING, D.C., MANESS, N.J.,  
 HABERMANN, B., TANAKA, E., BRYANT, S.V., GARDNER, D.M., PARICHY, D.M.  
 and VOSS, S.R.  
 TITLE From biomedicine to natural history research: EST resources for  
 ambystomatid salamanders  
 JOURNAL BMC Genomics 5 (1), 54 (2004)  
 COMMENT Contact: SR Voss

Department of Biology  
University of Kentucky  
TH Morgan Building, Lexington, KY 40506, USA  
Tel: 859 257 9888  
Fax: 859 257 1717  
Email: syros@uky.edu  
The EST is quality trimmed at the ends with a 20 base window and  
quality threshold of 15 (phred quality score). Please visit  
http://salamander.uky.edu for any information (trace, quality files  
etc) regarding this EST.

## FEATURES

source

1..716  
/organism="Ambystoma mexicanum"  
/mol\_type="mRNA"  
/db\_xref="taxon:8296"  
/tissue\_type="Limb Blastema and Proximal Limb Tissue  
collected from larvae on days 1-6 of regeneration"  
/clone\_lib="Match"

## ORIGIN

Query Match 72.2%; Score 13; DB 7; Length 716;  
Best Local Similarity 92.3%; Pred. No. 5.6e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNNN 18  
|||  
695 CCTGAGANNNNNN 683

RESULT 75 756 bp mRNA linear EST 29-NOV-2002  
BU438636 604145436F1 CSEQRBN11 Gallus gallus CDNA clone CHEST984h9 5', mRNA  
LOCUS  
DEFINITION  
ACCESSION BU438636  
VERSION BU438636.1 GI:25927947  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 756)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burr, D.W., Bosch, E.,  
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken CDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source

1..756  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer and broiler"  
/db\_xref="taxon:9031"  
/clone="CHEST984h9"  
/sex="Male and female"  
/tissue\_type="muscle"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQRBN11"  
/note="Vector: pBluescript II KS(+); Site 1: EcoRI;  
Site 2: NotI; This normalized library was constructed from  
1 million independent clones. cDNA synthesis was initiated  
using an oligo(dt) primer, using methylated C in the first

## ORIGIN

Query Match 72.2%; Score 13; DB 5; Length 756;  
Best Local Similarity 92.3%; Pred. No. 5.5e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGANNNNNN 18  
|||  
474 CCTGAGANNNNNN 486

RESULT 76 758 bp DNA linear GSS 16-JUL-1999  
AO745042 HS\_3506\_A1 B06 SP6 RPCI-11 Human Male BAC Library Homo sapiens  
LOCUS genomic clone Plate=1082 Col=11 Row=C, genomic survey sequence.  
DEFINITION  
ACCESSION AO745042  
VERSION AO745042.1 GI:5522487  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 758)  
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holman, T.,  
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and  
Hood, L.  
Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
10449764  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering/bac.htm)  
or from Research Genetics (info@resgen.com). BAC end Web Server:  
http://www.hsc.washington.edu  
Plate: 1082 row: C column: 11  
Seq primer: SP6  
Classes: BAC ends  
High quality sequence stop: 758.

## FEATURES

source

1..758  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="Plate=1082 Col=11 Row=C"  
/sex="male"  
/clone\_lib="RPCI-11 Human Male BAC Library"  
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRI methylase. Size selected DNA was cloned into the  
pBAC3.6 vector at EcoRI sites"

## ORIGIN

Query Match 72.2%; Score 13; DB 8; Length 758;  
 Best Local Similarity 92.3%; Pred. No. 5.5e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
 ||:|||||  
 Db 640 CCTGGAGNNNNNN 652

RESULT 77  
 LOCUS CN042530 783 bp mRNA linear EST 29-MAR-2004  
 DEFINITION vtl\_p42\_019\_c3\_010\_ab1 Match Ambystoma mexicanum cDNA, mRNA  
 sequence.  
 ACCESSION CN042530  
 VERSION CN042530.1 GI:45812901  
 KEYWORDS EST.  
 SOURCE Ambystoma mexicanum (axolotl)  
 ORGANISM Ambystoma mexicanum  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Caudata; Salamandridae; Ambystomatidae;  
 Ambystoma.  
 1 (bases 1 to 783)  
 Puta, S., Smith, J.J., Walker, J.A., Rondet, M., Weisrock, D.,  
 Monaghan, J., Samuels, A.K., Kump, K., King, D.C., Maness, N.J.,  
 Habermann, B., Tanaka, E., Bryant, S.V., Gardiner, D.M., Patchy, D.M.  
 and Voss, S.R.  
 From biomedicine to natural history research: EST resources for  
 ambystomatid salamanders  
 BMC Genomics 5 (1), 54 (2004)  
 Contact: SR Voss  
 Department of Biology  
 University of Kentucky  
 TH Morgan Building, Lexington, KY 40506, USA  
 Tel: 859 257 9888  
 Fax: 859 257 1717  
 Email: svoss@uky.edu  
 The EST is quality trimmed at the ends with a 20 base window and  
 quality threshold of 15 (phred quality score). Please visit  
 http://salamander.uky.edu for any information (trace, quality files  
 etc) regarding this EST.

FEATURES  
 source location/Qualifiers  
 1..783  
 /organism="Ambystoma mexicanum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8296"  
 /tissue\_type="Limb Blastema and Proximal Limb Tissue"  
 collected from larvae on days 1-6 of regeneration"  
 /clone\_lib="Match"

ORIGIN  
 Query Match 72.2%; Score 13; DB 7; Length 783;  
 Best Local Similarity 92.3%; Pred. No. 5.5e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
 ||:|||||  
 Db 3 CCTGGAGNNNNNN 15

RESULT 78  
 LOCUS AY111174 802 bp mRNA linear HTC 17-OCT-2002  
 DEFINITION Zee mayes CL27726\_1 mRNA sequence.  
 ACCESSION AY111174  
 VERSION AY111174.1 GI:21215764  
 KEYWORDS HTC.  
 SOURCE Zee mayes  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 802)  
 AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S.,  
 Arthur, L.M., Hanahey, M., Morgante, M. and Tingey, S.V.  
 TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of  
 Overgo Probes  
 JOURNAL Unpublished (2002)  
 REFERENCE 2 (bases 1 to 802)  
 AUTHORS Coe, E.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of  
 Missouri, Columbia, MO 65211, USA  
 COMMENT If you are interested in getting corresponding physical clones,  
 these are publicly available from ZmDB and may be found by BLAST  
 searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR,  
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the  
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat  
 Schnable, Iowa State, then clones may be requested from ZmDB:  
 www.zmdb.iastate.edu.

FEATURES  
 source location/Qualifiers  
 1..802  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /db\_xref="MaizeDB:631151"  
 /db\_xref="taxon:4577"  
 /clone\_lib="Maize Mapping Project/Dupont Consensus  
 Library"  
 /note="this sequence is part of a project of EST  
 assemblies resulting from the application of public  
 configs to seed Dupont configs; this resource was  
 assembled by Dupont as part of a collaboration for the  
 overgo addressing of BACs in conjunction with the Maize  
 Mapping Project"

ORIGIN  
 Query Match 72.2%; Score 13; DB 3; Length 802;  
 Best Local Similarity 92.3%; Pred. No. 5.5e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGAGNNNNNN 18  
 ||:|||||  
 Db 565 CCTGGAGNNNNNN 577

RESULT 79  
 LOCUS AY405397 825 bp DNA linear GSS 12-DEC-2003  
 DEFINITION Pan troglodytes HCM2210 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 genomic survey sequence.  
 ACCESSION AY405397  
 VERSION AY405397.1 GI:39761371  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 REFERENCE 1 (bases 1 to 825)  
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
 Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,  
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Slatney, J.J.,  
 Adams, M.D. and Cargill, M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 REFERENCE 2 (bases 1 to 825)  
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,  
 Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,  
 Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Slatney, J.J.,  
 Adams, M.D. and Cargill, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering

FEATURES      them based on alignment.  
 source      Location/Qualifiers  
             1..825  
             /organism="Pan troglodytes"  
             /mol\_type="genomic DNA"  
             /db\_xref="taxon:9598"  
             <1..>825  
             /locus\_tag="HCM2210"

Query Match      72.2%; Score 13; DB 9; Length 825;  
 Best Local Similarity      84.6%; Pred. No. 5.5e+03;  
 Matches      11; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

QY      3 GGCCGAGGAGNNN 15  
 ||:|||||  
 Db      506 GGTCCTGGAGNNN 518

RESULT 80  
 BQ948660/c  
 LOCUS      BQ948660      845 bp      mRNA      linear      EST 21-AUG-2002  
 DEFINITION      AGENCOURT 8784237 NIH\_MGC\_43 Homo sapiens cDNA clone IMAGE:6376418  
             5', mRNA sequence.  
 ACCESSION      BQ948660  
 VERSION      BQ948660.1      GI:22364138  
 KEYWORDS      EST.  
 SOURCE      Homo sapiens (human)  
 ORGANISM      Homo sapiens  
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
             Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE      1 (bases 1 to 845)  
 AUTHORS      NIH-MGC http://mgi.nci.nih.gov/  
 TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL      Unpublished (1999)  
 COMMENT      Contact: Robert Strausberg, Ph.D.  
             Email: cga@bbs-remail.nih.gov  
             Tissue Procurement: ATCC  
             cDNA Library Preparation: Rubin Laboratory  
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
             DNA Sequencing by: Agencourt Bioscience Corporation  
             Clone distribution: MGC clone distribution information can be  
             found through the I.M.A.G.E. Consortium/LNL at:  
             http://image.lnl.gov  
             Plate: L1CM2558      row: j      column: 03  
             High quality sequence stop: 534.  
             Location/Qualifiers  
             1..845  
             /organism="Homo sapiens"  
             /mol\_type="mRNA"  
             /db\_xref="taxon:9606"  
             /clone="IMAGE:6376418"  
             /tissue\_type="normal pigmented retinal epithelium"  
             /lab\_host="DH10B (phage-resistant)"  
             /clone\_lib="NIH\_MGC\_43"  
             /note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:  
             EcoRI; cDNA made by oligo-dT priming. Directionally  
             cloned into EcoRI/XhoI sites using the following 5'  
             adaptor: GGCACGAG(G). Library constructed by Ling Hong  
             in the laboratory of Gerald M. Rubin (University of  
             California, Berkeley) using ZAP-cDNA synthesis kit  
             (Stratagene) and Superscript II RT (Life Technologies).  
             Note: this is a NIH\_MGC Library. |"

FEATURES      source  
 1..845

ORIGIN

Query Match      72.2%; Score 13; DB 5; Length 845;  
 Best Local Similarity      92.3%; Pred. No. 5.5e+03;  
 Matches      12; Conservative      1; Mismatches      0; Indels      0; Gaps      0;

QY      6 CCUGAGGNNNNN 18  
 ||:|||||  
 Db      725 CCTGGAGNNNNN 713

RESULT 81  
 CC921276/c  
 LOCUS      CC921276      858 bp      DNA      linear      GSS 08-AUG-2003  
 DEFINITION      t047002ba.f1 TAMBT Bos taurus genomic clone t047002ba, genomic  
             survey sequence.  
 ACCESSION      CC921276  
 VERSION      CC921276.1      GI:33554634  
 KEYWORDS      GSS.  
 SOURCE      Bos taurus (cow)  
 ORGANISM      Bos taurus  
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
             Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
             Bovinae; Bos.  
 REFERENCE      1 (bases 1 to 858)  
 AUTHORS      Lin, S., Najjar, F.Z., Adelson, D., Gill, C.A. and Roe, B.A.  
 TITLE      Bovine BAC End Sequences from Library TAMBT  
 JOURNAL      Unpublished (2003)  
 COMMENT      Contact: Bruce A. Roe  
             Advanced Center for Genome Technology  
             University of Oklahoma Department of Chemistry and Biochemistry  
             620 Parrington Oval, Room 208, Norman, OK 73019, USA  
             Tel: 405 325 4912  
             Fax: 405 325 7762  
             Email: broe@ou.edu  
             Class: BAC ends  
             High quality sequence start: 119  
             High quality sequence stop: 441.  
             Location/Qualifiers  
             1..858  
             /organism="Bos taurus"  
             /mol\_type="genomic DNA"  
             /strain="Angus bull T A M U Shoshone Y6 11519666"  
             /db\_xref="taxon:9913"  
             /clone="t047002ba"  
             /sex="Male"  
             /cell\_type="B100d"  
             /clone\_lib="TAMBT"  
             /note="Vector: pBelBAC11; Site 1: HindIII; Site 2:  
             HindIII; TAMBT Bovine BAC library (Male) produced by Texas  
             A&M University, Department of Animal Science."

FEATURES      source

ORIGIN

Query Match      72.2%; Score 13; DB 9; Length 858;  
 Best Local Similarity      92.3%; Pred. No. 5.5e+03;  
 Matches      12; Conservative      1; Mismatches      0; Indels      0; Gaps      0;

QY      6 CCUGAGGNNNNN 18  
 ||:|||||  
 Db      104 CCTGGAGNNNNN 92

RESULT 82  
 BU957217/c  
 LOCUS      BU957217      873 bp      mRNA      linear      EST 21-OCT-2002  
 DEFINITION      AGENCOURT 10621575 NIH\_MGC\_107 Homo sapiens cDNA clone  
             IMAGE:6731210 5', mRNA sequence.  
 ACCESSION      BU957217  
 VERSION      BU957217.1      GI:24186789  
 KEYWORDS      EST.  
 SOURCE      Homo sapiens (human)  
 ORGANISM      Homo sapiens  
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
             Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE      1 (bases 1 to 873)  
 AUTHORS      NIH-MGC http://mgi.nci.nih.gov/  
 TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL      Unpublished (1999)  
 COMMENT      Contact: Robert Strausberg, Ph.D.  
             Email: cga@bbs-remail.nih.gov  
             Tissue Procurement: ATCC  
             cDNA Library Preparation: Rubin Laboratory  
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1CM3057 row: e column: 01  
 High quality sequence stop: 695.

## FEATURES

## SOURCE

1..873  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6731210"  
 /issue\_type="adenocarcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_107"  
 /note="Organ: breast; Vector: pOTB7; Site: 1: EcoRI;  
 Site: 2: XhoI; cDNA made by oligo-dT priming.  
 directionally cloned into EcoRI/XhoI sites using  
 following 5' adaptor: GGCACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 72.2%; Score 13; DB 5; Length 873;  
 Best Local Similarity 92.3%; Pred. No. 5.5e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGNNNNNN 18  
 ||:|||||||  
 Db 766 CCTGAGNNNNNN 754

RESULT 83  
 BUI96728/c  
 LOCUS BUI96728 895 bp mRNA linear EST 04-SEP-2002  
 DEFINITION AGNCOURT\_7974315 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6082172  
 5', mRNA sequence.  
 ACCESSION BUI96728  
 VERSION BUI96728.1 GI:22710712  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 895)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1CM2310 row: e column: 21  
 High quality sequence stop: 655.

## FEATURES

## SOURCE

1..895  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6082172"  
 /issue\_type="ductal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_110"  
 /note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI;  
 Site: 2: EcoRI; cDNA made by oligo-dT priming.  
 directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 72.2%; Score 13; DB 5; Length 895;  
 Best Local Similarity 92.3%; Pred. No. 5.5e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGNNNNNN 18  
 ||:|||||||  
 Db 840 CCTGAGNNNNNN 828

RESULT 84  
 AY110949  
 LOCUS AY110949 903 bp mRNA linear HTC 17-OCT-2002  
 DEFINITION Zea mays CL12681\_1 mRNA sequence.  
 ACCESSION AY110949  
 VERSION AY110949.1 GI:21215539  
 KEYWORDS HTC.

## SOURCE

Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

1 (bases 1 to 903)  
 Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitelitt, M.S.,  
 Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.

## TITLE

Maize Mapping Project/Dupont Consensus Sequences for Design of  
 Overgo Probes

## JOURNAL

Unpublished (2002)

## REFERENCE

2 (bases 1 to 903)  
 Coe, E.H.

## JOURNAL

Direct Submission  
 Submitted (25-APR-2002) Maize Mapping Project, University of

## TITLE

Missouri, Columbia, MO 65211, USA  
 If you are interested in getting corresponding physical clones,  
 these are publicly available from ZmDB and may be found by BLAST  
 searching at MSL, [maizemap.org](http://maizemap.org); ZmDB, [www.zmdb.iastate.edu](http://www.zmdb.iastate.edu); TIGR,  
[www.tigr.org](http://www.tigr.org); or NCBI, [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov). When the source of the  
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat  
 Schnable, Iowa State, then clones may be requested from ZmDB:  
[www.zmdb.iastate.edu](http://www.zmdb.iastate.edu).

## FEATURES

Location/Qualifiers

1..903  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4577"  
 /clone\_lib="Maize Mapping Project/Dupont Consensus  
 Library"  
 /note="this sequence is part of a project of EST  
 assemblies resulting from the application of public  
 contigs to seed Dupont contigs; this resource was  
 assembled by Dupont as part of a collaboration for the  
 overgo addressing of BACs in conjunction with the Maize  
 Mapping Project"

## ORIGIN

Query Match 72.2%; Score 13; DB 3; Length 903;  
 Best Local Similarity 92.3%; Pred. No. 5.5e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGNNNNNN 18  
 ||:|||||||  
 Db 514 CCTGAGNNNNNN 526

RESULT 85  
 AY110206/c

LOCUS AY110206 928 bp mRNA linear HTC 17-OCT-2002  
 DEFINITION Zea mays Cl25252\_1 mRNA sequence.  
 ACCESSION AY110206  
 VERSION AY110206.1 GI:21214366  
 KEYWORDS HTC.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 928)  
 Hailey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whiteside, M.S.,  
 Arthur, L.W., Hanfey, M., Morgante, M. and Tingey, S.V.  
 Maize Mapping Project/Dupont Consensus Sequences for Design of  
 Overgo Probes  
 Unpublished (2002)  
 2 (bases 1 to 928)  
 Coe, E.H.  
 Direct Submission  
 Submitted (25-APR-2002) Maize Mapping Project, University of  
 Missouri, Columbia, MO 65211, USA  
 If you are interested in getting corresponding physical clones,  
 these are publicly available from ZmDB and may be found by BLAST  
 searching at MSU, [maizemap.org](http://maizemap.org); ZmDB, [www.zmdb.iastate.edu](http://www.zmdb.iastate.edu); TIGR,  
[www.tigr.org](http://www.tigr.org); or NCBI, [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov). When the source of the  
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat  
 Schnable, Iowa State, then clones may be requested from ZmDB:  
[www.zmdb.iastate.edu](http://www.zmdb.iastate.edu).  
 Location/Qualifiers  
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 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4577"  
 /clone\_lib="Maize Mapping Project/Dupont Consensus  
 Library"  
 /note="this sequence is part of a project of EST  
 assemblies resulting from the application of public  
 configs to seed Dupont configs; this resource was  
 assembled by Dupont as part of a collaboration for the  
 overgo addressing of BACS in conjunction with the Maize  
 Mapping Project"

ORIGIN  
 Query Match 72.2%; Score 13; DB 3; Length 928;  
 Best Local Similarity 92.3%; Pred. No. 5.5e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCGGAGNNNNNN 18  
 ||:|||||||  
 Db 312 CCTGGAGNNNNNN 300

RESULT 86  
 LOCUS BO927240 990 bp mRNA linear EST 20-AUG-2002  
 DEFINITION AGENCOURT 8774505 NIH\_MGC\_18 Homo sapiens cDNA clone IMAGE:6370157  
 5', mRNA sequence.  
 ACCESSION BO927240  
 VERSION BO927240.1 GI:22342271  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
 Tissue Procurement: DCTD/DRP/Gazdar  
 cDNA Library Preparation: Rubin Laboratory

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

FEATURES  
 source  
 1..990  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6370157"  
 /tissue\_type="large cell carcinoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_18"  
 /note="Organ: Lung; Vector: pOT7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
 into EcoRI/XhoI sites using the following 5' adaptor:  
 GGCACGAG(G). Library constructed by Ling Hong in the  
 Laboratory of Gerald M. Rubin (University of California,  
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
 Superscript II RT (Life Technologies). Note: this is a  
 NIH\_MGC Library."

ORIGIN  
 Query Match 72.2%; Score 13; DB 5; Length 990;  
 Best Local Similarity 92.3%; Pred. No. 5.4e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCGGAGNNNNNN 18  
 ||:|||||||  
 Db 966 CCTGGAGNNNNNN 954

RESULT 87  
 LOCUS BU860039 1000 bp mRNA linear EST 16-OCT-2002  
 DEFINITION AGENCOURT 10435318 NIH\_MGC\_107 Homo sapiens cDNA clone  
 IMAGE:6651052 5', mRNA sequence.  
 ACCESSION BU860039  
 VERSION BU860039.1 GI:24045031  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
 Plate: L1CM2697 row: e column: 04  
 High quality sequence stop: 351.  
 Location/Qualifiers  
 1..1000  
 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:6651052"  
 /tissue\_type="adenocarcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_107"  
 /note="Organ: breast; Vector: pOT7; Site 1: EcoRI,



Site 2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 72.2%; Score 13; DB 5; Length 1000;  
Best Local Similarity 92.3%; Pred. No. 5.4e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGANNNNNN 18  
||:|||||  
Db 382 CCGAGANNNNNN 370

RESULT 88  
LOCUS B0062584/c 1073 bp mRNA linear EST 02-APR-2002  
DEFINITION AGENCOURT\_6827224 NIH\_MGC\_99 Homo sapiens cDNA clone IMAGE:5924077  
5', mRNA sequence.  
ACCESSION B0062584  
VERSION B0062584.1 GI:19889552  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1073)  
AUTHORS NIH-MGC http://mgi.mcg.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-r@mail.nih.gov  
Tissue Procurement: Lou Straube  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.lnl.gov

Plate: LNCM2093 row: j column: 14  
High quality sequence start: 116  
High quality sequence stop: 528.

FEATURES  
source location/Qualifiers

1..1073  
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/tissue\_type="lymphoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
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/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 72.2%; Score 13; DB 5; Length 1073;  
Best Local Similarity 92.3%; Pred. No. 5.4e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGANNNNNN 18  
||:|||||  
Db 837 CCGAGANNNNNN 825

RESULT 89  
LOCUS AY399238 1124 bp DNA linear GSS 15-DEC-2003  
DEFINITION Pan troglodytes CPE gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY399238  
VERSION AY399238.1 GI:39755227  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes

REFERENCE 1 (bases 1 to 1124)  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Cavello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
Title Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1124)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Cavello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
Title Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES  
source location/Qualifiers

1..1124  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
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## ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 1124;  
Best Local Similarity 92.3%; Pred. No. 5.4e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 CCUGAGANNNNNN 18  
||:|||||  
Db 660 CCGAGANNNNNN 672

RESULT 90  
LOCUS AY410559 1170 bp DNA linear GSS 16-DEC-2003  
DEFINITION Homo sapiens SLC14A1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY410559  
VERSION AY410559.1 GI:39766527  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1170)  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Cavello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
Title Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302

REFERENCE 2 (bases 1 to 1170)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
source  
1..1170  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
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/gene="SLC14A1"  
/locus\_tag="HCM3931"

ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 1170;  
Best Local Similarity 92.3%; Pred. No. 5.4e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGNNNNNN 18  
||:|||||  
657 CCTGAGNNNNNN 669

RESULT 91  
LOCUS AY410560 1170 bp DNA linear GSS 16-DEC-2003  
DEFINITION Pan troglodytes SLC14A1 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY410560  
VERSION AY410560.1 GI:39766528  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
1 (bases 1 to 1170)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
REFERENCE PubMed 14671302  
2 (bases 1 to 1170)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
source  
1..1170  
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/gene="SLC14A1"  
/locus\_tag="HCM3931"

ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 1170;  
Best Local Similarity 92.3%; Pred. No. 5.4e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGNNNNNN 18  
||:|||||  
Db 657 CCTGAGNNNNNN 669

RESULT 92  
LOCUS AY410561 1170 bp DNA linear GSS 16-DEC-2003  
DEFINITION Mus musculus SLC14A1 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY410561  
VERSION AY410561.1 GI:39766529  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 1170)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
REFERENCE PubMed 14671302  
2 (bases 1 to 1170)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
source  
1..1170  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
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/gene="SLC14A1"  
/locus\_tag="HCM3931"

ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 1170;  
Best Local Similarity 92.3%; Pred. No. 5.4e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGNNNNNN 18  
||:|||||  
Db 657 CCTGAGNNNNNN 669

RESULT 93  
LOCUS AY409438 1247 bp DNA linear GSS 12-DEC-2003  
DEFINITION Pan troglodytes HCM3557 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY409438  
VERSION AY409438.1 GI:39765406  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
1 (bases 1 to 1247)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE  
Infering nonneutral evolution from human-chimp-mouse orthologous  
gene trios

JOURNAL  
Science 302 (5652), 1960-1963 (2003)

REFERENCE  
PUBMED  
14671302

AUTHORS  
2 (bases 1 to 1247)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE  
Direct Submission

JOURNAL  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

COMMENT  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

FEATURES  
Source  
Location/Qualifiers  
1..1247  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
<1..>1247  
/locus\_tag="HCM3557"

ORIGIN  
gene

Query Match  
Best Local Similarity 92.3%; Pred. No. 5.3e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  
6 CCUGAGNNNNNN 18  
||:|||||||  
||:|||||||

Db  
667 CCTGGAGNNNNNN 655

RESULT 94  
AY409437/c

LOCUS  
1271 bp DNA linear GSS 12-DEC-2003

DEFINITION  
Homo sapiens HCM3557 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.

ACCESSION  
AY409437

VERSION  
AY409437.1 GI:39765405

KEYWORDS  
GSS.

SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 (bases 1 to 1271)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE  
Infering nonneutral evolution from human-chimp-mouse orthologous  
gene trios

JOURNAL  
Science 302 (5652), 1960-1963 (2003)

REFERENCE  
PUBMED  
14671302

AUTHORS  
2 (bases 1 to 1271)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE  
Direct Submission

JOURNAL  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

COMMENT  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

FEATURES  
Location/Qualifiers  
1..1271  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
<1..>1271  
/locus\_tag="HCM3557"

ORIGIN  
gene

Query Match  
Best Local Similarity 92.3%; Pred. No. 5.3e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  
6 CCUGAGNNNNNN 18  
||:|||||||  
||:|||||||

Db  
667 CCTGGAGNNNNNN 655

Best Local Similarity 92.3%; Pred. No. 5.3e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  
6 CCUGAGNNNNNN 18  
||:|||||||  
||:|||||||

Db  
667 CCTGGAGNNNNNN 655

RESULT 95  
AY421522

LOCUS  
1613 bp DNA linear GSS 17-DEC-2003

DEFINITION  
Pan troglodytes EYA2 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.

ACCESSION  
AY421522

VERSION  
AY421522.1 GI:39748381

KEYWORDS  
GSS.

SOURCE  
Pan troglodytes (chimpanzee)

ORGANISM  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE  
1 (bases 1 to 1613)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.

TITLE  
Direct Submission

JOURNAL  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA

COMMENT  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

FEATURES  
Location/Qualifiers  
1..1613  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
<1..>1613  
/gene="EYA2"  
/locus\_tag="HCM7585"

ORIGIN  
gene

Query Match  
Best Local Similarity 72.2%; Score 13; DB 9; Length 1613;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  
6 CCUGAGNNNNNN 18  
||:|||||||  
||:|||||||

Db  
968 CCTGGAGNNNNNN 980

RESULT 96  
AY409605

LOCUS  
1920 bp DNA linear GSS 16-DEC-2003

DEFINITION  
Homo sapiens EYA4 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.

ACCESSION  
AY409605

VERSION  
AY409605.1 GI:39765573

KEYWORDS  
GSS.

SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 (bases 1 to 1920)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

Periera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)  
2 (bases 1 to 1920)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,  
Periera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
Location/Qualifiers  
1..1920  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
<1..>1920  
/gene="EYA4"  
/locus\_tag="HCM3613"

Query Match 72.2%; Score 13; DB 9; Length 1920;  
Best Local Similarity 92.3%; Pred. No. 5.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 6 CCTGGAGNNNNNN 18  
||:|||||||  
Db 1101 CCTGGAGNNNNNN 1113

RESULT 97  
AY409606  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

AY409606 1920 bp DNA linear GSS 16-DEC-2003  
Pan troglodytes EYA4 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
AY409606 GI:39765574  
GSS.  
Pan troglodytes (chimpanzee)  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
1 (bases 1 to 1920)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,  
Periera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)  
2 (bases 1 to 1920)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,  
Periera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
Location/Qualifiers  
1..1920  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
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gene

ORIGIN  
/locus\_tag="HCM3613"

Query Match 72.2%; Score 13; DB 9; Length 1920;  
Best Local Similarity 92.3%; Pred. No. 5.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 6 CCTGGAGNNNNNN 18  
||:|||||||  
Db 1101 CCTGGAGNNNNNN 1113

RESULT 98  
AY402163/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

AY402163 2001 bp DNA linear GSS 15-DEC-2003  
Pan troglodytes PZD3 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
AY402163 GI:39758149  
GSS.  
Pan troglodytes (chimpanzee)  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
1 (bases 1 to 2001)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,  
Periera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)  
2 (bases 1 to 2001)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,  
Periera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
Location/Qualifiers  
1..2001  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
<1..>2001  
/gene="PZD3"  
/locus\_tag="HCM1132"

gene

ORIGIN

Query Match 72.2%; Score 13; DB 9; Length 2001;  
Best Local Similarity 84.6%; Pred. No. 5.1e+03;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 5 UCCUGAGNNNNNN 17  
||:|||||||  
Db 1586 TCCTGGAGNNNNNN 1574

RESULT 99  
AY405709  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AY405709 2036 bp DNA linear GSS 15-DEC-2003  
Pan troglodytes CY2N2 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
AY405709 GI:39761683  
GSS.  
Pan troglodytes (chimpanzee)  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 2036)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 2036)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
FEATURES  
source Location/Qualifiers  
1..2036  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
<1..>2036  
/gene="CYLN2"  
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ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 2036;  
Best Local Similarity 92.3%; Pred. No. 5.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGNNNNNN 18  
||:|||||  
Db 694 CCTGGAGNNNNN 706

RESULT 100  
AY417388  
LOCUS 2073 bp DNA linear GSS 17-DEC-2003  
DEFINITION Pan troglodytes TGM3 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY417388.1 GI:39773348  
VERSION  
KEYWORDS GSS.  
SOURCE  
ORGANISM Pan troglodytes (chimpanzee)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
1 (bases 1 to 2073)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 2073)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
FEATURES  
source Location/Qualifiers  
1..2073  
/organism="Pan troglodytes"

/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
<1..>2073  
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/locus\_tag="HCM6207"

ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 2073;  
Best Local Similarity 92.3%; Pred. No. 5.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGNNNNNN 18  
||:|||||  
Db 1787 CCTGGAGNNNNN 1797

RESULT 101  
AY417387  
LOCUS 2075 bp DNA linear GSS 17-DEC-2003  
DEFINITION Homo sapiens TGM3 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY417387  
VERSION AY417387.1 GI:39773347  
KEYWORDS GSS.  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 2075)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 2075)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
FEATURES  
source Location/Qualifiers  
1..2075  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
<1..>2075  
/gene="TGM3"  
/locus\_tag="HCM6207"

ORIGIN  
Query Match 72.2%; Score 13; DB 9; Length 2075;  
Best Local Similarity 92.3%; Pred. No. 5.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CCUGAGNNNNNN 18  
||:|||||  
Db 1787 CCTGGAGNNNNN 1799

RESULT 102  
AY417389  
LOCUS 2075 bp DNA linear GSS 17-DEC-2003  
DEFINITION Mus musculus TGM3 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY417389  
VERSION AY417389.1 GI:39773349

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 2075)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.J., Adams, M.D. and Cargill, M.  
TITLE Interfering nonneutral evolution from human-chimp-mouse orthologous gene tries  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 2075)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.J., Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
FEATURES  
Location/Qualifiers  
1..2075  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
<1..>2075  
/gene="RFX1"  
/locus\_tag="HCM6207"

Query Match 72.2%; Score 13; DB 9; Length 2075;  
Best Local Similarity 92.3%; Pred. No. 5.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
||:|||||  
Db 1787 CCTGAGNNNNNN 1799

RESULT 103  
LOCUS AY413512/c 2257 bp DNA linear GSS 17-DEC-2003  
DEFINITION Pan troglodytes RFX1 gene, VIRUTAL TRANSCRIPT, partial sequence, genomic survey sequence.  
ACCESSION AY413512  
VERSION AY413512.1 GI:39769474  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
AUTHORS 1 (bases 1 to 2257)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.J., Adams, M.D. and Cargill, M.  
TITLE Interfering nonneutral evolution from human-chimp-mouse orthologous gene tries  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 2257)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.J., Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering

them based on alignment.  
FEATURES  
Location/Qualifiers  
1..2257  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
<1..>2257  
/gene="RFX1"  
/locus\_tag="HCM4915"

Query Match 72.2%; Score 13; DB 9; Length 2257;  
Best Local Similarity 92.3%; Pred. No. 5.1e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
||:|||||  
Db 1264 CCTGAGNNNNNN 1252

RESULT 104  
LOCUS AY410786 2772 bp DNA linear GSS 12-DEC-2003  
DEFINITION Mus musculus HCM4006 gene, VIRUTAL TRANSCRIPT, partial sequence, genomic survey sequence.  
ACCESSION AY410786  
VERSION AY410786.1 GI:3976754  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 2772)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.J., Adams, M.D. and Cargill, M.  
TITLE Interfering nonneutral evolution from human-chimp-mouse orthologous gene tries  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 2772)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.J., Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
FEATURES  
Location/Qualifiers  
1..2772  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
<1..>2772  
/locus\_tag="HCM4006"

Query Match 72.2%; Score 13; DB 9; Length 2772;  
Best Local Similarity 92.3%; Pred. No. 5e+03;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 CCUGAGNNNNNN 18  
||:|||||  
Db 180 CCTGAGNNNNNN 192

RESULT 105  
LOCUS AY405708 3129 bp DNA linear GSS 15-DEC-2003  
DEFINITION Homo sapiens CYLN2 gene, VIRUTAL TRANSCRIPT, partial sequence,

ACCESSION genomic survey sequence.  
 AY405708  
 VERSION AY405708.1 GI:39761682  
 KEYWORDS GSS.  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 3129)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 3129)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
 FEATURES  
 source  
 1. .3129  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 <1. .>3129  
 /gene="CYLN2"  
 /locus\_tag="HCM2314"  
 ORIGIN  
 Query Match 72.2%; Score 13; DB 9; Length 3129;  
 Best Local Similarity 92.3%; Pred. No. 4.9e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 CCUGAGNNNNNN 18  
 ||:|||||||  
 Db 1374 CCTGAGNNNNNN 1386  
 RESULT 106  
 AY420125 3878 bp DNA linear GSS 17-DEC-2003  
 LOCUS Mus musculus LAMC1 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 DEFINITION AY420125  
 ACCESSION AY420125  
 VERSION AY420125.1 GI:39776082  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 3878)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 3878)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.  
 FEATURES  
 source  
 1. .3878  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 <1. .>3878  
 /gene="LAMC1"  
 /locus\_tag="HCM7119"  
 ORIGIN  
 Query Match 72.2%; Score 13; DB 9; Length 3878;  
 Best Local Similarity 92.3%; Pred. No. 4.8e+03;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 CCUGAGNNNNNN 18  
 ||:|||||||  
 Db 2891 CCTGAGNNNNNN 2903  
 RESULT 107  
 CG918361 69 bp DNA linear GSS 12-DEC-2003  
 LOCUS CH240\_143P18.TV CHORI-240 Bos taurus genomic clone CH240\_143P18,  
 DEFINITION genomic survey sequence.  
 ACCESSION CG918361  
 VERSION CG918361.1 GI:39778044  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 69)  
 AUTHORS Costa,J.N., Mota,M. and Caetano,A.R.  
 TITLE Brazil's Contribution to End-Sequencing the Bovine BAC Library CHORI-240  
 JOURNAL Unpublished (2003)  
 COMMENT Other GSSs: CH240\_143P18.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetan@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.choi.org/bacpac/ordering/information.htm).  
 Bases shown have phred quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong (pjejong@mail.cho.org).  
 Clones may be purchased from BACPAC Resources  
 (http://www.choi.org/bacpac/ordering/information.htm).  
 This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e Biotecnologia with financing from Conselho Nacional de Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
 Plate: 143 row: P column: 18  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 69.  
 FEATURES  
 source  
 1. .69  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="Bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_143P18"

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/sex="Male"
/cell_type="Blood"
/clone_id="CHORI-240"
/notes="Vector: PTARBA1.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN
Query Match      66.7%; Score 12; DB 9; Length 69;
Best Local Similarity 91.7%; Pred. No. 2.4e+04;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY
7 CUGAGANNNNNN 18
11:|||||
15 CTGAGANNNNNN 26

RESULT 108
AF219075      73 bp  DNA      linear  GSS 17-APR-2000
LOCUS         AF219075 Human Homo sapiens genomic clone Nf1, genomic survey
DEFINITION    AF219075 Human Homo sapiens genomic clone Nf1, genomic survey
ACCESSION     AF219075.1 GI:7581521
KEYWORDS      GSS.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 73)
AUTHORS       Hamshire, M., Cross, S., Daniels, M., Lennon, G. and Brook, J.D.
TITLE         A transcript map of a 10-Mb region of chromosome 19: A source of
              genes for human disorders, including candidates for genes involved
              in asthma, heart defects, and eye disorders
              Genomics 63 (3), 425-429 (2000)
JOURNAL       20171383
MEDLINE       10704290
PUBMED        Contact: Hamshire M
              Institute of Genetics
              University of Nottingham
              Queen's Medical Center, Nottingham, NG7 2LT, United Kingdom
              Class: exon-trapped.
              Location/Qualifiers
                1..73
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                /clone="Nf1"
                /clone_id="Human"

FEATURES
Source
  1..73
  /organism="Homo sapiens"
  /mol_type="genomic DNA"
  /db_xref="taxon:9606"
  /clone="Nf1"
  /clone_id="Human"

ORIGIN
Query Match      66.7%; Score 12; DB 8; Length 73;
Best Local Similarity 83.3%; Pred. No. 2.4e+04;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY
1 GGGGUCCTCGAG 12
11:|||||
20 GGGGCTCTCGAG 31

RESULT 109
AA929340      94 bp  mRNA      linear  EST 23-APR-1998
LOCUS         AA929340 r1 Soares_thymus_2NDMT Mus musculus cDNA clone
DEFINITION    v241d10.r1 Soares_thymus_2NDMT Mus musculus cDNA clone
ACCESSION     AA929340
KEYWORDS      IMAGE:1329018 5' similar to TR:035449 C35449 HYPOTHETICAL 31.4 KD
SOURCE        EST.
              AA929340.1 GI:3078649
              Mus musculus (house mouse)
              Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

ORIGIN

```

```

REFERENCE
AUTHORS      1 (bases 1 to 94)
              Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
              Gettel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
              Schellenberg, K., Stepien, M., Tan, F., Underwood, K., Moore, B.,
              Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
              Waterston, R.
TITLE         The WashU-HMT Mouse EST Project
JOURNAL       Unpublished (1996)
COMMENT       Contact: Marra M/Mouse EST Project
              WashU-HMT Mouse EST Project
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: mouseest@watson.wustl.edu
              This clone is available royalty-free through LNL; contact the
              IMAGE Consortium (info@image.lnl.gov) for further information.
              MGI:68562
              Possible reversed clone: similarity on wrong strand
              Seq primer: -28ml3 rev2 ET from Amersham
              High quality sequence stop: 78.
              Location/Qualifiers
                1..94
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="IMAGE:1329018"
                /sex="male"
                /tissue_type="thymus"
                /dev_stage="4 weeks"
                /lab_host="DH10B"
                /clone_id="Soares_thymus_2NDMT"
                /note="Vector: pT73D-Pac (Pharmacia) with a modified
                polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
                was primed with a Not I - oligo(dT) primer (5',
                TGTTCCATCTGAGTGGAGCGCCGCTTTTCTTTTCTTTTCTTTTCTTTT
                3'); double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not I and cloned into the Not I
                and Eco RI sites of the modified pT73 vector. RNA
                provided by Dr. Bertrand Jordan. Library went through two
                rounds of normalization, and was constructed by Bento
                Soares and M. Fatima Bonaldo."

ORIGIN
Query Match      66.7%; Score 12; DB 1; Length 94;
Best Local Similarity 83.3%; Pred. No. 2.3e+04;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY
1 GGGGUCCTCGAG 12
11:|||||
58 GGGGCTCTCGAG 47

RESULT 110
BF374161      100 bp  mRNA      linear  EST 24-NOV-2000
LOCUS         BF374161 MRO-SN0040-250500-004-b07 SN0040 Homo sapiens cDNA, mRNA sequence.
DEFINITION    BF374161
ACCESSION     BF374161
KEYWORDS      EST.
              BF374161.1 GI:11336095
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 100)
AUTHORS       Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
              Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
              Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
              Brunstein, A., de Oliveira, P.S., Bucher, F., Jongeneel, C.V.,
              O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
              Simpson, A.J.
TITLE         Shotgun sequencing of the human transcriptome with ORF expressed

```



JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the PAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR0&ct2=MR0-SN0040-  
250500-004-b07&ct3=2000-05-25&ct4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 15  
High quality sequence stop: 100.

# FEATURES

source

1..100  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="SN0040"  
/note="Organ: stomach normal; Vector: puc18; Site\_1: Sma1;  
Site\_2: Sma1; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

# ORIGIN

Query Match 66.7%; Score 12; DB 2; Length 100;  
Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
||||:|||||  
45 GGGGTCCTGGAG 56

RESULT 111  
CF537121/c 101 bp mRNA linear EST 12-SEP-2003  
LOCUS UI-M-FY0-chg-o-13-0-UI.r1 NIH BMAP\_FY0 Mus musculus cDNA clone  
DEFINITION IMAGE:30535932 5', mRNA sequence.  
ACCESSION CF537121 GI:34589101  
VERSION CF537121.1  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 101)  
REFERENCE NIH-MGC http://ngc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
AUTHORS Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cga@bbs-remail.nih.gov  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
http://genome.uiowa.edu/distribution/mouse1.html  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP).

FEATURES  
source  
Seq primer: pYX-5.  
Location/Qualifiers  
1..101

# ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 101;  
Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
||||:|||||  
82 GGGGTCCTGGAG 71

RESULT 112  
CK387998/c 102 bp mRNA linear EST 29-DEC-2003  
LOCUS L0923G09-5 NIA Mouse Newborn Kidney cDNA library (Long) Mus  
DEFINITION CK387998  
musculus cDNA clone NIA:L0923G09 IMAGE:30002288 5', mRNA sequence.  
ACCESSION CK387998.1 GI:40377001  
VERSION CK387998.1  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 102)  
REFERENCE Piao Y., Ko N.T., Lim M.K. and Ko M.S.H.  
Construction of long-transcript enriched cDNA libraries from  
submicrogram amounts of total RNAs by a universal PCR amplification  
method  
JOURNAL Genome Res. 11 (9), 1553-1558 (2001)  
MEDLINE 21429098  
PUBMED 11544199  
COMMENT Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@lsun-grc.nia.nih.gov  
Plate: L0923 row: G column: 09  
Seq primer: M13 Reverse  
High quality sequence stop: 102  
POLYA=No.

FEATURES  
source  
1..102  
/organism="Mus musculus"  
/mol\_type="mRNA"  
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/db\_xref="taxon:10090"  
/clone="IMAGE:30535932"  
/tissue\_type="whole brain"  
/dev\_stage="embryo 13.5,14.5,16.5,17.5dpc"  
/lab\_host="MDH10B (T1 phage resistant)"  
/clone\_lib="NIH BMAP FY0"  
/note="Organ: Brain; Vector: pYX-Asc; Site\_1: EcoR I;  
Site\_2: Not I; The library was constructed according  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction, ligated  
with EcoR I adaptor, digested with NotI and then cloned  
directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is AGCAGACAG. This library was created for the University  
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,  
program coordinator."



ORIGIN rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 66.7%; Score 12; DB 1; Length 107;  
Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
||||:|||||  
DB 88 GGGGTCCTGGAG 99

## RESULT 115

AZ557012 110 bp DNA linear GSS 20-NOV-2000  
DEFINITION RPI-23-179N14.TV RPI-23 Mus musculus genomic clone  
ACCESSION RPI-23-179N14, genomic survey sequence.  
VERSION AZ557012  
KEYWORDS AZ557012.1 GI:11236832

SOURCE GSS.  
ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 110)  
Zhao, S., Nierman, W., Feldblum, T., Malek, J., Shatman, S., Akhtar, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P., and Frazer, C.M.  
Mouse BAC End Sequences from Library RPI-23

TITLE Unpublished (1999)  
COMMENT Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@igf.org

Clones are derived from the mouse BAC library RPI-23. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Reseach Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac/ends/mouse/bac\_end\_intro.html  
Plate: 179 row: N column: 14  
Seq primer: 17  
Class: BAC ends.

FEATURES  
source Location/Qualifiers

1..110  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="RPI-23-179N14"  
/sex="Female"  
/lab\_host="DH10B"  
/clone\_lib="RPI-23"  
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methyase. Site selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

## ORIGIN

Query Match 66.7%; Score 12; DB 8; Length 110;

Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
||||:|||||  
DB 5 GGGGTCCTGGAG 16

## RESULT 116

AM326734 116 bp mRNA linear EST 25-APR-2001  
LOCUS 19665 MARC 280V Bos taurus cDNA 5', mRNA sequence.  
DEFINITION AM326734  
ACCESSION AM326734.1 GI:6762655  
VERSION EST.  
KEYWORDS Bos taurus (cow)

SOURCE Bos taurus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

## REFERENCE

AUTHORS 1 (bases 1 to 116)  
Smith, T.P.L., Grose, W.M., Fekling, B.A., Roberts, A.J., Stone, R.T., Caeas, E., Wray, J.E., White, J., Cho, J., Fahrnkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perte, G., Holt, I., Karaycheva, S., Liang, F., Quackenbush, J. and Keefe, J.W.  
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)

## TITLE

JOURNAL MEDLINE  
PUBMED 11282978

COMMENT Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@meat.marc.usda.gov  
Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 20 and -mismatch 12 options.

PCR primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCAGTCAGCAGC  
Plate: 10 row: O column: 13  
Seq primer: ATTAGTGACACTAATG.

FEATURES  
source Location/Qualifiers

1..116  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 280V"  
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

## ORIGIN

Query Match 66.7%; Score 12; DB 2; Length 116;  
Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
||||:|||||  
DB 83 GGGGTCCTGGAG 94

## RESULT 117

COS49288 121 bp mRNA linear EST 01-SEP-2004  
LOCUS LYEST6835 Sea lamprey LyEST Petromyzon marinus cDNA, mRNA sequence.  
DEFINITION COS49288  
ACCESSION COS49288.1 GI:51797604  
VERSION EST.  
KEYWORDS Petromyzon marinus (sea lamprey)

SOURCE Petromyzon marinus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia; Petromyzontiformes; Petromyzontidae; Petromyzon.

Petromyzontiformes; Petromyzontidae; Petromyzon.

REFERENCE 1 (bases 1 to 121)  
 AUTHORS Pancer, Z., Mayer, W.E., Klein, J. and Cooper, M.D.  
 TITLE Prototypic T-cell receptor and CD4-like coreceptor expressed in lymphocytes of the agnathan sea lamprey  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 101, 13273-13278 (2004)  
 COMMENT Contact: Pancer, Zeev  
 The University of Alabama at Birmingham  
 378 Wallace Tumor Institute, 1530 Third Avenue, South, Birmingham, AL 35294-3300  
 Tel: 205-975-5812  
 Fax: 205-975-7218  
 Email: zpancer@uab.edu.

FEATURES  
 source Location/Qualifiers  
 1..121  
 /organism="Petromyzon marinus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7757"  
 /cell\_type="lymphocyte"  
 /dev\_stage="unstimulated larvae"  
 /clone\_lib="Sea lamprey LyEST"  
 /note="Vector: Lambda ZAP Express; lymphocyte mRNA ESTs from unstimulated larvae. All are from arrayed colonies from a directionally cloned cDNA library in Lambda ZAP Express (Stratagene). All are single pass 5' sequences."

ORIGIN  
 Query Match 66.7%; Score 12; DB 7; Length 121;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 |||:|||||  
 Db 107 GGGGTCTTGAG 118

RESULT 118  
 CD286354 123 bp mRNA linear EST 27-MAY-2003  
 LOCUS 11 K23.abd POE14 (Day\_14\_pregnant\_ovine\_endometrium) Ovis aries  
 DEFINITION cDNA, mRNA sequence.  
 ACCESSION CD286354  
 VERSION CD286354.1 GI:31084397  
 KEYWORDS EST.  
 SOURCE Ovis aries (sheep)  
 ORGANISM Ovis aries  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.  
 1 (bases 1 to 123)  
 Gray, C.A., Adelson, D.L. and Spencer, T.E.  
 Ovine ESTs  
 Unpublished (2003)  
 Contact: Thomas E. Spencer  
 Center for Animal Biotechnology and Genomics  
 Texas A&M University  
 Animal Science Dept., TAMU-2471, College Station, TX 77843-2471, USA  
 Tel: 9798454896  
 Fax: 9798622662  
 Email: tspancer@anrc.tamu.edu.

FEATURES  
 source Location/Qualifiers  
 1..123  
 /organism="Ovis aries"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9940"  
 /sex="female"  
 /tissue\_type="endometrium"  
 /dev\_stage="Day 14 pregnant"  
 /clone\_lib="POE14 (Day 14 pregnant ovine endometrium)"  
 /note="Organ: uterus; Vector: Triplex2; Site 1: EcoRI; Site 2: XhoI; Non-normalized library, sequenced 5' with Triplex2 primer (CTCCGAGATCTGACGAGC). Library constructed

ORIGIN  
 Query Match 66.7%; Score 12; DB 6; Length 123;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 |||:|||||  
 Db 49 GGGGTCTTGAG 38

RESULT 119  
 AM480318 128 bp mRNA linear EST 09-JUL-2000  
 LOCUS 30824 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.  
 DEFINITION AM480318  
 ACCESSION AM480318.1 GI:7050424  
 VERSION  
 KEYWORDS EST.  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 1 (bases 1 to 128)  
 Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Perrea, G., Sultana, R., Quackenbush, J. and Keel, J.W.  
 Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly  
 Mamm. Genome 13 (8), 475-478 (2002)  
 22213789  
 JOURNAL MEDLINE  
 PUBMED 12226715

COMMENT  
 Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@mail.marc.usda.gov  
 Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 20 and -mismatch 12 options.  
 PCR Primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCGAGTACGACG  
 Place: 17 row: K column: 1  
 Seq primer: ATTGAGTGACATATAG.  
 Location/Qualifiers  
 1..128  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9823"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 2P1G"  
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."

ORIGIN  
 Query Match 66.7%; Score 12; DB 2; Length 128;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 |||:|||||  
 Db 52 GGGGTCTTGAG 63

RESULT 120  
 AM385180 133 bp mRNA linear EST 04-FEB-2000  
 LOCUS PM1-HT0452-291299-001-C01 HT0452 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION

ACCESSION AM285180  
 VERSION AM385180.1 GI:6889839  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 133)  
 HCCP <http://www.ludwig.org.br/ORESTES>.  
 TITLE The FAPESP/LICR Human Cancer Genome Project  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PMlet2=PM1-HT0452-291299-001-c01&t3=1999-12-29&t4=1>)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 133.

FEATURES  
 Location/Qualifiers  
 1..133  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /def\_stage="Adult"  
 /clone\_lib="HT0452"  
 /note="Organ: head\_neck; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN  
 Query Match 66.7%; Score 12; DB 2; Length 133;  
 Best Local Similarity 83.3%; Pred. No. 2.3e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCCCCGAG 12  
 |||||  
 2 GGGGTCTCTGGAG 13

RESULT 121  
 AI280744 134 bp mRNA linear EST 21-DEC-1998  
 LOCUS GW07C10.X1 NCI\_CGAP\_uc3 Homo sapiens cDNA clone IMAGE:190386 3',  
 DEFINITION mRNA sequence.  
 ACCESSION AI280744  
 VERSION AI280744.1 GI:3918977  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 134)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the [www.a.g.e.consortium/LNL.ac](http://www.a.g.e.consortium/LNL.ac):  
[www-bio.llnl.gov/bdrrp/image/image.html](http://www-bio.llnl.gov/bdrrp/image/image.html)  
 Insert Length: 1474 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 119.

FEATURES  
 Location/Qualifiers  
 1..134  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1990386"  
 /tissue\_type="poorly-differentiated endometrial adenocarcinoma, 2 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP uc3"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NciI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.45 kb. Life Technologies catalog #: 11541-018"

ORIGIN  
 Query Match 66.7%; Score 12; DB 1; Length 134;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCCCCGAG 12  
 |||||  
 109 GGGGTCTCTGGAG 120

RESULT 122  
 AM358302 134 bp mRNA linear EST 25-APR-2001  
 LOCUS 42366 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.  
 DEFINITION AM358302  
 ACCESSION AM358302  
 VERSION AM358302.1 GI:6862308  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 134)  
 Smith,T.P.L., Grosee,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pettes,G., Holt,I., Karanycheva,S., Liang,F., Quackenbush,J. and Keele,J.W.  
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle  
 Genome Res. 11 (4), 626-630 (2001)

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED 11282978

COMMENT Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: [smith@email.marc.usda.gov](mailto:smith@email.marc.usda.gov)  
 Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 20 and -minmatch 12 options.  
 PCR primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCACAGTCACGACG  
 Plate: 22 row: N column: 9  
 Seq primer: ATTGAGTGACACTATG.  
 Location/Qualifiers  
 1..134  
 /organism="Bos taurus"  
 /mol\_type="mRNA"

/db\_xref="taxon:9913"  
 /issue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 3BOV"  
 /note="Vector: PCMV SPOR6; Site 1: NotI; Site 2: SalI;  
 library made from pooled tissue from marrow, alveolar  
 macrophage, ovary, fetal semitendinosus muscle, and fetal  
 longissimus muscle."

ORIGIN  
 Query Match 66.7%; Score 12; DB 2; Length 134;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 |||:|:|:|:|:|  
 Db 73 GGGGTCCTGGAG 84

RESULT 123  
 CA378150 135 bp mRNA linear EST 06-NOV-2002  
 LOCUS 65698 NCCWA 1RT Oncorhynchus mykiss cDNA clone 1RT42H16\_D\_D08 5',  
 DEFINITION mRNA sequence.  
 CA378150  
 VERSION CA378150.1 GI:24697751  
 KEYWORDS EST.  
 SOURCE Oncorhynchus mykiss (rainbow trout)  
 ORGANISM Oncorhynchus mykiss  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 1 (bases 1 to 135)  
 Rexroad, C.E., 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Brown, G.,  
 koop, B., Gah, S.A., Palti, Y., and Quackenbush, J.  
 Sequence analysis of a rainbow trout cDNA library and creation of a  
 gene index

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 CytoGenet. Genome Res. 102 (1-4), 347-354 (2003)  
 Contact: Rexroad CE  
 USDA, ARS, National Center for Cool and Cold Water Aquaculture  
 11876 Leetown Road, Kearneysville, WV 25430, USA  
 Tel: 304 724 8340 x2129  
 Fax: 304 725 0351  
 Email: crexroad@nccwa.ars.usda.gov  
 Single pass sequencing. Bases called with phred v0.020425.c and  
 trimmed with the aid of the trim\_al option. Vector identified by  
 cross match v0.990329.  
 Seq primer: AGCGGATACCAATTTCACACAGCA.

FEATURES

SOURCE  
 1..135  
 /organism="Oncorhynchus mykiss"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8022"  
 /clone="1RT42H16\_D\_D08"  
 /issue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="NCCWA 1RT"  
 /note="Vector: PCMV SPOR6; Site 1: NotI; Site 2: SalI;  
 library made from pooled tissue from brain, gill, liver,  
 spleen, muscle, and kidney."

ORIGIN  
 Query Match 66.7%; Score 12; DB 6; Length 135;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 |||:|:|:|:|:|  
 Db 22 GGGGTCCTGGAG 33

RESULT 124  
 CL965510

LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

CL965510 141 bp DNA linear GSS 21-SEP-2004  
 OaIFCC03107 Oryza sativa Express Library Oryza sativa (indica  
 cultivar-group) genomic, genomic survey sequence.  
 CL965510  
 AC965510.1 GI:52385704  
 GSS.  
 Oryza sativa (indica cultivar-group)  
 Oryza sativa (indica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriarthrodaceae; Oryzoideae; Oryza.  
 1 (bases 1 to 141)  
 Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,  
 Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,  
 Wong, G.K.S., Deng, X.W., and Wang, J.  
 An analysis of transcriptional regulation of the rice genome and  
 its comparison to Arabidopsis  
 Unpublished (2004)

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Contact: Chen Chen  
 Department of Bioinformatic  
 Beijing Institute of Genomics  
 Chinese Academy of Sciences, Beijing 101300, China  
 Tel: 86-10-80481559  
 Fax: 86-10-80488676  
 Email: chenchen@genomics.org.cn  
 Rice genomic sequence.  
 Class: exon-trapped.  
 Location/Qualifiers

FEATURES  
 source  
 1..141  
 /organism="Oryza sativa (indica cultivar-group)"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:39946"  
 /clone\_lib="Oryza sativa Express library"  
 /note="Oryza sativa exon trapped genomic sequences"

ORIGIN  
 Query Match 66.7%; Score 12; DB 9; Length 141;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 |||:|:|:|:|:|  
 Db 50 GGGGTCCTGGAG 61

RESULT 125  
 BB606528 143 bp mRNA linear EST 06-DEC-2000  
 LOCUS BB606528 RIKEN full-length enriched, 0 day neonate eyeball Mus  
 DEFINITION musculus cDNA clone E130102K01 5', mRNA sequence.  
 BB606528  
 ACCESSION BB606528.1 GI:11560388  
 VERSION EST.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Scuriongnathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 143)  
 Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T.,  
 Carninci, P., Hanagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T.,  
 Hodojima, Y., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kawai, J.,  
 Kojima, Y., Kono, H., Kusakabe, M., Matsuyama, T., Miyazaki, A.,  
 Nakamura, M., Nihei, K., Nomura, K., Numazaki, R., Okazaki, Y.,  
 Okido, T., Owa, C., Sakai, C., Sakai, K., Sasaki, D., Sato, K.,  
 Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y.,  
 Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T.,  
 Watabiki, A., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshiki, A.,  
 Muramatsu, M., and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Aizawa, K. et al. 2000)  
 Unpublished (2000)  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute



Class: BAC ends  
High quality sequence stop: 147.  
Location/Qualifiers  
1. 147

FEATURES  
source  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_142J06"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: PTABAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

ORIGIN  
Query Match 66.7%; Score 12; DB 9; Length 147;  
Best Local Similarity 91.7%; Pred. No. 2.2e+04;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 7 CUGAGNNNNNN 18  
Db 72 CTGAGNNNNNN 61

RESULT 128  
LOCUS CG918034/c  
DEFINITION CH240\_136J13.TJ CHORI-240 Bos taurus genomic clone CH240\_136J13, genomic survey sequence.  
ACCESSION CG918034  
VERSION CG918034.1 GI:39777717  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 150)  
Costa, J.N., Mota, M. and Caetano, A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library CHORI-240  
Unpublished (2003)  
Other\_GSS: CH240\_136J13.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/S Norte, Brasilia-DF C.P. 02372-70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acetano@cena.gen.br  
Clones are derived from the bovine BAC library CHORI-240 (<http://www.chori.org/bacpac/bovine240.htm>).  
Bases with quality value below 20 were masked with 'N'.  
Bases shown have phred quality value equal to or higher than 20.  
Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/ordering/information.htm>).  
This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia with financing from Conselho Nacional de Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 136 row: J column: 13  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 150.  
Location/Qualifiers  
1. 150  
/organism="Bos taurus"  
/mol\_type="genomic DNA"

FEATURES  
source

ORIGIN  
Query Match 66.7%; Score 12; DB 9; Length 150;  
Best Local Similarity 91.7%; Pred. No. 2.2e+04;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 7 CUGAGNNNNNN 18  
Db 132 CTGAGNNNNNN 121

RESULT 129  
LOCUS BZ280016/c  
DEFINITION CH230-480K1.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone CH230-480K1, genomic survey sequence.  
ACCESSION BZ280016  
VERSION BZ280016.1 GI:24006179  
KEYWORDS GSS.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.  
1 (bases 1 to 151)  
Zhao, S., Shetty, V., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.  
Rat BAC End Sequences from Library CHORI-230 MboI segment Unpublished (1999)  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the rat BAC library CHORI-230 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/ordering/information.htm>). BAC end page: [http://www.tigr.org/cdb/bac\\_ends/rat/bac\\_end\\_intro.html](http://www.tigr.org/cdb/bac_ends/rat/bac_end_intro.html)  
Plate: 480 row: K column: 1  
Seq primer: SP6  
Class: BAC ends  
Location/Qualifiers  
1. 151  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/strain="BN/SnHsd/MCW"  
/db\_xref="taxon:10116"  
/clone="CH230-480K1"  
/sex="Female"  
/cell\_type="Brain"  
/clone\_lib="CHORI-230 Segment 2"  
/note="Vector: PTABAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source

ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 151;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;



QY 1 GGGGUCUGAG 12  
 |||||:  
 Db 98 GGGGTCCTGAG 87

RESULT 130  
 CE594318/c  
 LOCUS  
 DEFINITION tigr-gss-17000366530020 Dog library Canis familiaris genomic,  
 genomic survey sequence.

ACCESSION CE594318  
 VERSION CE594318.1 GI:36911099  
 KEYWORDS GSS  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris

REFERENCE  
 AUTHORS  
 1 (bases 1 to 151)  
 Kirkenes, R.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
 Ruch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M., and  
 Venter, J.C.

TITLE The dog genome: survey sequencing and comparative analysis  
 JOURNAL Science 301 (5641), 1898-1903 (2003)  
 MEDLINE 22875432  
 PUBMED 14512627

COMMENT

The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirkenes@tigr.org  
 Class: shotgun.

FEATURES  
 source Location/Qualifiers

1..151  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"

Query Match 66.7%; Score 12; DB 9; Length 151;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
 |||||:  
 Db 89 GGGGTCCTGAG 78

RESULT 131  
 CB482046/c  
 LOCUS  
 DEFINITION jn86.C03.f jns Sue scrofa cDNA 5', mRNA sequence.  
 ACCESSION CB482046  
 VERSION CB482046.1 GI:29288432  
 KEYWORDS EST  
 SOURCE Sue scrofa (pig)  
 ORGANISM Sue scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Sequence analysis of African swine fever virus infected and  
 non-infected porcine macrophage cDNA libraries  
 Unpublished (2003)  
 Contact: Neilan JG  
 Plum Island Animal Disease Center  
 US Department of Agriculture, Agricultural Research Service

PO Box 848, Greenport, NY 11944-848, USA  
 Tel: 631 323 3133  
 Fax: 631 323 3044

Email: jneilan@iadc.ars.usda.gov  
 Single pass sequencing. Bases called with phred v0.020425.c and  
 trimmed with the aid of the trim alt option. Vector identified by  
 cross match v0.990329 and Lucy v1.17p.

Seq primer: M13 Forward.

FEATURES  
 source Location/Qualifiers

1..152  
 /organism="Sue scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9623"  
 /tissue\_type="lymphoid"  
 /cell\_type="macrophage"  
 /lab\_host="DH10B"  
 /clone\_lib="jns"  
 /note="Vector: pSPOR1; Site 1: NotI; Site 2: SalI;  
 library made from pools of polyA selected RNA. Macrophages  
 were derived from peripheral blood mononuclear cells  
 cultured for 48 hrs on plastic in the presence of 30% L929  
 supernatant."

ORIGIN

Query Match 66.7%; Score 12; DB 6; Length 152;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
 |||||:  
 Db 141 GGGGTCCTGAG 130

RESULT 132  
 CG677253/c  
 LOCUS  
 DEFINITION tmf1008 tmf Aegilops tauschii genomic clone tmf17L06, genomic  
 survey sequence.

ACCESSION CG677253  
 VERSION CG677253.1 GI:37506320  
 KEYWORDS GSS  
 SOURCE Aegilops tauschii  
 ORGANISM Aegilops tauschii

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Aegilops.  
 1 (bases 1 to 155)  
 Li, W., Zhang, P., Fellner, J., Friebe, B. and Gill, B.S.

Sequence composition, organization and evolution of a basic  
 Triticeae genome of the grass family  
 Unpublished (2003)  
 Contact: Li, W

Dr. Bikram S. Gill's Lab  
 Wheat Genetics Resource Center, Kansas State University  
 4024 Throckmorton, Manhattan, KS 66506-5502, USA  
 Tel: 785-532-1108  
 Fax: 785-532-5692  
 Email: wli@ksu.edu

Seq primer: T7  
 Class: sheared ends.

FEATURES  
 source Location/Qualifiers

1..155  
 /organism="Aegilops tauschii"  
 /mol\_type="genomic DNA"  
 /strain="AL 8/78"  
 /db\_xref="taxon:37682"  
 /clone="tmf17L06"  
 /tissue\_type="leaves"  
 /dev\_stage="shoot"  
 /lab\_host="E. coli strain DH5alpha"  
 /clone\_lib="tmf"  
 /note="Vector: PCR 4Blunt-TOP; 0.8-1.2 kb methylation  
 filtered genomic DNA library"

ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 155;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
||||:|||||  
78 GGGGCTCTGAG 67

RESULT 133  
CL303190 155 bp mRNA linear GSS 30-JUN-2004  
LOCUS CL303190/c  
DEFINITION P005G12 GGTG Gene Trap Library GV08C05 Mus musculus cDNA clone  
P005G12, mRNA sequence.  
CL303190  
VERSION CL303190.1 GI:42744019  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Hansen, J., Floss, T., van Sloun, P., Fuchsbauer, E.M., Vauti, F.,  
Arnold, H.H., Schultgen, F., Mursel, W., Von Melchner, H. and Ruiz, P.  
A large-scale, gene-driven mutagenesis approach for the functional  
analysis of the mouse genome  
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)  
22810117  
12904583  
COMMENT Contact: GGTC  
German Genetrap Consortium (GGTC)  
Email: info@genetrap.de  
FlpRosaBetageo gene trap. Sequence tag generated by 5'RACE.  
Additional sequence information can be found at:  
'http://genetrap.gsf.de/project/web\_new/database/result\_clone.html?clone\_id=P005G12' ES cell line harboring insertion mutation of  
target gene is available at:  
'http://genetrap.gsf.de/project/web\_new/order\_clones/howtoorder.htm'  
1' Inhouse Sequence Identifier: 13210  
Class: Gene Trap

FEATURES  
source location/Qualifiers  
1..155  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129 Sv"  
/db\_xref="taxon:10090"  
/clone="P005G12"  
/sex="Male"  
/cell\_type="Embryonic stem cell"  
/cell\_line="ES cells [C57BL/6J x 129Sv/SvEvTac] F1"  
/clone\_id="GGTC Gene Trap Library GV08C05"  
/note="Vector: FlpRosaBetageo"

ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 155;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
||||:|||||  
60 GGGGCTCTGAG 49

RESULT 134  
CL607849 158 bp DNA linear GSS 17-JUN-2004  
LOCUS CL607849/c  
DEFINITION CH240\_174109 TJ CHORI-240 Bos taurus genomic clone CH240\_174109,  
genomic survey sequence.  
CL607849  
VERSION CL607849.1 GI:48875881  
KEYWORDS GSS.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 158)  
Costa, J.N., Mota, M., and Caetano, A.R.  
Brazil's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240  
Unpublished (2003)  
Other GSSs: CH240\_174109.TV  
Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, FinaI Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acaetano@cargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have Phred quality value equal to or higher than 20.  
Bases with quality value below 20 were masked with 'N'.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 174 row: 1 column: 09  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 158.

FEATURES  
source location/Qualifiers  
1..158  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_174109"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_id="CHORI-240"  
/note="Vector: pIRBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull l1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 158;  
Best Local Similarity 91.7%; Pred. No. 2.2e+04;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGNNNNN 18  
||||:|||||  
149 CTGAGNNNNN 138

RESULT 135  
CR081247 160 bp DNA linear GSS 05-JUL-2004  
LOCUS CR081247  
DEFINITION Reverse strand read from insert in 3'HPRT insertion targeting and  
chromosome engineering clone MHP68114, genomic survey sequence.  
CR081247  
VERSION CR081247.1 GI:49814836  
KEYWORDS GSS; genome survey sequence; MICE.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,

Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,  
Rogers, J. and Bradley, A.

TITLE Direct Submission  
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. <http://www.sanger.ac.uk/MICER>

FEATURES  
SOURCE Location/Qualifiers

1..160  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="MHPP68114"  
/clone\_lib="MHPP"

## ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 160;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUGAG 12  
||||:|||||  
DB 42 GGGGTCCTGGAG 53

RESULT 136  
BPE61925/c 161 bp mRNA linear EST 25-APR-2001  
LOCUS 275345 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.  
DEFINITION BPE61925  
ACCESSION BPE61925  
VERSION BPE61925.1 GI:11917055  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.

REFERENCE 1 (bases 1 to 161)  
AUTHORS Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,  
Cavaa, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,  
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,  
Chitko-McKown, C.G., Perte, G., Holt, I., Karaycheva, S., Liang, F.,  
Quackenbush, J. and Keefe, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA  
libraries and construction of a gene index for cattle  
Genome Res. 11 (4), 626-630 (2001)

JOURNAL 11282978  
MEDLINE  
PUBMED  
COMMENT Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: [smith@email.marc.usda.gov](mailto:smith@email.marc.usda.gov)  
Single pass sequencing. Bases called and alt crimed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -minmatch 12 options.

PCR primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACGTCACGACG  
Plate: 64 row: D column: 4  
Seq primer: ATTAGGACACTATAG.

FEATURES  
SOURCE Location/Qualifiers

1..161  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 3BOV"  
/note="Vector: PCMV SPORT6; Site\_1: NotI; Site\_2: SalI;  
Library made from pooled tissue from marrow, alveolar  
macrophage, ovary, fetal semitendoneous muscle, and fetal  
longissimus muscle."

ORIGIN

Query Match 66.7%; Score 12; DB 2; Length 161;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUGAG 12  
||||:|||||  
DB 86 GGGGTCCTGGAG 75

RESULT 137  
AM848479/c 163 bp mRNA linear EST 19-MAY-2000  
LOCUS IL3-CT0214-170200-006-D08 CT0214 Homo sapiens cDNA, mRNA sequence.  
DEFINITION AM848479  
ACCESSION AM848479  
VERSION AM848479.1 GI:7943996  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 163)  
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

## COMMENT

JOURNAL 10737800  
MEDLINE  
PUBMED  
CONTACT: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the PAPSP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l=il3-ct0214-170>)  
200-006-D08&t3=2000-02-17&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 163.

FEATURES  
SOURCE Location/Qualifiers

1..163  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="CT0214"  
/note="Organ: colon; Vector: puc18; Site\_1: SmaI; Site\_2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No.  
196,716 - Ludwig Institute for Cancer Research) profiles  
into the puc 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

## ORIGIN

Query Match 66.7%; Score 12; DB 2; Length 163;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUGAG 12  
||||:|||||  
DB 160 GGGGTCCTGGAG 149

RESULT 138

BB569306 168 bp, cDNA, 10 days embryo Mus musculus  
 BB569306 RIKEN full-length cDNA, 10 days embryo Mus musculus  
 cDNA clone 3426406E15 5', mRNA sequence.  
 BB569306  
 BB569306.1 GI:11460214  
 EST.  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 168)  
 Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T.,  
 Carninci, P., Hayashizaki, T., Hayatsu, N., Hiroaka, T., Hirozane, T.,  
 Hodoayama, Y., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kawai, J.,  
 Kojima, Y., Komoto, H., Kusakabe, M., Matsuyama, T., Miyazaki, A.,  
 Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y.,  
 Okido, T., Owa, C., Sakai, C., Sakai, K., Sasaki, D., Sato, K.,  
 Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y.,  
 Suzuki, H., Tagawa, A., Takanashi, F., Tanaka, T., Toyota, T.,  
 Watanishi, A., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshiki, A.,  
 Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Aizawa, K. et al. 2000)  
 Unpublished (2000)  
 Contact: Yoshinide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Saitama-cho, Tsukuba-Ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagoka, S.,  
 Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Thermosensitization and thermoactivation of thermolabile enzymes by  
 formalase and its application for the synthesis of full length  
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
 Itoh, M., Katsunari, T., Akiyama, S., Shibata, K., Izawa, M., Kawai, J.,  
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,  
 Okazaki, Y. and Hayashizaki, Y.  
 Automated filtration-based high-throughput plasmid preparation  
 system. Genome Res. 9 (5), 463-470 (1999)  
 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
 19-44 (1999)  
 Please visit our web site (http://genome.riken.go.jp) for  
 further details

Location/Qualifiers  
1. .168

```

/organism="Mus musculus"
/mol_type="cDNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="3426406E15"
/sex="mixed"
/dev_stage="10 days embryo"
/lab_host="MDH10B"
/clone_lib="RIKEN full-length enriched, 10 days embryo"
/name="Site 1: Salt; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGGAGAGAGAGATCCAAAGAGCTCTTTTTTTTTTTTTN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGGAGAGAGATTCGACGTATAATTAAATTAATCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pluescript KS(+) after bulk excision from Lambda

```

[illegible]

### Source

```

/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D03A06"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN"
/note="Vector: pBluscript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

```

Query Match	66.7%	Score 12;	DB 6;	Length 171;
Best Local Similarity	83.3%	Pred. NO. 2.2e+04;		
Matches 10; Conservative	2;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 GGGGUCCTUGAG 12  
|||:|:|  
Db 57 GGGGTCCTGGAG 46

RESULT 140

LOCUS	171 bp	DNA	linear	GSS 26-SRP-2003
DEFINITION	C8350113	tigr-gss-dog-1700033418375	Dog	Library Canis familiaris genomic,
		genomic survey sequence.		

ACCESSION	CE350113
VERSION	CE350113.1
	GI:36184115

SOURCE	Canis familiaris (dog)
ORGANISM	Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 171)  
AUTHORS Kirkness E.F., Rafni, V., Halpern, A.L., Levy, S., Remington, K., Ruesch, D.B., Delcher, A.L., Fop, M., Wang, W., Fraser, C.M. and Venter, J.C.  
TITLE The dog genome: survey sequencing and comparative analysis  
JOURNAL Science 301 (5641), 1898-1903 (2003)  
MEDLINE 22875432  
PUBMED 14512627  
COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org  
Class: Shotgun.  
FEATURES  
source 1..171  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"  
ORIGIN  
Query Match 66.7%; Score 12; DB 9; Length 171;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 110 GGGGTCCTGGAG 121  
RESULT 141  
LOCUS CD557019 172 bp mRNA linear EST 11-JUN-2003  
DEFINITION AGNCOURT\_14400763 NIH\_MGC\_179 Homo sapiens cDNA clone  
IMAGE:30392397 5', mRNA sequence.  
ACCESSION CD557019  
VERSION CD557019.1 GI:31583087  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 172)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
CDNA Library Preparation: Invitrogen Corp  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov  
Plate: NDAM467 row: j column: 22  
High quality sequence start: 4  
High quality sequence stop: 172.  
Location/Qualifiers  
1..172  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
FEATURES  
source 1..172  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 66.7%; Score 12; DB 9; Length 171;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

/clone="IMAGE:30392397"  
/issue\_type="Pituitary"  
/lab\_host="DH10B-Ton A ( T1 and T5 phage resistances)"  
/clone\_lib="NIH\_MGC\_179"  
/note="Organ: brain; Vector: pCMV-Sport6.1; Site 1: EcoRV  
(destroyed); Site 2: NotI; Library is oligo-dT primed and  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.1 kb. Library was  
constructed by (Invitrogen). Note: this is a NIH\_MGC  
Library."  
ORIGIN  
Query Match 66.7%; Score 12; DB 6; Length 172;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 44 GGGGTCCTGGAG 55  
RESULT 142  
LOCUS CD519554 173 bp mRNA linear EST 06-JUN-2003  
DEFINITION AGNCOURT\_14369178 NIH\_MGC\_181 Homo sapiens cDNA clone  
IMAGE:30356597 5', mRNA sequence.  
ACCESSION CD519554  
VERSION CD519554.1 GI:31451296  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 173)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
CDNA Library Preparation: Invitrogen Corp  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov  
Plate: NDAM478 row: j column: 22  
High quality sequence start: 4  
High quality sequence stop: 173.  
Location/Qualifiers  
1..173  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30396597"  
/issue\_type="White Matter"  
/dev\_stage="Unknown"  
/lab\_host="DH10B-Ton A ( T1 and T5 phage resistances)"  
/clone\_lib="NIH\_MGC\_181"  
/note="Vector: pCMV-Sport6.1; Site 1: NotI; Site 2: EcoRV  
(destroyed); Library is oligo-dT primed and directionally  
cloned (EcoRV site is destroyed upon cloning). Average  
insert size 1.42 kb. Library was constructed by  
(Invitrogen). Note: this is a NIH\_MGC Library."  
ORIGIN  
Query Match 66.7%; Score 12; DB 6; Length 173;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;



Query Match 66.7%; Score 12; DB 5; Length 174;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
 |||||:  
 Db 130 GGGGTCCTGGAG 141

RESULT 145  
 CL303253 174 bp mRNA linear GSS 30-JUN-2004  
 LOCUS P005A07 GGTC Gene Trap Library GV08C05 Mus musculus cDNA clone  
 DEFINITION P005A07, mRNA sequence.  
 ACCESSION CL303253  
 VERSION CL303253.1 GI:42744082  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Hansen, J., Flores, T., van Sloun, P., Fuchsbauer, E.M., Vauti, F.,  
 Arnold, H.H., Schnitgen, F., Mursli, W., Von Melchner, H. and Ruiz, P.  
 A large-scale, gene-driven mutagenesis approach for the functional  
 analysis of the mouse genome  
 Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)  
 JOURNAL MEDLINE 12904583  
 PUBMED 12904583

COMMENT Contact: GGTC  
 German Genetrap Consortium (GGTC)  
 Email: info@genetrap.de  
 FliProSAbetaGeo gene trap. Sequence tag generated by 5'RACE.  
 Additional sequence information can be found at:  
 'http://genetrap.gsf.de/project/web\_new/database/result\_clone.html?clone\_id=P005A07'. ES cell line harboring insertion mutation of target gene is available at:  
 'http://genetrap.gsf.de/project/web\_new/order\_clones/howtoorder.htm'. Inhouse Sequence Identifier: 13255  
 Class: Gene Trap.  
 Location/Qualifiers  
 1..174  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129 Sv"  
 /db\_xref="taxon:10090"  
 /clone="P005A07"  
 /sex="Male"  
 /cell\_type="Embryonic stem cell"  
 /cell\_line="ES cells [C57BL/6J x 129Sv/SvEvTac] F1"  
 /clone\_lib="GGTC Gene Trap Library GV08C05"  
 /note="Vector: FliProSAbetaGeo"

ORIGIN  
 Query Match 66.7%; Score 12; DB 9; Length 174;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
 |||||:  
 Db 79 GGGGTCCTGGAG 68

RESULT 146  
 BE926972 175 bp mRNA linear EST 02-OCT-2000  
 LOCUS RCO-CN0026-300800-012-e10 CN0026 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION BE926972  
 ACCESSION BE926972.1 GI:10453152  
 VERSION BE926972.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 175)  
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
 Goldman, G.H., Carvalho, A.F., Matukuma, A., Bata, G.S., Simpson, D.H.,  
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.J.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000).  
 JOURNAL MEDLINE 20202663  
 PUBMED 10737800

COMMENT Contact: Simpson A.J.J.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the PAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=at2-RCO-CN0026-300  
 800-012-e10&t3=2000-08-30&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 16  
 High quality sequence stop: 175.  
 Location/Qualifiers  
 1..175  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="CN0026"  
 /note="Organ: colon normal; Vector: puc18; Site\_1: SmaI;  
 Site\_2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

ORIGIN  
 Query Match 66.7%; Score 12; DB 2; Length 175;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
 |||||:  
 Db 90 GGGGTCCTGGAG 79

RESULT 147  
 T20038 175 bp mRNA linear EST 28-NOV-1994  
 LOCUS B300R Heart Homo sapiens cDNA clone B300, mRNA sequence.  
 DEFINITION T20038  
 ACCESSION T20038  
 VERSION T20038.1 GI:597783  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 175)  
 Ilew, C.C., Hwang, D.M., Fung, Y.W., Laurensen, C., Cukerman, E.,  
 Teui, S. and Lee, C.Y.  
 A catalogue of genes in the cardiovascular system as identified by  
 expressed sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 91, 10645-10649 (1994)  
 JOURNAL MEDLINE 95024171  
 PUBMED 7938007

COMMENT Other ESTs: B300F  
Contact: Ilev CC  
Brigham and Women's Hospital  
Harvard Medical School  
75 Francis St., Boston, MA 02115, USA  
Tel: 6177328915  
Fax: 6179750995  
Email: cleveland@bwh.harvard.edu  
Seq primer: GACACGACCACTGGTATG.  
Location/Qualifiers

FEATURES  
source  
1..175  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="B300"  
/lab\_host="E.coli Y1090"  
/clone\_1lb="Heart"  
/note="Vector: Lambda gtl1, Site\_1: EcoRI, Site\_2: EcoRI"

ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 175;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUCUGAG 12  
||||:|||||  
50 GGGGTCTCTGGAG 61

Db

RESULT 148  
LOCUS B0348169 176 bp mRNA linear EST 20-MAY-2002  
DEFINITION RC-HT0295-141199-011-e06 HT0295 Homo sapiens cDNA, mRNA sequence.  
ACCESSION B0348169  
VERSION B0348169.1 GI:21012225  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 176)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,  
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, São Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC0&t2=RC0-HT0295-  
141199-011-e06&t3=1999-11-14&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 86  
High quality sequence stop: 121.  
Location/Qualifiers  
1..176  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"

FEATURES  
source

COMMENT /clone\_1lb="HT0295"  
/note="Organ: head neck; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESMS PCR (U.S. Letters Patent application  
No.196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

ORIGIN

Query Match 66.7%; Score 12; DB 5; Length 176;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUCUGAG 12  
||||:|||||  
78 GGGGTCTCTGGAG 67

Db

RESULT 149  
LOCUS CE745681 176 bp DNA linear GSS 30-SEP-2003  
DEFINITION tigr-gss-dog-17000369548879 Dog library Canis familiaris genomic.  
ACCESSION CE745681  
VERSION CE745681.1 GI:37086028  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
1 (bases 1 to 179)  
Kirkness, E.F., Batina, V., Halpern, A.L., Levy, S., Remington, K.,  
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
Venter, J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)  
22875432  
14512627  
Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org  
Classes: Shotgun.  
Location/Qualifiers  
1..179  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_1lb="Dog library"  
/note="Site 1: BstXI; Libraries were prepared from  
peripheral blood"

ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 179;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUCUGAG 12  
||||:|||||  
66 GGGGTCTCTGGAG 77

Db

RESULT 150  
LOCUS AJ463066 180 bp mRNA linear EST 24-MAY-2002  
DEFINITION AJ463066 S00002 Hordeum vulgare subsp. vulgare cDNA clone  
S0000200024F08FL, mRNA sequence.  
ACCESSION AJ463066



VERSION AJ463066.1 GI:21061986  
 KEYWORDS EST.  
 SOURCE Hordeum vulgare subsp. vulgare  
 ORGANISM Hordeum vulgare subsp. vulgare  
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Hordeum.  
 REFERENCE 1 (bases 1 to 180)  
 AUTHORS Saren,A.-M., Tanskainen,J., Paulin,L. and Schulman,A.H.  
 TITLE Barley EST<sup>8</sup>  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Schulman AH  
 Institute of Biotechnology  
 University of Helsinki  
 P.O.Box 56 (Valkinkuuri 6A), University of Helsinki FIN-00014,  
 Finland.  
 FEATURES  
 source 1..180  
 Location/Qualifiers  
 /organism="Hordeum vulgare subsp. vulgare"  
 /mol\_type="mRNA"  
 /cultivar="Saana"  
 /sub\_species="vulgare"  
 /db\_xref="taxon:112509"  
 /clone="S0000200024F08F1"  
 /dev\_stage="Embryo"  
 /clone\_idb="S00002"  
 /note="1 day after pollination"  
 ORIGIN  
 Query Match 66.7%; Score 12; DB 1; Length 180;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTGGAG 12  
 |||||:  
 DB 63 GGGGCTCTGGAG 52  
 |||||:  
 RESULT 151  
 BG062863 182 bp mRNA linear EST 10-JUN-2003  
 LOCUS L0958H12-5 NIA Mouse Newborn Kidney cDNA Library2 (Short) Mus  
 DEFINITION musculus cDNA clone L0958H12 5', mRNA sequence.  
 ACCESSION BG062863  
 VERSION BG062863.2 GI:31577341  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 182)  
 AUTHORS Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.  
 TITLE Construction of long-transcript enriched cDNA libraries from  
 submicrogram amounts of total RNAs by a universal PCR amplification  
 method  
 JOURNAL Genome Res. 11 (9), 1553-1558 (2001)  
 MEDLINE 21429098  
 PUBMED 11544199  
 COMMENT On Jan 25, 2001 this sequence version replaced gi:12533767.  
 Other ESTs: L0958H12-3  
 Contact: George J. Kargul  
 Laboratory of Genetics  
 National Institute on Aging/National Institutes of Health  
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
 Email: cdna@igun.grc.nia.nih.gov  
 niaEST (http://igun.grc.nia.nih.gov/cDNA/cDNA.html)  
 Plate: L0958 row: H column: 12  
 Seq primer: -21M3 Reverse  
 High quality sequence stop: 192  
 POLYA=No.  
 FEATURES  
 source 1..182  
 Location/Qualifiers  
 /organism="Mus musculus"

/mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="niaEST:L0958H12-5"  
 /db\_xref="taxon:10090"  
 /clone="L0958H12"  
 /issue\_type="Newborn kidney"  
 /dev\_stage="Newborn"  
 /lab\_host="DH10B"  
 /clone\_idb="NIA Mouse Newborn Kidney cDNA Library2  
 (Short)"  
 /note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:  
 NotI; Mouse cDNA project by the Laboratory of Genetics,  
 National Institute on Aging (NIA), Intramural Research  
 Program, NIH (http://igun.grc.nia.nih.gov/cDNA). This is  
 a short-transcript enriched cDNA library (Ref. Genome Res.  
 11: 1553-1558 (2001). [PMID: 11544199]). In brief,  
 double-stranded cDNAs were synthesized with an Oligo (dT)  
 primer (Invitrogen: 5'-  
 pGACTACTTCAGATCGGAGCGCCCTTTT-3') from 26  
 ug of total RNA, created with T4 DNA polymerase, and  
 purified by ethanol-precipitation. The cDNAs were ligated  
 to lone-linker L1-SalI, purified by phenol/chloroform, and  
 separated from free linkers by Centricon 100. Then, the  
 cDNAs were amplified by long-range high fidelity PCR using  
 Ex Taq polymerase (Takara) with a primer SalI-L. The  
 products were purified by phenol/chloroform and Centricon  
 100. The cDNAs were digested with SalI and NotI enzymes  
 and cloned into SalI/NotI site of pSPORT1 plasmid vector.  
 The DH10B E. coli host was transformed with the ligation  
 mixture by the standard chemical method. The average  
 insert size is about 1.5 kb. The library was constructed  
 by Yulan Piao(NIA)."  
 ORIGIN  
 Query Match 66.7%; Score 12; DB 4; Length 182;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCCTGGAG 12  
 |||||:  
 DB 141 GGGGCTCTGGAG 152  
 |||||:  
 RESULT 152  
 BW183955 182 bp mRNA linear EST 05-NOV-2002  
 LOCUS BW183955 Nori Satoh unpublished cDNA library, heart Ciona  
 DEFINITION intestinalis cDNA clone rc1hc001m03 3', mRNA sequence.  
 ACCESSION BW183955  
 VERSION BW183955.1 GI:24574216  
 KEYWORDS EST.  
 SOURCE Ciona intestinalis  
 ORGANISM Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
 Phlebobranchia; Cionidae; Ciona.  
 REFERENCE 1 (bases 1 to 182)  
 AUTHORS Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.  
 TITLE Expressed genes in Ciona intestinalis (2002c)  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Nori Satoh  
 Department of Zoology  
 Kyoto University  
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
 Tel: 81-75-753-4081  
 Fax: 81-75-705-1113  
 Email: satoh@ascidian.zool.kyoto-u.ac.jp.  
 FEATURES  
 source 1..182  
 Location/Qualifiers  
 /organism="Ciona intestinalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7719"  
 /clone="rc1hc001m03"  
 /issue\_type="heart"



## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hullman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, P., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE  
JOURNAL  
COMMENT

The Mashu-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu

Insert Size: 1066  
High quality sequence stops: 118  
Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert Length: 1066 Std Error: 0.00  
Seq primer: M13Rpl

High quality sequence stop: 118.

## FEATURES

## source

Location/Qualifiers

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1..185
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3830487"
/db_xref="taxon:9606"
/clone="IMAGE:192271"
/sex="Male"
/dev_stage="55-year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares adult brain N294HB5Y"
/note="Organ: brain; Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M. Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."
```

## ORIGIN

## Query Match

Best Local Similarity 83.3%; Score 12; DB 7; Length 185;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGGAG 12  
||||:|||||

Db 38 GGGGTCTCTGGAG 27

## RESULT 156

## BB281821

186 bp

mRNA

linear

EST 01-AUG-2000

## DEFINITION

## BB281821

BB281821 RIKEN full-length enriched, adult retina Mus musculus cDNA

## ACCESSION

BB281821

## VERSION

BB281821.1 GI:8982270

EST.

## KEYWORDS

Mus musculus (house mouse)

## SOURCE

Mus musculus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS

1 (bases 1 to 186)

Komno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kodaira, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saico, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toyota, T., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yamashita, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

TITLE  
JOURNAL  
COMMENT

RIKEN Mouse ESTs (Komno, H., et al.)  
Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216

Email: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/  
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Thermolabile and thermolabile activation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh, M., Kikuchi, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

## FEATURES

## source

Location/Qualifiers

```
1..186
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A93003K16"
/tissue_type="retina"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult retina"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATCTTCGACTTATTAATAATATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda PUC I. -Retina RNA was provided by Stefano Guarnieri, Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA, whose assistance we gratefully acknowledge."
```

## ORIGIN

## Query Match

Best Local Similarity 83.3%; Score 12; DB 2; Length 186;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 |||||:|||||  
 Db 102 GGGGTCCTGGAG 113

RESULT 157  
 CE739078 188 bp DNA linear GSS 30-SEP-2003  
 LOCUS tigr-gss-dog-17000330307476 Dog library Canis familiaris genomic,  
 DEFINITION genomic survey sequence.  
 ACCESSION CE739078  
 VERSION CE739078.1 GI:37079340  
 KEYWORDS GSS.  
 SOURCE  
 ORGANISM Canis familiaris (dog)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 1 (bases 1 to 188)  
 Kirchner,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
 Ruesch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
 Venter,J.C.  
 The dog genome: survey sequencing and comparative analysis  
 Science 301 (5641), 1898-1903 (2003)  
 14512627  
 Contact: Kirchner EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirchner@tigr.org  
 Class: shotgun.

FEATURES  
 source location/Qualifiers  
 1..188  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"

ORIGIN  
 Query Match 66.7%; Score 12; DB 9; Length 188;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 |||||:|||||  
 Db 1 GGGGTCCTGGAG 12

RESULT 158  
 CD016191 189 bp mRNA linear EST 07-MAY-2003  
 LOCUS NCBI 029 C01 F NCXI (NsF Xylem Compression wood Inclined) Pinus  
 DEFINITION taeda cDNA clone NCXI\_029\_C01 5', mRNA sequence.  
 ACCESSION CD016191  
 VERSION CD016191.1 GI:30354841  
 KEYWORDS EST.  
 SOURCE Pinus taeda (loblolly pine)  
 ORGANISM Pinus taeda  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
 1 (bases 1 to 189)  
 Sederoff,R.  
 Molecular Basis of Wood Formation in the Pine Megagenome  
 Unpublished (2000)  
 Contact: Sederoff, Ron  
 Forest Biotechnology

North Carolina State University  
 840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,  
 NC 27695, USA  
 Tel: 919 515 7800  
 Fax: 919 515 7801  
 Email: ron\_sederoff@ncsu.edu, jerril\_johnson@ncsu.edu  
 Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further  
 information.  
 Seq primer: T3.

FEATURES  
 source location/Qualifiers  
 1..189  
 /organism="Pinus taeda"  
 /mol\_type="mRNA"  
 /strain="Coastal plain loblolly pine from North Carolina"  
 /db\_xref="taxon:3352"  
 /clone="NCXI 029 C01"  
 /tissue\_type="Xylem"  
 /cell\_type="Compression"  
 /dev\_stage="Juvenile"  
 /lab\_host="X11-Blue"  
 /clone\_lib="NCXI (NsF Xylem Compression wood Inclined)"  
 /note="Vector: Bluescript SK; Site 1: Eco RI; Site 2:  
 XhoI; The library is from early (spring) wood, taken from  
 three six-year old trees (three different genotypes), in  
 the juvenile phase. These trees were induced to form  
 compression wood by bending to a 45 degree angle and tying  
 them to the ground. Differentiating xylem was harvested  
 from the bottoms of the inclined stems, and a mixture of  
 all three genotypes was used for the library. oligo-dr  
 primed cDNA was directionally cloned into the EcoRI-XhoI  
 Bluescript SK vector arms. NOTE: The sequences contain a  
 'cDNA adapter' between the EcoRI site and the start of the  
 EST. The adapter sequence is 'AATTCGACACGAG.'"

ORIGIN  
 Query Match 66.7%; Score 12; DB 6; Length 189;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 |||||:|||||  
 Db 63 GGGGTCCTGGAG 74

RESULT 159  
 CD612432/c 190 bp mRNA linear EST 12-JAN-2004  
 LOCUS 56086375H1 FLP Homo sapiens cDNA, mRNA sequence.  
 DEFINITION CD612432  
 ACCESSION CD612432  
 VERSION CD612432.1 GI:40260696  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 190)  
 Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.  
 Circular rapid amplification of cDNA ends for high-throughput  
 extension cloning of partial genes  
 Genomics 84 (1), 205-210 (2004)  
 Contact: Fu GK  
 Incyte Genomics, Inc.  
 3160 Porter Dr., Palo Alto, CA 94304, USA  
 Tel: 6508654102  
 Email: gfu@incyte.com.

FEATURES  
 source location/Qualifiers  
 1..190  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="FLP"  
 /note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 66.7%; Score 12; DB 6; Length 190;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUCGAG 12  
 |||||:  
 Db 21 GGGGTCCTGGAG 10

RESULT 160  
 CE683453 190 bp DNA linear GSS 29-SEP-2003  
 LOCUS tigr-gss-dog-17000314478830 Dog library Canis familiaris genomic,  
 CE683453 genomic survey sequence.  
 ACCESSION CE683453.1 GI:37002489  
 VERSION GSS.  
 KEYWORDS  
 SOURCE Canis familiaris (dog)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 1 (bases 1 to 190)  
 Kirksnes,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
 Venter,J.C.  
 TITLE The dog genome: survey sequencing and comparative analysis  
 JOURNAL Science 301 (5641), 1898-1903 (2003)  
 MEDLINE 14512627  
 PUBMED  
 COMMENT Contact: Kirksnes EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirksne@tigr.org  
 Class: shotgun.  
 Location/Qualifiers  
 1..190  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog library"  
 /note="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"

ORIGIN  
 Location/Qualifiers  
 1..190  
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 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog library"  
 /note="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"

Query Match 66.7%; Score 12; DB 9; Length 190;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUCGAG 12  
 |||||:  
 Db 158 GGGGTCCTGGAG 169

RESULT 161  
 BF832234 191 bp mRNA linear EST 13-JAN-2001  
 LOCUS PM3-HT0925-181000-004-c12 HT0925 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION BF832234  
 ACCESSION BF832234.1 GI:12180760  
 VERSION EST.  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 191)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zagdo,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matukuma,A., Bata,G.S., Simpson,D.H.,

Brustrein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 JOURNAL 20202663  
 MEDLINE 10737800  
 PUBMED  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM5&st=PM3-HT0925-  
 181000-004-c12&t3=2000-10-18&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 3  
 High quality sequence stop: 191.  
 Location/Qualifiers  
 1..191  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="HT0925"  
 /note="Organ: head neck; Vector: puc18; Site 1: SmaI;  
 Site 2: SmaI; A mini-library was made by cloning products  
 derived from ORSTS PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

ORIGIN  
 Location/Qualifiers  
 1..191  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="HT0925"  
 /note="Organ: head neck; Vector: puc18; Site 1: SmaI;  
 Site 2: SmaI; A mini-library was made by cloning products  
 derived from ORSTS PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

Query Match 66.7%; Score 12; DB 2; Length 191;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUCGAG 12  
 |||||:  
 Db 142 GGGGTCCTGGAG 153

RESULT 162  
 CD612433 191 bp mRNA linear EST 12-JAN-2004  
 LOCUS 5608637501 FLP Homo sapiens cDNA, mRNA sequence.  
 DEFINITION CD612433  
 ACCESSION CD612433  
 VERSION CD612433.1 GI:40260697  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 191)  
 Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.  
 Circular rapid amplification of cDNA ends for high-throughput  
 extension cloning of partial genes  
 Genomics 84 (1), 205-210 (2004)  
 JOURNAL Contact: Fu GK  
 Incyte Genomics, Inc.  
 3160 Porter Dr., Palo Alto, CA 94304, USA  
 Tel: 6508454102  
 Email: gfu@incyte.com  
 Location/Qualifiers  
 1..191  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"

ORIGIN  
 /db\_xref="taxon:9606"  
 /clone\_lib="FLP"  
 /note="Vector: pDrive Cloning Vector"

Query Match 66.7%; Score 12; DB 6; Length 191;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 ||||:||||  
 170 GGGGTCCTGGAG 181

RESULT 163  
 CV298789/c 191 bp mRNA linear EST 23-SEP-2004

LOCUS CV298789/c petunia floral post-pollination cDNA library Petunia x hybrida cDNA clone Petunia-PP-12-D03 5' end, mRNA sequence.

ACCESSION CV298789  
 VERSION CV298789.1 GI:52592435  
 KEYWORDS EST.

SOURCE  
 ORGANISM Petunia x hybrida

REFERENCE  
 AUTHORS Petunia x hybrida  
 Shibusawa, K., Underwood, B., Loucas, H., Farmerie, W., Jones, M. and Clark, D.

TITLE  
 JOURNAL Petunia x hybrida EST collection  
 COMMENT Unpublished (2004)  
 Contact: David Clark  
 UF Agriculture Biotechnology Lab  
 University of Florida  
 Environmental Horticulture Department, 1545 Fifield Hall, Box 110670, Gainesville, FL 32611-0670, USA  
 Tel: 352-392-1831 x370  
 Fax: 352-392-3870  
 Email: dclark@mail.ifas.ufl.edu  
 Contact Dr. Clark (dclark@mail.ifas.ufl.edu) for clone information  
 Seq primer: T3 primer.

FEATURES  
 source  
 Location/Qualifiers  
 1..191

/organism="Petunia x hybrida"  
 /mol\_type="mRNA"  
 /cultivar="Mitchell Diploid (aka. Mitchell, aka W15 in Europe)"  
 /db\_xref="taxon:4102"  
 /clone="Petunia-PP-12-D03"  
 /tissue\_type="all floral organs"  
 /lab\_host="lambda ZAP11 unidirectional"  
 /clone\_lib="petunia floral post-pollination cDNA library"  
 /note="vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; supplier: Petunia x hybrida cv. Mitchell Diploid plants were grown from seeds to a fully flowering stage under standard greenhouse conditions. Flowers at anthesis stage were self-pollinated and entire flowers were collected at 0, 5, 10, 24, 36 and 48 hours after pollination from plants grown in standard greenhouses. Total RNA was extracted from each sample, and 100 micrograms of each sample was combined for subsequent poly A+ mRNA selection and cDNA synthesis."

## ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 191;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 ||||:||||  
 43 GGGGTCCTGGAG 32

Db

RESULT 164  
 CF613742

LOCUS CF613742 192 bp mRNA linear EST 01-OCT-2003  
 DEFINITION CES007966 Bos taurus fat cDNA library Bos taurus cDNA clone

ACCESSION CF613742  
 VERSION CF613742.1 GI:37238840  
 KEYWORDS EST.

SOURCE  
 ORGANISM Bos taurus (cow)

REFERENCE  
 AUTHORS Bos taurus  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

TITLE  
 JOURNAL Transcription profiling of bovine skeletal muscle and subcutaneous fat

COMMENT  
 Unpublished (2003)  
 Contact: Dr Sigrid Lehnert  
 Functional Genomics Lab  
 CSIRO Livestock Industries  
 level 5, Queensland Bioscience Precinct, University of Queensland,  
 306 Carmody Road, St. Lucia QLD Australia  
 Tel: 07 3214 2445  
 Fax: 07 3214 2480  
 Email: sigrid.lehnert@csiro.au  
 Plate: 02 row: H column: 02.

FEATURES  
 source  
 Location/Qualifiers  
 1..192

/organism="Bos taurus"  
 /mol\_type="mRNA"  
 /strain="Angus"  
 /db\_xref="taxon:9913"  
 /clone="CC1007966"  
 /sex="male"  
 /tissue\_type="subcutaneous fat tissue"  
 /dev\_stage="Young Adult"  
 /lab\_host="XLI-BlueMRF strain"  
 /clone\_lib="Bos taurus fat cDNA library"  
 /note="vector: Uni-ZAPXR; Site 1: EcoRI; Site 2: Xho I; library made from subcutaneous fat of a 14 month old Angus steer."

## ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 192;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
 ||||:||||  
 27 GGGGTCCTGGAG 38

RESULT 165  
 CG987201/c

LOCUS CG987201/c 192 bp DNA linear GSS 15-DEC-2003  
 DEFINITION CH240\_158J01.TJ CHORI-240 Bos taurus genomic clone CH240\_158J01,  
 genomic survey sequence.

ACCESSION CG987201  
 VERSION CG987201.1 GI:39912980  
 KEYWORDS GSS.

SOURCE  
 ORGANISM Bos taurus (cow)

REFERENCE  
 AUTHORS Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.

TITLE  
 JOURNAL 1 (bases 1 to 192)  
 Costa, J.N., Mota, M. and Gaetano, A.R.  
 Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 CHORI-240  
 Unpublished (2003)

## COMMENT

Other GSSs: CH240\_158J01.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658

Email: acetanoc@embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm).  
 Bases shown have Phred quality value equal to or higher than 20.  
 For BAC library availability, please contact Pieter de Jong  
 (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering/information.htm).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Cientifico e Tecnológico (CNPq), Brazil  
 Plate: 158 row: J column: 01  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 192.

## FEATURES

source Location/Qualifiers

1..192  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_158J01"  
 /sex="Male"

/cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /note="Vector: pPARBAC1.3; Site 1: MboI; Site 2: MboI;  
 Hereford bull LI Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match

Best Local Similarity 91.7%; Pred. No. 2.2e+04;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGANNNNN 18

Db 39 CTGAGANNNNN 28

RESULT 166  
 CE424526

LOCUS CE424526 193 bp DNA linear GSS 27-SEP-2003  
 DEFINITION tigr-gss-dog-17000362791914 Dog library Canis familiaris genomic,  
 genomic survey sequence.

ACCESSION CE424526  
 VERSION CE424526.1 GI:36692430

KEYWORDS GSS.  
 SOURCE Canis familiaris (dog)

## ORGANISM

Canis familiaris  
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Eukaryota; Euteleostomi; Carnivora; Fissipedia; Canidae; Canis.  
 1 (bases 1 to 193)  
 Kirkness, E.F., Batina, V., Halpern, A.L., Levy, S., Remington, K.,  
 Risch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
 Venter, J.C.

The dog genome: survey sequencing and comparative analysis  
 Science 301 (5641), 1898-1903 (2003)

## COMMENT

TITLE JOURNAL  
 MEDLINE 22875432  
 PUBMED 14512627  
 Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA

## FEATURES

source

Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirkness@tigr.org  
 Class: shotgun.  
 Location/Qualifiers

1..193  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"

## ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 193;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12

Db 82 GGGGTCCTGGAG 93

RESULT 167  
 BM238031

LOCUS BM238031 194 bp mRNA linear EST 07-JUN-2003  
 DEFINITION K0511B01-3 NIA Mouse Hematopoietic Stem Cell (Lin-/C-Kit+/Sca-1+)  
 cDNA library (Long) Mus musculus cDNA clone NIA:K0511B01

IMAGE:30064908 3', mRNA sequence.

ACCESSION BM238031  
 VERSION BM238031.2 GI:31494579

KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Euteleostomi; Rodentia; Scuriognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 194)  
 Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.  
 Construction of long-transcript enriched cDNA libraries from  
 submicrogram amounts of total RNAs by a universal PCR amplification  
 method

Genome Res. 11 (9), 1553-1558 (2001)

JOURNAL  
 MEDLINE 21429098  
 PUBMED 11544199

COMMENT On Dec 17, 2001 this sequence version replaced gi:17873301.

Other ESTs: K0511B01-5N  
 Contact: Dawood B. Dudekula

Laboratory of Genetics  
 National Institute on Aging/National Institutes of Health  
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
 Email: cdna@igsun-grc.nia.nih.gov  
 Plate: K0511 row: B column: 01  
 Seq primer: -21M13 Forward  
 High quality sequence stop: 194  
 PolyA=yes.

## FEATURES

source

Location/Qualifiers

1..194  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6NCR"  
 /db\_xref="nabEST:K0511B01-3"  
 /db\_xref="taxon:10090"  
 /clone="NIA:K0511B01 IMAGE:30064908"  
 /issue\_type="Hematopoietic Stem Cell  
 (Lin-/C-Kit+/Sca-1+)"  
 /dev\_stage="Age approx. 10 weeks old"

/lab\_host="DHI08"  
 /clone\_lib="NIA Mouse Hematopoietic Stem Cell  
 (Lin-/C-Kit+/Sca-1+) cDNA library (Long)"  
 /note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:  
 NotI; Mouse cDNA project by the Laboratory of Genetics,  
 National Institute on Aging (NIA), Intramural Research

ORIGIN

QY 1 GGGGUCCTGGAG 12  
|||:|:|  
Db 57 GGGGCTCTGGAG 68

RESULT 168					
BB017291/c					
LOCUS	BB017291	195 bp	mRNA	linear	EST 22-JUN-2000
DEFINITION	BB017291	RIKEN full-length enriched, adult male testis			Mus
ACCESSION	BB017291	musculus cDNA clone 4930567J02 3', mRNA sequence.			

KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

REFERENCE  
1 (bases 1 to 195)  
Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

Carninci, P., Endo, T., Fukuda, S., Fukuyama, J., Aikawa, T., Hirose, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koyano, S., Kurikawa, C., Kusabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shingawa, A., Shiraki, T., Takahashi, F., Tomimaga, N., Toyota, T., Tsunoda, Y., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasutshiki, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashitaki, Y.

TITLE	ESTS (Konno, H., et al.)
RIKEN Mouse	
Unpublished (2000)	

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9226  
Email: genome-reesgsc.riken.jp, URL: <http://genome.gsc.riken.jp/>  
Carinanci, P., Nishiyama, Y., Westover, A., Itoh M., Nagao, S.,  
Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Thermoeutabolization and thermoactivation of thermolabile enzymes by  
trehalose and its application for the synthesis of full length  
cDNA. *Proc. Natl. Acad. Sci. U.S.A.* 95 (1998), 520-524 (1998)

**FEATURES**  
**SOURCE**

Itoh, M., Kikunai, T., Akiyama, T., Shibata, K., Iwawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. *Genome Res.* 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303, 19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

**SOURCE**

`organism="Mus musculus"
mol_type="rRNA"
strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4930567J02"
/sex="male"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male testis (DH10B)"
/notes="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5']
GAGGAGAGGAAGATCCACCAAGCGCTTTTTTTTTTTTTTTTNN 3']. cDNA was prepared by using rNeolase thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adaptor of sequence [5']
GAGGAGAGAGATTCGCGATTAATTAATTAATTCGCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from LambdaBLC1. Cloning sites, 5' end: SalI, 3' end: BamHI."`

## ORIGIN

Query Match	66.7%	Score 12;	DB 2;	Length 195;
Best Local Similarity	83.3%	Pred. No. 2.2e+04;		
Matches 10; Conservative	2;	Mismatches 0;	Indels 0;	Gaps 0;

```

QY      1 GGGGUCCTGGAG 12
          ||||:|||||
Db      51 GGGGTCCTGGAG 40

```

RESULT 169  
BI047499

LOCUS BT07499 195 bp mRNA, linear EST 14-JUN-2001  
DEFINITION MR4-ST0240-080101-024-g07 ST0240 Homo sapiens CDNA, mRNA sequence.  
ACCESSION BI067499  
VERSION BI067499.1 GI:14454121  
KEYWORDS EST.

ORGANISM

## REFERENCE AUTHORS

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
PUBMED	10737800



## COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR4&t2=MR4-ST0240-080101-024-g07&t3=2001-01-08&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 35  
High quality sequence stop: 195.

## FEATURES

Location/Qualifiers  
1..195  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="ST0240"

/note="Organ: stomach; Vector: puc18; Site: 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 66.7%; Score 12; DB 4; Length 195;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
||||:|||||  
184 GGGCTCTGGAG 195

Db 184 GGGCTCTGGAG 195

## RESULT 170

CV025592 195 bp mRNA linear EST 20-AUG-2004

LOCUS 3313 Full length cDNA from the mammalian Gene Collection Homo

sapiens cDNA 5' similar to BC002622, mRNA sequence.

ACCESSION CV025592

VERSION CV025592.1 GI:51483533

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Marc Vidal laboratory  
Dana Farber Cancer Institute  
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
Tel: 617 632 5180  
Fax: 617 632 5739  
Email: Marc.Vidal@dfci.harvard.edu  
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as template DNA and ORF specific primers  
PCR Primers  
FORWARD: ATGAGCTGAGAGATCGT  
BACKWARD: TATGCGTATCAGCATCATGTA

Insert Length: 195 Std Error: 130.00  
Plate: 11084 row: 06 column: A  
Seq primer: ACTGCGCTGCTTTACACATCTGCTGAGGAAAC  
High quality sequence start: 99  
High quality sequence stop: 194  
POLYA=No.

## FEATURES

## source

Location/Qualifiers  
1..195  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="mixed"  
/clone\_lib="Full length cDNA from the Mammalian Gene Collection"  
/note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 Donor vector. Reference: MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"

## ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 195;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
||||:|||||  
109 GGGCTCTGGAG 120

Db 109 GGGCTCTGGAG 120

## RESULT 171

D45320 195 bp mRNA linear EST 30-DEC-1995

LOCUS HUMHG5144 Human cerebral cortex Homo sapiens cDNA, mRNA sequence.

ACCESSION D45320

VERSION D45320.1 GI:1136722

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

PUBMED

Contact: Nobuaki Takahashi  
Institute of Medical Science  
University of Tokyo  
Shirokanedai 4-6-1, Minato-ku, Tokyo, Japan 108  
Tel: 03-5449-5625  
Fax: 03-5449-5445.

## FEATURES

## source

Location/Qualifiers  
1..195  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="Human cerebral cortex"  
/note="Adult male cerebral cortex tissue."

## ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 195;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
||||:|||||  
9 GGGCTCTGGAG 20

Db 9 GGGCTCTGGAG 20

RESULT 172  
 AM836385 196 bp mRNA linear EST 18-MAY-2000  
 DEFINITION PM0-LT0030-101299-001-h04 LT0030 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AM836385  
 VERSION AM836385.1 GI:7930359  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 196)  
 Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 JOURNAL MEDLINE 20202663  
 PUBMED 10737800  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=et2-PM0-LT0030-101299-001-h04&t3=199-12-10&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 3  
 Location/Qualifiers  
 1..196  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="LT0030"  
 /note="Organ: leiomyos; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORSTS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
 ORIGIN  
 Query Match 66.7%; Score 12; DB 2; Length 196;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCGUGAG 12  
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 Db 37 GGGGCTCTGGAG 48

ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 197)  
 Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.  
 Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method  
 Genome Res. 11 (9), 1553-1558 (2001)  
 JOURNAL MEDLINE 21429098  
 PUBMED 11544199  
 COMMENT Contact: Dawood B. Dudekula  
 Laboratory of Genetics  
 National Institute on Aging/National Institutes of Health  
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
 Email: chnald@nigam.nih.gov  
 Plate: B0715 row: A column: 10  
 Seq primer: M13 Reverse  
 High quality sequence stop: 197  
 POLYA=No.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /catalin="C57BL/6J"  
 /db\_xref="taeEST:B0715A10-5"  
 /db\_xref="taxon:10090"  
 /clone="NIA:B0715A10 IMAGE:30459273"  
 /sex="male"  
 /dev\_stage="embryonic day 8"  
 /lab\_host="DH10B"  
 /clone\_lib="NIA Mouse Embryonic Germ Cell cDNA Library (long)"  
 /note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Dr. Mark G. Carter (NIH/NIA-IRP). B6 cells were cultured at 37. C, 5% CO2 in DMEM supplemented with 15% ES cell-qualified FBS, 0.1mM non-essential amino acids, 1 mM glutamine, penicillin/streptomycin, 1 mM sodium pyruvate, 0.1 mM beta-mercaptoethanol, and 1000000 units of LIF per liter. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen):  
 5'-POACTAGTCTAGATCGGACGGCGCCCTTTT-3' from 2.5 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LR-Sa14, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 4.0 kb. The library was constructed by Yulan Piao."  
 ORIGIN  
 Query Match 66.7%; Score 12; DB 7; Length 197;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGUCGUGAG 12  
 |||||  
 Db 102 GGGGCTCTGGAG 91

RESULT 174

AA337180 200 bp mRNA linear EST 21-APR-1997  
 LOCUS AA337180 Endometrial tumor Homo sapiens cDNA 5' end, mRNA sequence.  
 ACCESSION AA337180  
 VERSION AA337180.1 GI:1989417  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 200)  
 AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-ai,C., Clifton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,T.M., Fritchman,U.L., Geoghegan,N.S., Gladek,A., Ghehri,C.B., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanges,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dinke,D., Feng,D.-F., Ferris,A., Fischer,C., Hastings,G.A., He,M.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weisner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,M.A., Fields,C., Fraser,C.M., and Venter,J.C.  
 TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence  
 JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)  
 MEDLINE 96026280  
 PUBMED 7566098  
 COMMENT Other\_ESTs: THC193172  
 Contact: Kerlavage, AR  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse  
 Location/Qualifiers  
 1..200  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="ATCC (inhost):138909"  
 /db\_xref="taxon:9606"  
 /sex="female"  
 /dev\_stage="adult"  
 /clone\_lib="Endometrial tumor"  
 /note="Organ: endometrium; Vector: pBluescript SK-"  
 Site\_1: EcoRI; Site\_2: XhoI

ORIGIN

Query Match 66.7%; Score 12; DB 1; Length 200;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Y 1 GGGGUCCTGGAG 12  
 |||:|||||  
 Db 22 GGGGCTCTGGAG 33

RESULT 175  
 BE398334/c 200 bp mRNA linear EST 21-JUN-2000  
 LOCUS BE398334 Wheat Endosperm Library Triticum  
 DEFINITION WHE0010.E12P000701 ITTC WHE Wheat Endosperm Library Triticum  
 aestivum cDNA clone WHE0010.E12, mRNA sequence.  
 ACCESSION BE398334

VERSION BE398334.1 GI:9357808  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)  
 ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poidea; Triticaceae; Triticum.  
 REFERENCE 1 (bases 1 to 200)  
 AUTHORS Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Hermann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Lagridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrelle,M., Warburton,M., and Wenzel,G.  
 International Triticaceae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticaceae Unpublished (2000)  
 CONTACT: Anderson OA  
 USDA ARS WRC  
 800 Buchanan Street, Albany, CA 94710-1105 USA  
 Tel: 510 559 5773  
 Fax: 510 559 5818  
 Email: oanderson@wrc.usda.gov  
 International Triticaceae EST Cooperative (ITEC)  
<http://wheat.pw.usda.gov/genome>.  
 Location/Qualifiers  
 1..200  
 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /cultivar="Cheyenne"  
 /db\_xref="taxon:4565"  
 /clone="WHE0010.E12"  
 /tissue="endosperm"  
 /dev\_stage="5-30 days post anthesis"  
 /clone\_lib="ITEC WHE Wheat Endosperm Library"  
 /note="Vector: Lambda ZAP1; Wheat Endosperm Library constructed in Lambda ZAP1 with 8-mer adapter."

ORIGIN

Query Match 66.7%; Score 12; DB 2; Length 200;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Y 1 GGGGUCCTGGAG 12  
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 Db 167 GGGGCTCTGGAG 156

RESULT 176  
 BE1047779 200 bp mRNA linear EST 14-JUN-2001  
 LOCUS BE1047779 M4-ST0240-310101-029-e01 ST0240 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION BE1047779  
 ACCESSION BE1047779  
 VERSION BE1047779.1 GI:14454401  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 200)  
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Bionesi,M.R., Negai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.P., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J., and Simpson,A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 PUBMED 10737800  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR4&t2=MR4-ST0240-  
310101-029-e01&t3=2001-01-31&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 68  
High quality sequence stop: 200.  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="ST0240"  
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORSTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Query Match 66.7%; Score 12; DB 4; Length 200;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUCGAG 12  
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Db 161 GGGGTCCTGGAG 172

RESULT 177  
LOCUS A2791991 201 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M0043H07F Mouse 10kb plasmid UGCLM library Mus musculus genomic  
clone UGCLM0043H07 F, genomic survey sequence.  
ACCESSION A2791991  
VERSION A2791991.1 GI:12935458  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 201)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Iellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Niederhauser, A., and Wright, D., Weis, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
CONTACT: Robert B. Weiss  
UNIVERSITY OF UTAH  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0043 row: H column: 07  
Seq primer: CGTTGTAAACGACGCGCACT  
Class: plasmid ends  
High quality sequence stop: 201.  
Location/Qualifiers  
1..201

## ORIGIN

Query Match 66.7%; Score 12; DB 8; Length 201;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUCGAG 12  
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Db 62 GGGGTCCTGGAG 73

RESULT 178  
LOCUS A1503108/c 203 bp mRNA linear EST 11-MAR-1999  
DEFINITION vm92a11.x1 Knowles Solter mouse blastocyst B1 Mus musculus cDNA  
clone IMAGE:1005692 3', mRNA sequence.  
ACCESSION A1503108  
VERSION A1503108.1 GI:4400959  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 203)  
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
Underwood, K., Steptoe, M., Thaising, B., Allen, M., Bowers, Y.,  
Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R.,  
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
Waterston, R. and Wilson, R.  
The WashU-NCI Mouse EST Project 1999  
Unpublished (1999)  
CONTACT: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LINT; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:569908  
This clone was previously sequenced on the 5' end only, this new  
data is from the 3' end  
Seq primer: Primer name ambiguous.  
Location/Qualifiers  
1..203  
/organism="Mus musculus"

/mol\_type="mrna"  
/strain="CS7BL/6J x DBA/2J F1"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1005692"  
/libsize\_type="blastocyst"  
/dev\_stage="embryo (pre-implantation)"  
/lab\_host="DH10B"  
/clone\_lib="Knowles Solter mouse blastocyst B1"  
/note="Organ: embryo; Vector: pSPORT; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally from mRNA prepared from 800 blastocysts. Primer: SalI(5'-CGTCCGACCGTCGACCGTCTTTTCTTTT-3', CDNA were cloned into the NotI/SalI sites of a pSPORT vector (Life Technologies). Two different size selections: B1 (larger inserts) and B3."

ORIGIN

Query Match 66.7%; Score 12; DB 1; Length 203;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCGAG 12  
||||:|||||

Db 167 GGGGTCCTCGAG 156

RESULT 179  
AW204396 203 bp mRNA linear EST 02-DEC-1999  
LOCUS U-H-B11-adv-d-04-0-UI.s1 NCI CGAP\_Sub3 Homo sapiens CDNA clone  
DEFINITION IMAGE:2718007 3', mRNA sequence.  
ACCESSION AW204396  
VERSION AW204396.1 GI:6503868  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 203)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/BLND at: www.bio.litl.gov/bdnp/image/image.html  
Seq primer: M13 Forward  
POLYA=Yes.

FEATURES  
source

1..203  
/organism="Homo sapiens"  
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/clone\_lib="NCI CGAP Sub3"  
/note="Vector: pT7TD-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; The NCI CGAP Sub3 library is a subcloned library derived from the NCI CGAP Sub1 library, which is a subcloned library normalized or subcloned NCI CGAP libraries:  
NCI CGAP Co4, NCI CGAP Pr22, NCI CGAP Pr28, NCI CGAP Co10, NCI CGAP Co16, NCI CGAP Kid5, NCI CGAP Kid12, NCI CGAP Kid3, NCI CGAP Kid1, NCI CGAP Lym2, NCI CGAP Br2, NCI CGAP Co8, NCI CGAP CUL1, NCI CGAP Le12, NCI CGAP Brn23, NCI CGAP Lu5, NCI CGAP Lu24,

NCI CGAP Lu19, NCI CGAP GC4, NCI CGAP GC6, NCI CGAP Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:  
NCI CGAP Kid3 pool 1 LAM 3334-3337, 3682-3683, 3798-3803 (IMAGE Clonides 1322376-1323911, 1456008-1456775, 1505552-1502855); NCI CGAP Kid5 pool 1 LAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonides 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI CGAP Lu5 pool 1 LAM 3575-3582, 3851-3854 (IMAGE Clonides 1414920-1417991, 1520904-1522439); NCI CGAP GC4 pool 1 LAM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonides 1257096-1258631, 1459064-1470983, LAM 2457-2459, 1475592-1476743); NCI CGAP Pr22 pool 1 LAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonides 985608-986759, 1101192-1101959, 1217928-1220615); NCI CGAP Co10 pool 1 LAM 2644-2653, 2871-2872 (IMAGE Clonides 1057416-1061255, 114584-1145351). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches to Facilitate Gene Discovery, Genome Research 6, 791-806.  
TAG TISSUE=kidney  
TAG LIB=NCI CGAP\_Kid3  
TAG\_SEQ=ATGCG"

ORIGIN

Query Match 66.7%; Score 12; DB 2; Length 203;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCGAG 12  
||||:|||||

Db 129 GGGGTCCTCGAG 118

RESULT 180  
BB246707 203 bp mRNA linear EST 06-JUL-2000  
LOCUS BB246707  
DEFINITION BB246707 RIKEN full-length enriched, 7 days neonate cerebellum Mus musculus CDNA clone A730015X23 3', mRNA sequence.  
ACCESSION BB246707  
VERSION BB246707.1 GI:8939453  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 203)  
Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadoya, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toyota, T., Tsunoda, Y., Wachihi, A., Watanabe, S., Yamamura, T., Yamashita, I., Yano, R., Yasunishi, A., Yokota, Y., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Kono, H., et al.)  
Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9226  
Fax: 81-45-503-9216  
Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/  
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S.,

Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Thermosensitization and thermostabilization of the tobacco etch virus RNAse by the addition of a 5' cap. *FEBS Lett.* 360: 111-114 (1995).

Chen, S. and Naik, S. Application of the thermophilic DNA polymerase I from *Thermococcus* sp. to the synthesis of full-length cDNA. *Proc. Natl. Acad. Sci. U.S.A.* 95 (2), 520-524 (1998).

Itchō, M., Katsunari, T., Akiyama, U., Shibata, K., Iwawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation system. *Genome Res.* 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

## FEATURES

**source**

1. .203  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
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/tissue\_type="cerebellum"  
/dev\_stage="7 days neonate"  
/lab\_host="DH10B"  
/clone\_id="RIKEN full-length enriched, 7 days neonate cerebellum"  
/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genetic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer 15'  
GAGGAGAGAAGATCCACAACGCTCTTTTTCCTTTTTTTTAA 3'. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence 15' GAGGAGAGATTCTCGACTTAATTAATTAATCCCCCCCCCCC 3'. cDNA was cleaved with XhoI and BamHI. Vector: a modified plasmid KS(+) after bulk excision from Lambda LVC I."

## ORIGIN

Query Match	66.7%	Score 12;	DB 2;	Length 203;
Best Local Similarity	83.3%	Pred. No. 2.2e+04;		
Matches 10;	Conservative 2;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	GGGUCCTUGGAG	12
		: :	
Db	119	GGGCTCTGGAG	130

RESULT 181	
BB523008/c	
LOCUS	BB523008
DEFINITION	BB523008 RIKEN full-length enriched, 15 days embryo head Mus musculus CDNA clone D930011G06 3', mRNA sequence.
ACCESSION	BB523008
	204 bp mRNA linear EST 28-JUL-2000

ORGANISM

## REFERENCE AUTHORS

## AUTHORS

Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hiroane, T., Hori, F., Ishii, Y., Ishikawa, U., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusabata, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,

TITLE  
JOURNAL  
COMMENT

Sogabe, K., Shihata, Y., Shigemoto, Y., Shingagawa, A., Shiraki, T., Shibata, Y., Sugihara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomihaga, N., Toya, T., Tsunoda, Y., Watanishi, A., Watanabe, S., Yamamura, T., Yamahara, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.

RIKEN Mouse ESrrs (Konno, H., et al.)

Unpublished (2000)

Contact: Yoshinide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216

Email: genome-resgsc.riken.jp, URL: <http://genome.gsc.riken.jp/>  
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.

The thermolabile and thermoactivation of thermolabile enzymes by thermalase and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh, M., Kitsumai, T., Atiyama, J., Shihata, K., Irawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

## FEATURES

**Source**

```

location/Qualifiers
1. 204
   /organism="Mus musculus"
   /mol_type="rRNA"
   /strain="C57BL/6J"
   /db_xref="taxon:10090"
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head"
note="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGGAGAGGAAGATCTCAAGAAGTCTTTTTCCTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5',
GAGGAGAGATCTCCAGATTAAATTAATTAAATCCCCCCCCCCC 3'}. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pbluescript KS(+) after bulk excision from Lambda
phage I"

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ORIGIN

Query Match	66.7%	Score 12;	DB 2;	Length 204;
Best Local Similarity	83.3%	Pred. No. 2.2e+04;		
Matches 10; Conservative	2;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	GGGGUCCUGGAG	12
		:	
Db	78	GGGGTCTGGAG	67

RESULT 182  
CB935713

LOCUS CB935713 205 bp mRNA linear EST 29-APR-2003  
 DEFINITION tab5a01.x1 Hydra EST -III Hydra magnipapillata cDNA 3' similar to  
 ACCESSION TR:000484 Q00484 MINI-COLLAGEN PRECURSOR.; mRNA sequence.  
 VERSION CB935713  
 KEYWORDS EST.  
 SOURCE GI:30221104  
 ORGANISM Hydra magnipapillata  
 Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;  
 Hydridae; Hydra.  
 1 (bases 1 to 205)  
 Bode H., Blumberg B., Steele R., Wigge P., Gee L., Nguyen O.,  
 Martinez D., Kibler D., Hampson S., Clifton S., Pape D., Marra M.,  
 Hillier L., Martin J., Wyllie T., Dante M., Theising B., Bowers Y.,  
 Gibbons M., Ritter E., Bennett J., Komko I., Teagataishvili R.,  
 Maguire L., Kennedy S., Waterston R. and Wilson R.  
 WASHU Hydra EST Project  
 Unpublished (2002)  
 TITLE WASHU Hydra EST Project  
 JOURNAL  
 COMMENT Contact: Hans Bode  
 WASHU Hydra EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Library was constructed by Bruce Blumberg & Jisong Pang, Univ. of  
 Calif. Irvine Library materials provided by Hans Bode & Lydia Gee,  
 Univ. of Calif., Irvine DNA sequencing by: Washington University  
 Genome Sequencing Center For information on obtaining a clone  
 please contact: Hans Bode (hrobde@uci.edu)  
 Trace considered overall poor quality  
 Seq primer: -40bp from Gibco  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..205  
 /organism="Hydra magnipapillata"  
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 /db\_xref="taxon:6085"  
 /lab\_host="DH10B"  
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 /note="Vector: pCS22; Site 1: XhoI; Site 2: PstI; a) 1st  
 strand cDNA was primed with a XhoI oligo (dr) primer (5'  
 ACTAAGGGCTCGAG(T)18NN(3'; b) Double-stranded cDNA was  
 ligated to PstI linker, digested with PstI and XhoI and  
 cloned into the PstI and XhoI sites of a pCS22 vector,  
 which is a modified pCS2+ vector. c) The pCS22 vector  
 contains a T7 promoter site [standard from Bluescript] at  
 the 5' end of the cloning site, and a T3 promoter site  
 [standard from pBluescript] at the 3' end of the cloning  
 site. d) The ligation mix was transformed into TOP10P  
 cells (= DH10B cells). e) The cells were grown in SOC =  
 5% yeast, 20% tryptone, 0.5% NaCl, 10mM MgSO4, 10mM MgCl,  
 0.2% glucose/liter, (no antibiotic). f) The frequency of  
 vectors containing inserts is >90% [42 of 42]. g) The  
 average size of the 42 inserts is 1075 +/- 8501."

ORIGIN  
 Query Match 66.7%; Score 12; DB 6; Length 205;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GGGGUCCTCGAG 12  
 Db 124 GGGGCTCTCGAG 135

RESULT 183  
 AM553129 206 bp mRNA linear EST 25-APR-2001  
 LOCUS AM553129  
 DEFINITION 34973 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.  
 ACCESSION AM553129  
 VERSION AM553129.1 GI:6852119  
 KEYWORDS EST.

SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (bases 1 to 206)  
 Smith T.P.L., Grose W.M., Freking B.A., Roberts A.J., Stone R.T.,  
 Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C.,  
 Bennett G.L., Heaton M.P., Laegreid W.W., Rohrer G.A.,  
 Chitko-McKown C.G., Perte G., Holt I., Karaycheva S., Liang F.,  
 Quackenbush J. and Keefe J.W.  
 Sequence evaluation of four pooled-tissue normalized bovine cDNA  
 libraries and construction of a gene index for cattle  
 Genome Res. 11 (4), 626-630 (2001)  
 21180013  
 11282978  
 TITLE JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov  
 Single pass sequencing. Bases called and trimmed with phred  
 v0.980904.e. Vector identified by cross\_match with the -minscore 20  
 and -mismatch 12 options.  
 PCR primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCACACTCAGCAG  
 Plate: 16 row: H column: 13  
 Seq primer: ATTGAGTGACACTATAG.  
 Location/Qualifiers  
 1..206  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /clone\_lib="MARC 2BOV"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;  
 Library made from pooled tissue from testis, thymus,  
 semitendinosus muscle, longissimus muscle, pancreas,  
 adrenal, and endometrium."

ORIGIN  
 Query Match 66.7%; Score 12; DB 2; Length 206;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GGGGUCCTCGAG 12  
 Db 40 GGGGCTCTCGAG 29

RESULT 184  
 N84369 207 bp mRNA linear EST 01-APR-1996  
 LOCUS N84369  
 DEFINITION KX8245F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA  
 clone KX8245 5' similar to EST(Y163C04.R1), mRNA sequence.  
 ACCESSION N84369  
 VERSION N84369.1 GI:1259994  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 207)  
 Liew C.C.  
 cDNAs from fetal heart (1996)  
 Unpublished (1996)  
 TITLE JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT Contact: Liew CC  
 Brigham and Women's Hospital  
 Harvard Medical School  
 75 Francis St. Boston, MA 02115, USA

Tel: 6177328915  
Fax: 6179750995

Email: c1iewerics.bwh.harvard.edu  
Seq primer: GAATTAACCTCCTACTAAGG.

## FEATURES

source

1..207

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="XK8245"

/lab\_host="E. coli XL1-Blue"

/clone\_lib="Human fetal heart, Lambda ZAP Express"

/note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2: XhoI; mRNA was synthesized using a XhoI-01100 cT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested lambda ZAP Express."

## ORIGIN

Query Match

Best Local Similarity 83.3%; Score 12; DB 7; Length 207;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12

Db 55 GGGGTCCTCGAG 66

## RESULT 185

AM353798/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

12226715

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred

vo.980904.e. Vector identified by cross\_match with the -minscore 20

and -mismatch 12 options.

PCR Primers

FORWARD: AGGAACAGCTATGACCAT

BACKWARD: GTTTCCTCAGTACAGC

Plate: 19

Row: C

Column: 20

Seq primer: ATTAGGTGACACTATAG.

Location/Qualifiers

1..208

/organism="Sus scrofa"

/mol\_type="mRNA"

/db\_xref="taxon:9823"

/tissue\_type="pooled"

/lab\_host="DH10B"

/clone\_lib="MARC 2P1G"

/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;

Library made from pooled tissue from testis, ovary,

## ORIGIN

endometrium, hypothalamus, pituitary, and placenta."

Query Match

Best Local Similarity 83.3%; Score 12; DB 2; Length 208;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12

Db 164 GGGGTCCTCGAG 153

## RESULT 186

BI017022

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

10737800

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the RAP8P/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?el=PM3&t2=PM3-ET0207-

300301-012-c03&t3=2001-03-30&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 8

High quality sequence stop: 183.

Location/Qualifiers

1..208

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="ET0207"

/note="Organ: lung\_tumor; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORST35 PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

ORIGIN

Query Match

Best Local Similarity 83.3%; Score 12; DB 4; Length 208;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12

Db 184 GGGGTCCTCGAG 195



RESULT 187  
CE614056/C  
LOCUS  
DEFINITION CE614056 208 bp mRNA linear EST 01-OCT-2003  
CE5013429 Bos taurus fat cDNA library Bos taurus cDNA clone  
CC011537 NULL, mRNA sequence.  
ACCESSION CE614056  
VERSION CE614056.1 GI:37239434  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos.  
1 (bases 1 to 208)  
Wang,Y.H., Byrne,K., Vuocolo,T., Tan,S.H., McWilliam,S., Dierens,L.  
and Lehnert,S.  
Transcription profiling of bovine skeletal muscle and subcutaneous  
fat  
TITLE Unpublished (2003)  
JOURNAL  
COMMENT Contact: Dr Sigrid Lehnert  
Functional Genomics Lab  
CSIRO Livestock Industries  
Level 5, Queensland Bioscience Precinct, University of Queensland,  
306 Carmody Road St. Lucia QLD Australia  
Tel: 07 3214 2445  
Fax: 07 3214 2480  
Email: Sigrid.Lehnert@csiro.au  
Plate: 25 row: H column: 11.  
FEATURES  
source  
1..208  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/strain="Angus"  
/db\_xref="taxon:9913"  
/clone="CCL011537"  
/sex="male"  
/tissue\_type="subcutaneous fat tissue"  
/dev\_stage="Young Adult"  
/lab\_host="XL1-BlueMRF'strain"  
/clone\_lib="Bos taurus fat cDNA library"  
/note="Vector: Uni-ZAPXR; Site 1: EcoRI; Site 2: Xho I;  
library made from subcutaneous fat of a 14 month old Angus  
steer."  
ORIGIN  
Query Match 66.7%; Score 12; DB 7; Length 208;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUGAG 12  
||||:||||  
Db 76 GGGGTCCTGAG 65  
RESULT 188  
CE743112  
LOCUS  
DEFINITION CE743112 208 bp DNA linear GSS 30-SEP-2003  
tigr-gss-dog-17000315835346 dog library Canis familiaris genomic,  
genomic survey sequence.  
ACCESSION CE743112  
VERSION CE743112.1 GI:37083459  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
1 (bases 1 to 208)  
Kirkness,E.F., Balfour,V., Halpern,A.L., Levy,S., Remington,K.,  
Ruech,D.B., Delcher,A.L., Pop,M., Wang,W., Frazer,C.M. and  
Venter,J.C.  
The dog genome: survey sequencing and comparative analysis  
TITLE

JOURNAL Science 301 (5641), 1898-1903 (2003)  
MEDLINE 22875432  
PUBMED 14512627  
COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org  
Class: shotgun.  
FEATURES  
source  
location/Qualifiers  
1..208  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BclXI; Libraries were prepared from  
peripheral blood"  
ORIGIN  
Query Match 66.7%; Score 12; DB 9; Length 208;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUGAG 12  
||||:||||  
Db 165 GGGGTCCTGAG 176  
RESULT 189  
A1594283  
LOCUS  
DEFINITION A1594283 209 bp mRNA linear EST 21-APR-1999  
vm2a11.y1 Knowles Solter mouse blastocyst B1 Mus musculus cDNA  
clone IMAGE:1005692 5', mRNA sequence.  
ACCESSION A1594283  
VERSION A1594283.1 GI:4603331  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.  
1 (bases 1 to 209)  
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,  
Underwood,K., Slepoe,M., Theising,B., Allen,M., Bowers,Y.,  
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,  
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,  
Waterston,R. and Wilson,R.  
The WashU-NCI Mouse EST Project 1999  
Unpublished (1999)  
Contact: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LIND; contact the  
IMAGE Consortium (info@image.lind.gov) for further information.  
MGI:569908  
This read is a RESSEQUENCE of a previously sequenced mouse clone  
correct orientation)  
Seq primer: -40RP.  
FEATURES  
source  
location/Qualifiers  
1..209  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J x DBA/2J F1"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1005692"  
/tissue\_type="blastocyst"  
/dev\_stage="embryo (pre-implantation)"

/lab host="DH10B"  
 /clone.lib="Knowles Solter mouse blastocyst B1"  
 /note="Organ: embryo; Vector: pSPORT; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally from mRNA prepared  
 from 800 blastocysts. Primer: SalI(dT):  
 5'-CGGTCGACCGTCGACCGTTTCTTTT-3'. cDNAs were  
 cloned into the NotI/SalI sites of a pSPORT vector (Life  
 Technologies). Two different size selections: B1 (larger  
 inserts) and B3."

## ORIGIN

Query Match 66.7%; Score 12; DB 1; Length 209;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTCGAG 12  
 |||||:|||||  
 Db 47 GGGGTCCTCGAG 58

RESULT 190  
 CV337093/C

LOCUS CV337093 209 bp mRNA linear EST 24-SEP-2004  
 DEFINITION IL5-HT0702-160600-098-907 HT0702 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION CV337093  
 VERSION CV337093.1 GI:52660307  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

## REFERENCE

AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
 Goldman, G.H., Carvalho, A.F., Matsumura, A., Bata, G.S., Simpson, D.H.,  
 Bruneisen, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
 Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 2020263  
 PUBMED 10737800  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. http://www.ludwig.org.br.

## FEATURES

## source

1..209  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone.lib="HT0702"  
 /note="Organ: head, neck; Vector: puc18; Site\_1: SmaI;  
 Site\_2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

## ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 209;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTCGAG 12  
 |||||:|||||  
 Db 86 GGGGTCCTCGAG 75

RESULT 191

LOCUS CL603743 209 bp DNA linear GSS 17-JUN-2004  
 DEFINITION CH240\_179103.TV CHORI-240 Bos taurus genomic clone CH240\_179103,  
 genomic survey sequence.  
 ACCESSION CL603743  
 VERSION CL603743.1 GI:48871775  
 KEYWORDS GSS.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

## REFERENCE

AUTHORS Costa, J.N., Mota, M. and Caetano, A.R.  
 TITLE Brazil's Contribution to Ent-Sequencing the Bovine BAC Library  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final AV. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetano@cenargen.embrapa.br

Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.htm).  
 Bases shown have phred quality value equal to or higher than 20.  
 Bases with quality value below 20 were masked with 'N'.  
 For BAC library availability, please contact Pieter de Jong  
 (pdejong@mail.choi.org).  
 Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering/information.html).  
 This work was undertaken as part of the International Bovine BAC  
 Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e  
 Biotecnologia with financing from Conselho Nacional de  
 Desenvolvimento Cientifico e Tecnológico (CNPq), Brazil  
 Plate: 179 row: 1 column: 03  
 Seq primer: T7  
 Class: BAC ends  
 High quality sequence stop: 209.  
 Location/Qualifiers

## FEATURES

## source

1..209  
 /organism="Bos taurus"  
 /mol\_type="genomic DNA"  
 /strain="bred: Hereford"  
 /db\_xref="taxon:9913"  
 /clone="CH240\_179103"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone.lib="CHORI-240"  
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 Hereford bull 11 Domino 99375; CHORI-240 Bovine BAC  
 library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 209;  
 Best Local Similarity 91.7%; Pred. No. 2.2e+04;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CTGGAGNNNNN 18  
 |||||:|||||  
 Db 149 CTGGAGNNNNN 160

RESULT 192

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS
BBO082813/C		BBO082813		
	musculus CDNA clone g930177G07 3' similar to D29763 Mouse mRNA for seizure-related gene product 6, mRNA sequence.	BBO082813		
		BBO082813.1	GI:8647873	
				EST.
		Mus musculus		
		Mus musculus (house mouse)		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
		1 (bases 1 to 210)		
REFERENCE		Kono H., Aizawa K., Akahira S., Akiyama J., Arakawa T., Carninci P., Endo T., Fukuda S., Fukuishi Y., Harai A., Hayatsu N., Hirozane T., Horii F., Ishii Y., Ishikawa J., Ishikawa T., Itoh M., Izawa M., Kadota K., Kagawa I., Kai C., Kawai J., Kikuchi N., Kiyoasa H., Kojima Y., Kondo S., Koya S., Kurihara C., Kusabeke M., Matsuyama T., Mihi R., Mizuno Y., Nakamura M., Oda H., Okazaki Y., Ono T., Owa C., Satto H., Sekai C., Seto K., Shibata K., Shibata Y., Shigenoto Y., Shingawar A., Shiraki T., Sogabe Y., Sugahara Y., Suzuki H., Suzuki H., Tagawa A., Takahashi F., Tomimaga N., Toya T., Tsunoda Y., Watanishi A., Watanabe S., Yamamura T., Yamataka I., Yano R., Yasunishi A., Yokota T., Yoshida K., Yoshiki A., Yoshino M., Muramatsu M. and Hayashizaki Y.		
TITLE		Riken Mouse ESTs (Kono H., et al.)		
JOURNAL		Unpublished (2000)		
COMMENT		Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-resgsc.riken.jp, URL:http://genome.gsc.riken.jp/ Carninci P., Nishiyama Y., Westover A., Itoh M., Nagoka S., Sasaki N., Okazaki Y., Muramatsu M. and Hayashizaki Y. Thermozestabilization and thermocatalytic activation of thermostable enzymes by chitosanose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh M., Katsunami T., Akiyama J., Shibata K., Izawa M., Kawai J., Tomaru Y., Carninci P., Shibata Y., Ozawa Y., Muramatsu M., Okazaki Y. and Hayashizaki Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci P. and Hayashizaki Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site ( <a href="http://genome.rtc.riken.go.jp">http://genome.rtc.riken.go.jp</a> ) for further details.		
FEATURES				
SOURCE				
		Location/Qualifiers		
		1..210		
		/organism="Mus musculus"		
		/mol_type="mRNA"		
		/strain="C57BL/6J"		
		/db_xref="taxon:10090"		
		/clone="g930177G07"		
		/sex="male"		
		/tissue_type="dienecephalon"		
		/dev_stage="adult"		
		/lab_host="DH10B"		
		/clone_lib="RIKEN full-length enriched, adult male dienecephalon"		
		/note="Site 1: SalI, Site 2: BamHI. CDNA library was prepared and sequenced in House Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'-GAGGAGAGAGATCCAGAAGCTCTTTTTCCTTTTTTTTNN 3'] cDNA was prepared by using transcriptase thermo-activated reverse		

ORIGIN	Query Match	66.7%; Score 12; DB 2; Length 210;
Db	Best Local Similarity 83.3%; Pred. No. 2,2e+04; Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	
QY	1 GGGGCCCCGAG 12     :	
RESULT 193	AL764056 210 bp DNA linear GSS 01-APR-2004	
LOCUS	Arabidopsis thaliana T-DNA flanking sequence GK-045H01-015475,	
DEFINITION	genomic survey sequence.	
VERSION	AL764056	
KEYWORDS	AL764056.1 GI:21515877	
SOURCE	GSS.	
ORGANISM	Arabidopsis thaliana (thale cress)	
REFERENCE	1 Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B. GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana Bioinformatics 19 (11), 1441-1442 (2003)	
AUTHORS	2 Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B. An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics Plant Mol. Biol. 53 (1-2), 247-259 (2003)	
JOURNAL	3 Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weisshaar,B. High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines Biotechniques 35 (6), 1164-1168 (2003)	
MEDLINE	4 (bases 1 to 210) Strizhov,N., Li,Y., Rosso,M.G. and Weisshaar,B. Direct Submission Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linn-Weeg 10, Koeln, 50829, Germany. This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene AT3G23810. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <a href="http://www.mpiz-koeln.mpg.de/GABI-Kat/">http://www.mpiz-koeln.mpg.de/GABI-Kat/</a> .	
COMMENT	location/Qualifiers	
JOURNAL	1. 210	
REFERENCE	/organism="Arabidopsis thaliana"	
FEATURES	/mol_type="genomic DNA"	
source		

## ORIGIN

/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

Query Match 66.7%; Score 12; DB 9; Length 210;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
DB 175 GGGGTCCTGGAG 164

RESULT 194  
CG988556/c 210 bp DNA linear GSS 15-DEC-2003  
LOCUS CH240\_145E01.TV CHORI-240 Bos taurus genomic clone CH240\_145E01,  
DEFINITION genomic survey sequence.  
ACCESSION CG988556  
VERSION CG988556.1 GI:39914335  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus

REFERENCE  
AUTHORS Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
1 (bases 1 to 210)  
Costa, J.N., Mota, M. and Caetano, A.R.  
Brazili's Contribution to End-Sequencing the Bovine BAC Library  
CHORI-240  
Unpublished (2003)  
JOURNAL Other GSSs: CH240\_145E01.TJ  
COMMENT Contact: Caetano AR  
Department of Biotechnology  
Embrapa Recursos Geneticos e Biotecnologia  
Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
02372, 70770-900 Brasil  
Tel: 55 61 448 4778  
Fax: 55 61 340 3658  
Email: acaetano@cenargen.embrapa.br  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm).  
Bases shown have phred quality value equal to or higher than 20.  
For BAC library availability, please contact Pieter de Jong  
(pdejong@mail.cno.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm).  
This work was undertaken as part of the International Bovine BAC  
Mapping Consortium (IBMC) by Embrapa Recursos Geneticos e  
Biotecnologia with financing from Conselho Nacional de  
Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil  
Plate: 145 row: E column: 01  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 210.  
Location/Qualifiers  
1..210

## FEATURES

source  
1..210  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="Breed: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_145E01"

## ORIGIN

/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: PTARBAC1.3; site 1: MboI; site 2: MboI;  
Hereford bull U Dominio 99373; CHORI-240 Bovine BAC  
Library (Male) produced by Pieter de Jong"

Query Match 66.7%; Score 12; DB 9; Length 210;  
Best Local Similarity 91.7%; Pred. No. 2.2e+04;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CTGAGNNNNN 18  
DB 164 CTGAGNNNNN 153

RESULT 195  
AA607115 211 bp mRNA linear EST 30-SEP-1997  
LOCUS VM92a11.r1 Knowles Solter mouse blastocyst B1 Mus musculus cDNA  
DEFINITION clone IMAGE:1005692.5', mRNA sequence.  
ACCESSION AA607115  
VERSION AA607115.1 GI:2456008  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 211)  
Marrs, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubague, T.,  
Schellendberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
JOURNAL Contact: Marrs M/Mouse EST Project  
COMMENT WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:569908  
putative full length read  
vector to vector length is 212.

## FEATURES

source  
1..211  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J x DBA/2J F1"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1005692"  
/tissue\_type="blastocyst"  
/dev\_stage="embryo (pre-implantation)"  
/lab\_host="DH10B"  
/clone\_lib="Knowles Solter mouse blastocyst B1"  
/note="Organ: embryo; Vector: pSPORT; site 1: NotI;  
site 2: SalI; Cloned unidirectionally from mRNA prepared  
from 800 blastocysts. Primer: SalI(dT):  
5'-CGGTCGACGCGACCGCTTTTCTTTT-3'. cDNAs were  
cloned into the NotI/SalI sites of a pSPORT vector (Life  
Technologies). Two different size selections: B1 (larger  
inserts) and B3."

## ORIGIN

Query Match 66.7%; Score 12; DB 1; Length 211;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCGAG 12  
 ||||:||||  
 Db 47 GGGGTCTCGAG 58

RESULT 196  
 LOCUS BM705448  
 DEFINITION UT-E-C11-afg-a-01-0-UI.R2 UI-E-C11 Homo sapiens cDNA clone  
 UT-E-C11-afg-a-01-0-UI 5', mRNA sequence.  
 ACCESSION BM705448  
 VERSION BM705448  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 211)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 8889548

## COMMENT

Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu

Tissue procurement: Dr. Gregg Hageman  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com).  
 Seq primer: M13 Reverse

## FEATURES

Location/Qualifiers  
 1..211

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UT-E-C11-afg-a-01-0-UI"  
 /tissue\_type="RPE and Choroid"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-E-C11"  
 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a  
 modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
 UT-E-C11 is a normalized cDNA library containing the  
 following tissue(s): RPE and Choroid. The library was  
 constructed according to Bonaldo, Lennon and Soares,  
 Genome Research, 6:791-806, 1996. First strand cDNA  
 synthesis was primed with an oligo-dT primer containing a  
 Not I site. Double stranded cDNA was ligated to an EcoR I  
 adaptor, digested with Not I, and cloned directionally  
 into pT73-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand cDNA contains a library tag  
 sequence that is located between the Not I site and the  
 (dT)18 tail. The sequence tag for this library is ACCGA.  
 This library was created for the program, Gene Discovery  
 in the Visual System, supported by National Eye Institute  
 (NEI)."

## ORIGIN

Query Match 66.7%; Score 12; DB 4; Length 211;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GGGGUCGAG 12  
 ||||:||||  
 Db 9 GGGGTCTCGAG 20

RESULT 197  
 LOCUS CV494873/C  
 DEFINITION 39970.1 Cold Sweetening B Solanum tuberosum cDNA clone 39970 5',  
 mRNA sequence.  
 ACCESSION CV494873  
 VERSION CV494873.1  
 KEYWORDS EST.  
 SOURCE Solanum tuberosum (potato)  
 ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; Lamiales; Solanales; Solanaceae; Solanum.

REFERENCE 1 (bases 1 to 211)  
 AUTHORS Flinn,B., Rochwell,C., Sardana,R., Griffiths,R., Laue,M., De  
 Koeijer,D., Audy,P., Goyer,C., Li,X-Q., Wang-Pruski,G. and Regan,S.  
 TITLE Generation of ESTs from tubers following 3 months storage at 4  
 degrees Celsius, and 95% relative humidity  
 JOURNAL Unpublished (2004)

## COMMENT

Contact: Barry Flinn  
 The Canadian Potato Genome Project - BioAtlantic  
 921 College Hill Rd, Fredericton, ON, E3B 6Z9, CANADA  
 Email: bflinn@bioatlantech.nb.ca  
 Seq primer: T3.

## FEATURES

Location/Qualifiers  
 1..211

/organism="Solanum tuberosum"  
 /mol\_type="mRNA"  
 /cultivar="Shepody"  
 /db\_xref="taxon:4113"  
 /clone="39970"  
 /tissue\_type="Tubers"  
 /lab\_host="X110-Gold"  
 /clone\_lib="Cold Sweetening B"  
 /note="Vector: pBluescript II SK(+); XR; Site\_1: EcoRI;  
 Site\_2: XhoI; supplier: Developmental series. Plants from  
 pathogen-free Solanum tuberosum var. Shepody, clone 1756,  
 nuclear stock were grown in a greenhouse under natural  
 conditions. Mature, harvested tubers were stored in the  
 dark at 4C, 95% relative humidity for 3 months. RNA was  
 isolated for library construction. A normalized library  
 was constructed following a modified protocol of Bonaldo  
 et al. (1996. Genome Research 6: 791-806)."

## ORIGIN

Query Match 66.7%; Score 12; DB 7; Length 211;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GGGGUCGAG 12  
 ||||:||||  
 Db 101 GGGGTCTCGAG 90

RESULT 198  
 LOCUS AV152436/C  
 DEFINITION 212 bp mRNA linear EST 07-JUL-1999  
 AV152436 Mus musculus hippocampus C57BL/6J adult Mus musculus cDNA  
 clone 2900037B13, mRNA sequence.  
 ACCESSION AV152436  
 VERSION AV152436.1  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)

## ORIGIN

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 212)  
 AUTHORS Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,  
 Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T.,  
 Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M.,  
 Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Nitsunuma,H., Oda,H.,

Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Suganara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Yoshino, M., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
 RIKEN Mouse ESTs  
 Unpublished (1999)  
 Contact: Chie Owa  
 Genome Science Laboratory  
 RIKEN  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: 81-298-36-9145  
 Fax: 81-298-36-9098  
 Email: genome-res@rtc.riken.go.jp

Thermotabilization and thermactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))  
 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))  
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details

# FEATURES

## source

Location/Qualifiers  
 1..212  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="2900037B13"  
 /sex="male"  
 /tissue\_type="hippocampus"  
 /dev\_stage="adult"  
 /clone\_lib="Mus musculus hippocampus C57BL/6J adult"

## ORIGIN

Query Match 66.7%; Score 12; DB 1; Length 212;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCCGAG 12  
 ||||:||||  
 Db 109 GGGGTCCTGGAG 98

RESULT 199 212 bp mRNA linear EST 04-MAR-2002  
 BM756685 K-EST003393 S6SNU620 Homo sapiens cDNA clone S6SNU620-26-F01 5',  
 LOCUS mRNA sequence.  
 DEFINITION  
 mRNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Homo sapiens (human)  
 EST.  
 BM756685.1 GI:19086300  
 Homo sapiens (human)  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 212)  
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and  
 Kim, Y.S.

21C Frontier Korean EST Project 2001  
 Unpublished (2002)  
 Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 26 row: F column: 01  
 High quality sequence stop: 212.

## FEATURES

Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"

## ORIGIN

Query Match 66.7%; Score 12; DB 4; Length 212;  
 Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCCGAG 12  
 ||||:||||  
 Db 200 GGGGTCCTGGAG 211

RESULT 200 212 bp DNA linear GSS 25-SEP-2003  
 CE204336 tigr-gss-dog-17000372580913 Dog library Canis familiaris genomic,  
 LOCUS genomic survey sequence.  
 DEFINITION  
 genomic survey sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Canis familiaris (dog)  
 Canis familiaris  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 1 (bases 1 to 212)  
 Kirhnes, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Frazer, C.M. and  
 Venter, J.C.

The dog genome: survey sequencing and comparative analysis  
 Science 301 (5641), 1898-1903 (2003)  
 22875432  
 14512627  
 Contact: Kirhnes EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirhnes@tigr.org  
 Class: shotgun.

## FEATURES

Location/Qualifiers  
 1..212  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from peripheral blood"

## ORIGIN

Query Match 66.7%; Score 12; DB 9; Length 212;  
Best Local Similarity 83.3%; Pred. No. 2.2e+04;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGUCUCUGAG 12  
|||:|:|  
Db 177 GGGGTCCTCGAG 188

Search completed: April 25, 2005, 14:50:29  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 25, 2005, 13:09:45 ; Search time 68.6842 Seconds  
(without alignments)  
428.817 Million cell updates/sec

Title: US-08-887-505B-38

Perfect score: 18  
Sequence: 1 GCGGCCCGAGGNNNNN 18

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database:

Issued Patents NA: \*  
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2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCITUS.COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13	72.2	59479	4	US-09-949-016-16910
C 2	12	66.7	12	4	US-09-647-344A-43
C 3	12	66.7	14	3	US-08-650-093C-97
C 4	12	66.7	16	3	US-08-954-210-39
C 5	12	66.7	16	3	US-09-431-419A-39
C 6	12	66.7	19	4	US-09-782-361-14
C 7	12	66.7	20	2	US-08-483-695-22
C 8	12	66.7	20	2	US-07-965-285-22
C 9	12	66.7	20	2	US-08-487-231-22
C 10	12	66.7	20	3	US-09-201-912-22
C 11	12	66.7	20	3	US-08-397-220B-38
C 12	12	66.7	20	3	US-08-397-220B-39
C 13	12	66.7	20	3	US-08-397-220B-40
C 14	12	66.7	20	3	US-08-397-220B-41
C 15	12	66.7	20	3	US-08-397-220B-44
C 16	12	66.7	20	3	US-08-650-093C-38
C 17	12	66.7	20	3	US-08-650-093C-39
C 18	12	66.7	20	3	US-08-650-093C-40
C 19	12	66.7	20	3	US-08-650-093C-41
C 20	12	66.7	20	3	US-08-650-093C-44
C 21	12	66.7	20	4	US-09-647-344A-49
C 22	12	66.7	22	4	US-09-647
C 23	12	66.7	24	2	US-08-639-080-22
C 24	12	66.7	25	4	US-09-647
C 25	12	66.7	25	4	US-09-647-344A-47
C 26	12	66.7	26	3	US-08-397-220B-98
C 27	12	66.7	26	3	US-08-650-093C-98

C 28	12	66.7	30	1	US-08-240-547-7	Sequence 7, Appl
C 29	12	66.7	39	1	US-08-530-492-66	Sequence 66, Appl
C 30	12	66.7	39	3	US-08-906-517-66	Sequence 66, Appl
C 31	12	66.7	46	4	US-09-647-344A-48	Sequence 48, Appl
C 32	12	66.7	47	4	US-09-422-978-2597	Sequence 2597, Ap
C 33	12	66.7	61	4	US-09-621-976-10142	Sequence 10142, A
C 34	12	66.7	155	3	US-08-474-700B-81	Sequence 41, Appl
C 35	12	66.7	177	2	US-08-256-568B-61	Sequence 61, Appl
C 36	12	66.7	177	2	US-08-256-568B-67	Sequence 67, Appl
C 37	12	66.7	177	2	US-08-256-568B-68	Sequence 68, Appl
C 38	12	66.7	177	2	US-08-256-568B-69	Sequence 69, Appl
C 39	12	66.7	177	2	US-08-256-568B-70	Sequence 70, Appl
C 40	12	66.7	177	2	US-08-256-568B-72	Sequence 72, Appl
C 41	12	66.7	177	2	US-08-256-568B-73	Sequence 73, Appl
C 42	12	66.7	177	2	US-08-256-568B-74	Sequence 74, Appl
C 43	12	66.7	177	2	US-08-256-568B-75	Sequence 75, Appl
C 44	12	66.7	177	2	US-08-256-568B-76	Sequence 76, Appl
C 45	12	66.7	177	2	US-08-256-568B-77	Sequence 77, Appl
C 46	12	66.7	177	2	US-08-256-568B-78	Sequence 78, Appl
C 47	12	66.7	177	2	US-08-256-568B-79	Sequence 79, Appl
C 48	12	66.7	177	2	US-08-256-568B-80	Sequence 80, Appl
C 49	12	66.7	177	3	US-09-038-369B-61	Sequence 61, Appl
C 50	12	66.7	177	3	US-09-038-369B-67	Sequence 67, Appl
C 51	12	66.7	177	3	US-09-038-369B-68	Sequence 68, Appl
C 52	12	66.7	177	3	US-09-038-369B-69	Sequence 69, Appl
C 53	12	66.7	177	3	US-09-038-369B-70	Sequence 70, Appl
C 54	12	66.7	177	3	US-09-038-369B-72	Sequence 72, Appl
C 55	12	66.7	177	3	US-09-038-369B-73	Sequence 73, Appl
C 56	12	66.7	177	3	US-09-038-369B-74	Sequence 74, Appl
C 57	12	66.7	177	3	US-09-038-369B-75	Sequence 75, Appl
C 58	12	66.7	177	3	US-09-038-369B-76	Sequence 76, Appl
C 59	12	66.7	177	3	US-09-038-369B-77	Sequence 77, Appl
C 60	12	66.7	177	3	US-09-038-369B-78	Sequence 78, Appl
C 61	12	66.7	177	3	US-09-038-369B-79	Sequence 79, Appl
C 62	12	66.7	177	3	US-09-038-369B-80	Sequence 80, Appl
C 63	12	66.7	177	4	US-09-378-900A-61	Sequence 61, Appl
C 64	12	66.7	177	4	US-09-378-900A-67	Sequence 67, Appl
C 65	12	66.7	177	4	US-09-378-900A-68	Sequence 68, Appl
C 66	12	66.7	177	4	US-09-378-900A-69	Sequence 69, Appl
C 67	12	66.7	177	4	US-09-378-900A-70	Sequence 70, Appl
C 68	12	66.7	177	4	US-09-378-900A-72	Sequence 72, Appl
C 69	12	66.7	177	4	US-09-378-900A-73	Sequence 73, Appl
C 70	12	66.7	177	4	US-09-378-900A-74	Sequence 74, Appl
C 71	12	66.7	177	4	US-09-378-900A-75	Sequence 75, Appl
C 72	12	66.7	177	4	US-09-378-900A-76	Sequence 76, Appl
C 73	12	66.7	177	4	US-09-378-900A-77	Sequence 77, Appl
C 74	12	66.7	177	4	US-09-378-900A-78	Sequence 78, Appl
C 75	12	66.7	177	4	US-09-378-900A-79	Sequence 79, Appl
C 76	12	66.7	177	4	US-09-378-900A-80	Sequence 80, Appl
C 77	12	66.7	177	4	US-09-899-044-61	Sequence 61, Appl
C 78	12	66.7	177	4	US-09-899-044-67	Sequence 67, Appl
C 79	12	66.7	177	4	US-09-899-044-68	Sequence 68, Appl
C 80	12	66.7	177	4	US-09-899-044-69	Sequence 69, Appl
C 81	12	66.7	177	4	US-09-899-044-70	Sequence 70, Appl
C 82	12	66.7	177	4	US-09-899-044-72	Sequence 72, Appl
C 83	12	66.7	177	4	US-09-899-044-73	Sequence 73, Appl
C 84	12	66.7	177	4	US-09-899-044-74	Sequence 74, Appl
C 85	12	66.7	177	4	US-09-899-044-75	Sequence 75, Appl
C 86	12	66.7	177	4	US-09-899-044-76	Sequence 76, Appl
C 87	12	66.7	177	4	US-09-899-044-77	Sequence 77, Appl
C 88	12	66.7	177	4	US-09-899-044-78	Sequence 78, Appl
C 89	12	66.7	177	4	US-09-899-044-79	Sequence 79, Appl
C 90	12	66.7	177	4	US-09-899-044-80	Sequence 80, Appl
C 91	12	66.7	178	2	US-08-256-568B-59	Sequence 59, Appl
C 92	12	66.7	178	2	US-08-256-568B-71	Sequence 71, Appl
C 93	12	66.7	178	3	US-09-038-369B-59	Sequence 59, Appl
C 94	12	66.7	178	3	US-09-038-369B-71	Sequence 71, Appl
C 95	12	66.7	178	4	US-09-378-900A-59	Sequence 59, Appl
C 96	12	66.7	178	4	US-09-378-900A-71	Sequence 71, Appl
C 97	12	66.7	178	4	US-09-899-044-59	Sequence 59, Appl
C 98	12	66.7	180	4	US-09-899-044-71	Sequence 71, Appl
C 99	12	66.7	180	3	US-08-441-971-50	Sequence 50, Appl
C 100	12	66.7	180	3	US-08-441-971-51	Sequence 51, Appl

C 101	12	66.7	180	3	US-08-221-653-50	Sequence 50, Appl	C 174	12	66.7	244	4	US-09-825-574-26	Sequence 26, Appl
C 102	12	66.7	180	3	US-08-221-653-51	Sequence 51, Appl	C 175	12	66.7	244	4	US-09-825-574-29	Sequence 29, Appl
C 103	12	66.7	180	3	US-08-442-144A-50	Sequence 50, Appl	C 176	12	66.7	244	4	US-09-825-574-31	Sequence 31, Appl
C 104	12	66.7	180	3	US-08-442-144A-51	Sequence 51, Appl	C 177	12	66.7	244	4	US-09-676-768-26	Sequence 26, Appl
C 105	12	66.7	180	3	US-08-441-970-50	Sequence 50, Appl	C 178	12	66.7	244	4	US-09-676-768-29	Sequence 29, Appl
C 106	12	66.7	180	3	US-08-441-970-51	Sequence 51, Appl	C 179	12	66.7	244	4	US-09-676-768-31	Sequence 31, Appl
C 107	12	66.7	194	2	US-08-634-797-46	Sequence 46, Appl	C 180	12	66.7	252	3	US-08-441-971-33	Sequence 33, Appl
C 108	12	66.7	194	2	US-08-634-797-47	Sequence 47, Appl	C 181	12	66.7	252	3	US-08-441-971-34	Sequence 34, Appl
C 109	12	66.7	194	2	US-08-634-797-48	Sequence 48, Appl	C 182	12	66.7	252	3	US-08-441-971-35	Sequence 35, Appl
C 110	12	66.7	201	4	US-09-767-28457	Sequence 28457, A	C 183	12	66.7	252	3	US-08-441-971-36	Sequence 36, Appl
C 111	12	66.7	201	4	US-09-513-999C-29549	Sequence 29549, A	C 184	12	66.7	252	3	US-08-441-971-37	Sequence 37, Appl
C 112	12	66.7	232	3	US-09-034-205-37	Sequence 37, Appl	C 185	12	66.7	252	3	US-08-441-971-38	Sequence 38, Appl
C 113	12	66.7	232	3	US-08-934-097A-37	Sequence 37, Appl	C 186	12	66.7	252	3	US-08-441-971-39	Sequence 39, Appl
C 114	12	66.7	232	3	US-08-851-588-37	Sequence 37, Appl	C 187	12	66.7	252	3	US-08-441-971-40	Sequence 40, Appl
C 115	12	66.7	232	3	US-09-677-218B-37	Sequence 37, Appl	C 188	12	66.7	252	3	US-08-441-971-41	Sequence 41, Appl
C 116	12	66.7	232	3	US-09-677-192-37	Sequence 37, Appl	C 189	12	66.7	252	3	US-08-441-971-42	Sequence 42, Appl
C 117	12	66.7	232	4	US-09-402-618B-37	Sequence 37, Appl	C 190	12	66.7	252	3	US-08-441-971-43	Sequence 43, Appl
C 118	12	66.7	232	4	US-09-825-574-37	Sequence 37, Appl	C 191	12	66.7	252	3	US-08-441-971-44	Sequence 44, Appl
C 119	12	66.7	232	4	US-09-676-768-37	Sequence 37, Appl	C 192	12	66.7	252	3	US-08-441-971-45	Sequence 45, Appl
C 120	12	66.7	239	3	US-09-034-205-32	Sequence 32, Appl	C 193	12	66.7	252	3	US-08-441-971-46	Sequence 46, Appl
C 121	12	66.7	239	3	US-09-034-205-36	Sequence 36, Appl	C 194	12	66.7	252	3	US-08-221-653-33	Sequence 33, Appl
C 122	12	66.7	239	3	US-08-934-097A-32	Sequence 32, Appl	C 195	12	66.7	252	3	US-08-221-653-34	Sequence 34, Appl
C 123	12	66.7	239	3	US-08-934-097A-36	Sequence 36, Appl	C 196	12	66.7	252	3	US-08-221-653-35	Sequence 35, Appl
C 124	12	66.7	239	3	US-08-851-588-32	Sequence 32, Appl	C 197	12	66.7	252	3	US-08-221-653-36	Sequence 36, Appl
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C 126	12	66.7	239	3	US-09-677-218B-32	Sequence 32, Appl	C 199	12	66.7	252	3	US-08-221-653-38	Sequence 38, Appl
C 127	12	66.7	239	3	US-09-677-218B-36	Sequence 36, Appl	C 200	12	66.7	252	3	US-08-221-653-39	Sequence 39, Appl
C 128	12	66.7	239	3	US-09-677-192-32	Sequence 32, Appl	C 201	12	66.7	252	3	US-08-221-653-40	Sequence 40, Appl
C 129	12	66.7	239	3	US-09-677-192-36	Sequence 36, Appl	C 202	12	66.7	252	3	US-08-221-653-41	Sequence 41, Appl
C 130	12	66.7	239	4	US-09-402-618B-32	Sequence 32, Appl	C 203	12	66.7	252	3	US-08-221-653-42	Sequence 42, Appl
C 131	12	66.7	239	4	US-09-402-618B-36	Sequence 36, Appl	C 204	12	66.7	252	3	US-08-221-653-43	Sequence 43, Appl
C 132	12	66.7	239	4	US-09-825-574-32	Sequence 32, Appl	C 205	12	66.7	252	3	US-08-221-653-44	Sequence 44, Appl
C 133	12	66.7	239	4	US-09-825-574-36	Sequence 36, Appl	C 206	12	66.7	252	3	US-08-221-653-45	Sequence 45, Appl
C 134	12	66.7	239	4	US-09-676-768-36	Sequence 36, Appl	C 207	12	66.7	252	3	US-08-221-653-46	Sequence 46, Appl
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C 136	12	66.7	240	3	US-09-034-205-38	Sequence 38, Appl	C 209	12	66.7	252	3	US-08-442-144A-34	Sequence 34, Appl
C 137	12	66.7	240	3	US-09-034-205-33	Sequence 33, Appl	C 210	12	66.7	252	3	US-08-442-144A-35	Sequence 35, Appl
C 138	12	66.7	240	3	US-08-934-097A-33	Sequence 33, Appl	C 211	12	66.7	252	3	US-08-442-144A-36	Sequence 36, Appl
C 139	12	66.7	240	3	US-08-934-097A-38	Sequence 38, Appl	C 212	12	66.7	252	3	US-08-442-144A-37	Sequence 37, Appl
C 140	12	66.7	240	3	US-08-851-588-33	Sequence 33, Appl	C 213	12	66.7	252	3	US-08-442-144A-38	Sequence 38, Appl
C 141	12	66.7	240	3	US-08-851-588-38	Sequence 38, Appl	C 214	12	66.7	252	3	US-08-442-144A-39	Sequence 39, Appl
C 142	12	66.7	240	3	US-09-677-218B-33	Sequence 33, Appl	C 215	12	66.7	252	3	US-08-442-144A-40	Sequence 40, Appl
C 143	12	66.7	240	3	US-09-677-218B-38	Sequence 38, Appl	C 216	12	66.7	252	3	US-08-442-144A-41	Sequence 41, Appl
C 144	12	66.7	240	3	US-09-677-192-33	Sequence 33, Appl	C 217	12	66.7	252	3	US-08-442-144A-42	Sequence 42, Appl
C 145	12	66.7	240	3	US-09-677-192-38	Sequence 38, Appl	C 218	12	66.7	252	3	US-08-442-144A-43	Sequence 43, Appl
C 146	12	66.7	240	4	US-09-402-618B-33	Sequence 33, Appl	C 219	12	66.7	252	3	US-08-442-144A-44	Sequence 44, Appl
C 147	12	66.7	240	4	US-09-402-618B-38	Sequence 38, Appl	C 220	12	66.7	252	3	US-08-442-144A-45	Sequence 45, Appl
C 148	12	66.7	240	4	US-09-825-574-33	Sequence 33, Appl	C 221	12	66.7	252	3	US-08-442-144A-49	Sequence 49, Appl
C 149	12	66.7	240	4	US-09-825-574-38	Sequence 38, Appl	C 222	12	66.7	252	3	US-08-441-970-33	Sequence 33, Appl
C 150	12	66.7	240	4	US-09-676-768-33	Sequence 33, Appl	C 223	12	66.7	252	3	US-08-441-970-34	Sequence 34, Appl
C 151	12	66.7	240	4	US-09-676-768-38	Sequence 38, Appl	C 224	12	66.7	252	3	US-08-441-970-35	Sequence 35, Appl
C 152	12	66.7	242	2	US-08-335-595-1	Sequence 1, Appl1	C 225	12	66.7	252	3	US-08-441-970-36	Sequence 36, Appl
C 153	12	66.7	244	3	US-09-034-205-26	Sequence 26, Appl	C 226	12	66.7	252	3	US-08-441-970-37	Sequence 37, Appl
C 154	12	66.7	244	3	US-09-034-205-29	Sequence 29, Appl	C 227	12	66.7	252	3	US-08-441-970-38	Sequence 38, Appl
C 155	12	66.7	244	3	US-09-034-205-31	Sequence 31, Appl	C 228	12	66.7	252	3	US-08-441-970-39	Sequence 39, Appl
C 156	12	66.7	244	3	US-08-934-097A-26	Sequence 26, Appl	C 229	12	66.7	252	3	US-08-441-970-40	Sequence 40, Appl
C 157	12	66.7	244	3	US-08-934-097A-29	Sequence 29, Appl	C 230	12	66.7	252	3	US-08-441-970-41	Sequence 41, Appl
C 158	12	66.7	244	3	US-08-934-097A-31	Sequence 31, Appl	C 231	12	66.7	252	3	US-08-441-970-42	Sequence 42, Appl
C 159	12	66.7	244	3	US-08-851-588-26	Sequence 26, Appl	C 232	12	66.7	252	3	US-08-441-970-43	Sequence 43, Appl
C 160	12	66.7	244	3	US-08-851-588-29	Sequence 29, Appl	C 233	12	66.7	252	3	US-08-441-970-44	Sequence 44, Appl
C 161	12	66.7	244	3	US-08-851-588-31	Sequence 31, Appl	C 234	12	66.7	252	3	US-08-441-970-45	Sequence 45, Appl
C 162	12	66.7	244	3	US-09-677-218B-26	Sequence 26, Appl	C 235	12	66.7	252	3	US-08-441-970-46	Sequence 46, Appl
C 163	12	66.7	244	3	US-09-677-218B-29	Sequence 29, Appl	C 236	12	66.7	252	3	US-08-441-970-47	Sequence 47, Appl
C 164	12	66.7	244	3	US-09-677-218B-31	Sequence 31, Appl	C 237	12	66.7	252	2	US-08-441-970-48	Sequence 48, Appl
C 165	12	66.7	244	3	US-09-677-192-26	Sequence 26, Appl	C 238	12	66.7	252	2	US-08-441-970-49	Sequence 49, Appl
C 166	12	66.7	244	3	US-09-677-192-29	Sequence 29, Appl	C 239	12	66.7	252	2	US-08-441-970-50	Sequence 50, Appl
C 167	12	66.7	244	4	US-09-677-192-31	Sequence 31, Appl	C 240	12	66.7	252	2	US-07-965-285-1	Sequence 1, Appl1
C 168	12	66.7	244	4	US-09-402-618B-26	Sequence 26, Appl	C 241	12	66.7	252	2	US-07-965-285-24	Sequence 24, Appl
C 169	12	66.7	244	4	US-09-402-618B-29	Sequence 29, Appl	C 242	12	66.7	252	2	US-07-965-285-25	Sequence 25, Appl
C 170	12	66.7	244	4	US-09-402-618B-31	Sequence 31, Appl	C 243	12	66.7	252	2	US-07-965-285-26	Sequence 26, Appl
C 171	12	66.7	244	4	US-09-402-618B-124	Sequence 124, App	C 244	12	66.7	252	2	US-07-965-285-46	Sequence 46, Appl
C 172	12	66.7	244	4	US-09-402-618B-127	Sequence 127, App	C 245	12	66.7	252	2	US-08-487-231-24	Sequence 24, Appl
C 173	12	66.7	244	4	US-09-402-618B-128	Sequence 128, App	C 246	12	66.7	252	2	US-08-487-231-25	Sequence 25, Appl

C 247	12	66.7	256	2	US-08-487-231-36	Sequence 26, App1	C 320	12	66.7	341	4	US-09-814-351-3	Sequence 3, App1
C 248	12	66.7	256	3	US-09-201-912-1	Sequence 1, App1	C 321	12	66.7	341	5	PCT-US95-13552-4	Sequence 4, App1
C 249	12	66.7	256	3	US-09-201-912-4	Sequence 24, App1	C 322	12	66.7	342	3	US-08-474-1008-39	Sequence 3, App1
C 250	12	66.7	256	3	US-09-201-912-25	Sequence 25, App1	C 323	12	66.7	347	4	US-08-150-0148-100	Sequence 100, App
C 251	12	66.7	256	3	US-09-201-912-26	Sequence 26, App1	C 324	12	66.7	350	2	US-07-863-622-1	Sequence 1, App1
C 252	12	66.7	260	3	US-08-474-7008-40	Sequence 40, App1	C 325	12	66.7	350	5	PCT-US93-03266-1	Sequence 1, App1
C 253	12	66.7	281	2	US-08-757-653-121	Sequence 121, App	C 326	12	66.7	359	4	US-09-513-999C-11161	Sequence 1161, A
C 254	12	66.7	281	2	US-08-757-653-126	Sequence 126, App	C 327	12	66.7	359	4	US-08-150-2048-99	Sequence 99, App1
C 255	12	66.7	281	2	US-08-757-653-127	Sequence 127, App	C 328	12	66.7	360	4	US-08-150-2048-98	Sequence 98, App1
C 256	12	66.7	281	2	US-08-757-653-128	Sequence 128, App	C 329	12	66.7	370	4	US-09-621-976-1980	Sequence 180, App
C 257	12	66.7	281	2	US-08-757-653-132	Sequence 132, App	C 330	12	66.7	366	2	US-08-757-653-122	Sequence 122, App
C 258	12	66.7	281	3	US-08-520-946-121	Sequence 121, App	C 331	12	66.7	366	3	US-08-520-946-122	Sequence 122, App
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C 260	12	66.7	281	3	US-08-520-946-127	Sequence 127, App	C 333	12	66.7	401	3	US-09-643-597-264	Sequence 264, App
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C 265	12	66.7	281	4	US-09-655-378A-127	Sequence 127, App	C 338	12	66.7	447	4	US-09-902-540-5709	Sequence 5709, App
C 266	12	66.7	281	4	US-09-655-378A-128	Sequence 128, App	C 339	12	66.7	447	4	US-09-621-976-17212	Sequence 17212, A
C 267	12	66.7	281	4	US-09-655-378A-132	Sequence 132, App	C 340	12	66.7	461	3	US-08-836-0758-103	Sequence 103, App
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C 270	12	66.7	282	3	US-08-520-946-124	Sequence 124, App	C 343	12	66.7	584	3	US-08-191-160-18	Sequence 18, App1
C 271	12	66.7	282	3	US-08-520-946-130	Sequence 130, App	C 344	12	66.7	587	4	US-09-720-201A-2	Sequence 2, App1
C 272	12	66.7	282	4	US-09-655-378A-124	Sequence 124, App	C 345	12	66.7	601	4	US-09-949-016-19009	Sequence 19009, A
C 273	12	66.7	282	4	US-09-655-378A-130	Sequence 130, App	C 346	12	66.7	601	4	US-09-949-016-22177	Sequence 22177, A
C 274	12	66.7	289	3	US-09-034-205-20	Sequence 20, App1	C 347	12	66.7	601	4	US-09-949-016-23106	Sequence 23106, A
C 275	12	66.7	289	3	US-09-034-205-23	Sequence 23, App1	C 348	12	66.7	601	4	US-09-949-016-27838	Sequence 27838, A
C 276	12	66.7	289	3	US-08-934-097A-20	Sequence 20, App1	C 349	12	66.7	601	4	US-09-949-016-35419	Sequence 35419, A
C 277	12	66.7	289	3	US-08-934-097A-23	Sequence 23, App1	C 350	12	66.7	601	4	US-09-949-016-35420	Sequence 35420, A
C 278	12	66.7	289	3	US-08-851-588-20	Sequence 20, App1	C 351	12	66.7	601	4	US-09-949-016-35421	Sequence 35421, A
C 279	12	66.7	289	3	US-08-851-588-23	Sequence 23, App1	C 352	12	66.7	601	4	US-09-949-016-35422	Sequence 35422, A
C 280	12	66.7	289	3	US-09-677-218B-20	Sequence 20, App1	C 353	12	66.7	601	4	US-09-949-016-47089	Sequence 47089, A
C 281	12	66.7	289	3	US-09-677-218B-23	Sequence 23, App1	C 354	12	66.7	601	4	US-09-949-016-48640	Sequence 48640, A
C 282	12	66.7	289	3	US-09-677-192-20	Sequence 20, App1	C 355	12	66.7	601	4	US-09-949-016-555193	Sequence 55193, A
C 283	12	66.7	289	3	US-09-677-192-23	Sequence 23, App1	C 356	12	66.7	601	4	US-09-949-016-55671	Sequence 55671, A
C 284	12	66.7	289	4	US-09-402-618B-20	Sequence 20, App1	C 357	12	66.7	601	4	US-09-949-016-58990	Sequence 58990, A
C 285	12	66.7	289	4	US-09-402-618B-23	Sequence 23, App1	C 358	12	66.7	601	4	US-09-949-016-63043	Sequence 63043, A
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C 287	12	66.7	289	4	US-09-825-574-23	Sequence 23, App1	C 360	12	66.7	601	4	US-09-949-016-81230	Sequence 81230, A
C 288	12	66.7	289	4	US-09-825-574-20	Sequence 20, App1	C 361	12	66.7	601	4	US-09-949-016-82531	Sequence 82531, A
C 289	12	66.7	289	4	US-09-676-768-23	Sequence 23, App1	C 362	12	66.7	601	4	US-09-949-016-94155	Sequence 94155, A
C 290	12	66.7	305	1	US-08-332-616A-1	Sequence 1, App1	C 363	12	66.7	601	4	US-09-949-016-116947	Sequence 116947, A
C 291	12	66.7	305	1	US-08-317-220-1	Sequence 1, App1	C 364	12	66.7	601	4	US-09-949-016-127463	Sequence 127463, A
C 292	12	66.7	308	3	US-08-444-818-108	Sequence 108, App	C 365	12	66.7	601	4	US-09-949-016-131124	Sequence 131124, A
C 293	12	66.7	308	3	US-08-444-818-109	Sequence 109, App	C 366	12	66.7	601	4	US-09-949-016-131125	Sequence 131125, A
C 294	12	66.7	308	3	US-08-444-818-110	Sequence 110, App	C 367	12	66.7	601	4	US-09-949-016-132404	Sequence 132404, A
C 295	12	66.7	308	3	US-08-444-818-112	Sequence 112, App	C 368	12	66.7	601	4	US-09-949-016-132405	Sequence 132405, A
C 296	12	66.7	308	3	US-08-444-818-114	Sequence 114, App	C 369	12	66.7	601	4	US-09-949-016-177691	Sequence 177691, A
C 297	12	66.7	308	3	US-08-444-818-116	Sequence 116, App	C 370	12	66.7	601	4	US-09-949-016-178899	Sequence 178899, A
C 298	12	66.7	308	3	US-08-444-818-118	Sequence 118, App	C 371	12	66.7	601	4	US-09-949-016-179483	Sequence 179483, A
C 299	12	66.7	309	4	US-09-513-999C-15853	Sequence 15853, A	C 372	12	66.7	601	4	US-09-949-016-179484	Sequence 179484, A
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C 301	12	66.7	324	2	US-08-470-426B-15	Sequence 15, App1	C 374	12	66.7	601	4	US-09-949-016-179486	Sequence 179486, A
C 302	12	66.7	337	2	US-08-756-386-56	Sequence 56, App1	C 375	12	66.7	601	4	US-09-949-016-183217	Sequence 183217, A
C 303	12	66.7	337	2	US-08-823-516-45	Sequence 45, App1	C 376	12	66.7	601	4	US-09-949-016-184414	Sequence 184414, A
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C 305	12	66.7	337	3	US-08-759-038-56	Sequence 56, App1	C 378	12	66.7	601	4	US-09-949-016-198333	Sequence 198333, A
C 306	12	66.7	337	3	US-08-758-314-56	Sequence 56, App1	C 379	12	66.7	601	4	US-09-949-016-203551	Sequence 203551, A
C 307	12	66.7	337	3	US-09-350-309-56	Sequence 56, App1	C 380	12	66.7	601	4	US-09-949-016-203552	Sequence 203552, A
C 308	12	66.7	337	4	US-09-684-938-56	Sequence 56, App1	C 381	12	66.7	601	4	US-08-836-0758-59	Sequence 59, App1
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C 311	12	66.7	337	4	US-09-333-145-56	Sequence 56, App1	C 384	12	66.7	601	4	US-08-444-818-98	Sequence 98, App1
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C 313	12	66.7	341	2	US-08-440-209-1	Sequence 1, App1	C 386	12	66.7	601	4	US-08-444-818-102	Sequence 102, App
C 314	12	66.7	341	3	US-08-854-531-4	Sequence 4, App1	C 387	12	66.7	601	4	US-09-690-936-37	Sequence 37, App1
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C 318	12	66.7	341	3	US-09-014-416-49	Sequence 49, App1	C 391	12	66.7	601	4	US-09-720-201A-3	Sequence 3, App1
C 319	12	66.7	341	3	US-08-864-380-4	Sequence 4, App1	C 392	12	66.7	702	4		

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C 394	12	66.7	736	4	US-09-328-475C-294	Sequence 294, App	C 467	12	66.7	2589	2	US-08-482-728B-3	Sequence 3, Appl1
C 395	12	66.7	780	3	US-08-474-700B-45	Sequence 45, Appl1	468	12	66.7	2674	4	US-10-066-130-19	Sequence 19, Appl1
C 396	12	66.7	789	3	US-09-109-204-11	Sequence 11, Appl1	469	12	66.7	2733	4	US-09-976-594-517	Sequence 517, App
C 397	12	66.7	789	4	US-09-490-032-11	Sequence 11, Appl1	C 470	12	66.7	2733	4	US-09-976-594-517	Sequence 512, App
C 398	12	66.7	789	4	US-09-949-016-2067	Sequence 2067, App	C 471	12	66.7	2771	4	US-09-949-016-512	Sequence 18, Appl1
C 399	12	66.7	803	1	US-08-157-235-1	Sequence 1, Appl1	C 472	12	66.7	2826	4	US-09-949-016-3926	Sequence 3926, App
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C 405	12	66.7	819	4	US-09-620-461-20	Sequence 20, Appl1	C 478	12	66.7	3181	4	US-09-620-312D-856	Sequence 856, App
C 406	12	66.7	821	3	US-09-342-681C-7	Sequence 7, Appl1	C 479	12	66.7	3264	4	US-09-949-016-1268	Sequence 1268, App
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C 408	12	66.7	923	5	PCT-US95-13552-14	Sequence 14, Appl1	C 481	12	66.7	3304	4	US-09-673-395A-539	Sequence 539, App
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C 410	12	66.7	1024	4	US-09-949-016-5707	Sequence 5707, App	C 483	12	66.7	3478	4	US-08-530-492-1	Sequence 1, Appl1
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C 413	12	66.7	1105	4	US-09-016-434-1481	Sequence 1481, App	C 486	12	66.7	3484	3	US-08-906-517-105	Sequence 105, App
C 414	12	66.7	1131	3	US-09-247-155-146	Sequence 146, App	C 487	12	66.7	3604	4	US-09-016-434-1180	Sequence 1180, App
C 415	12	66.7	1176	3	US-09-342-681C-14	Sequence 14, Appl1	C 488	12	66.7	3650	4	US-09-949-016-3694	Sequence 3694, App
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C 421	12	66.7	1340	4	US-09-673-395A-54	Sequence 54, Appl1	C 494	12	66.7	4636	4	US-09-949-016-5248	Sequence 5248, App
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C 428	12	66.7	1608	5	PCT-US94-02891-68	Sequence 68, App	C 501	12	66.7	5307	4	US-09-949-016-203	Sequence 203, App
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C 432	12	66.7	1752	3	US-09-360-779-1	Sequence 1, Appl1	C 505	12	66.7	5660	4	US-10-056-130-17	Sequence 17, Appl1
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C 434	12	66.7	1773	3	US-09-818-780-71	Sequence 71, Appl1	C 507	12	66.7	6139	4	US-08-843-076D-33	Sequence 33, Appl1
C 435	12	66.7	1863	2	US-08-470-426B-13	Sequence 13, Appl1	C 508	12	66.7	6717	4	US-10-082-272-1	Sequence 1, Appl1
C 436	12	66.7	1863	2	US-08-470-426B-14	Sequence 14, Appl1	C 509	12	66.7	6728	4	US-09-949-016-1103	Sequence 1103, A
C 437	12	66.7	1968	4	US-09-902-540-3231	Sequence 3231, App	C 510	12	66.7	6800	4	US-09-949-016-14697	Sequence 14697, A
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C 445	12	66.7	2106	3	US-10-008-960-1	Sequence 1, Appl1	C 518	12	66.7	7989	4	US-09-519-601-7	Sequence 7, Appl1
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C 447	12	66.7	2106	5	PCT-US94-09700-1	Sequence 1, Appl1	C 520	12	66.7	8001	4	US-09-519-601-16	Sequence 16, Appl1
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C 451	12	66.7	2177	4	US-09-919-039-124	Sequence 124, App	C 524	12	66.7	8596	4	US-09-949-016-14493	Sequence 14493, A
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C 453	12	66.7	2229	4	US-09-810-174B-309	Sequence 309, App	C 526	12	66.7	8638	4	US-10-029-907-6	Sequence 6, Appl1
C 454	12	66.7	2229	4	US-09-620-461-1	Sequence 1, Appl1	C 527	12	66.7	8638	4	US-10-029-907-7	Sequence 7, Appl1
C 455	12	66.7	2235	4	US-09-949-016-3736	Sequence 3736, App	C 528	12	66.7	8638	4	US-10-029-907-24	Sequence 24, Appl1
C 456	12	66.7	2246	4	US-09-949-016-4937	Sequence 4937, App	C 529	12	66.7	8638	4	US-10-029-907-25	Sequence 25, Appl1
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C 465	12	66.7	2505	4	US-09-799-451-179		C 538	12	66.7	9185	3		

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C 542	12	66.7	9379	3	US-09-388-874-1	Sequence 1, Appli	C 615	12	66.7	26050	4	US-09-949-016-17449	Sequence 17449, A
C 543	12	66.7	9379	4	US-09-916-359-1	Sequence 1, Appli	C 616	12	66.7	26433	4	US-09-949-016-15401	Sequence 15401, A
C 544	12	66.7	9401	1	US-07-910-760-9	Sequence 9, Appli	C 617	12	66.7	27600	4	US-09-949-016-15200	Sequence 15200, A
C 545	12	66.7	9401	1	US-08-440-519-9	Sequence 9, Appli	C 618	12	66.7	28933	4	US-09-949-016-16095	Sequence 16095, A
C 546	12	66.7	9401	2	US-08-433-693-1	Sequence 9, Appli	C 619	12	66.7	29133	4	US-09-949-016-12604	Sequence 12604, A
C 547	12	66.7	9401	3	US-08-440-549-9	Sequence 9, Appli	C 620	12	66.7	29171	4	US-09-949-016-12823	Sequence 12823, A
C 548	12	66.7	9401	3	US-08-823-895A-25	Sequence 25, Appli	C 621	12	66.7	29171	4	US-09-949-016-13509	Sequence 13509, A
C 549	12	66.7	9401	5	PCT-US91-02225-9	Sequence 9, Appli	C 622	12	66.7	29558	4	US-09-949-016-15607	Sequence 15607, A
C 550	12	66.7	9413	4	US-09-827-668-6	Sequence 6, Appli	C 623	12	66.7	31414	4	US-09-949-016-12717	Sequence 12717, A
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C 552	12	66.7	9416	2	US-08-384-616-1	Sequence 1, Appli	C 625	12	66.7	36387	4	US-09-949-016-13862	Sequence 13862, A
C 553	12	66.7	9416	2	US-08-904-686A-1	Sequence 1, Appli	C 626	12	66.7	36387	4	US-09-949-016-16730	Sequence 16730, A
C 554	12	66.7	9416	3	US-08-811-566-19	Sequence 19, Appli	C 627	12	66.7	38657	4	US-09-949-016-16267	Sequence 16267, A
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C 556	12	66.7	9416	3	US-09-034-756-19	Sequence 19, Appli	C 629	12	66.7	40905	4	US-09-949-016-16864	Sequence 16864, A
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C 833	11	61.1	219	4	US-09-493-795B-102	Sequence 102, Ap	906	11	61.1	443	4	US-08-485-942A-96	Sequence 96, Appl
C 834	11	61.1	220	3	US-09-488-799-92	Sequence 92, Appl	907	11	61.1	454	3	US-08-488-214A-96	Sequence 96, Appl
C 835	11	61.1	220	3	US-09-488-799-96	Sequence 96, Appl	908	11	61.1	454	3	US-08-488-208A-96	Sequence 96, Appl
C 836	11	61.1	220	3	US-09-488-799-98	Sequence 98, Appl	909	11	61.1	454	3	US-08-483-211A-96	Sequence 96, Appl
C 837	11	61.1	220	4	US-09-493-795B-130	Sequence 130, Appl	910	11	61.1	454	3	US-08-488-223A-96	Sequence 96, Appl
C 838	11	61.1	220	4	US-09-493-795B-135	Sequence 135, Appl	911	11	61.1	454	3	US-08-438-431A-96	Sequence 96, Appl
C 839	11	61.1	220	4	US-09-493-795B-152	Sequence 152, Appl	912	11	61.1	454	3	US-08-488-225A-96	Sequence 96, Appl
C 840	11	61.1	220	4	US-09-493-795B-289	Sequence 289, Appl	913	11	61.1	456	4	US-09-640-211A-1894	Sequence 1894, Ap
C 841	11	61.1	221	3	US-09-488-799-40	Sequence 40, Appl	914	11	61.1	456	4	US-09-640-211A-1895	Sequence 1895, Ap
C 842	11	61.1	222	4	US-09-248-795B-64	Sequence 6827, Ap	C 915	11	61.1	457	4	US-09-621-976-1454	Sequence 1454, Ap
C 843	11	61.1	223	4	US-09-493-795B-68	Sequence 64, Appl	C 916	11	61.1	458	4	US-09-621-976-1989	Sequence 1889, Ap
C 844	11	61.1	223	4	US-09-493-795B-70	Sequence 68, Appl	918	11	61.1	459	4	US-09-640-211A-1857	Sequence 1857, Ap
C 845	11	61.1	223	4	US-09-493-795B-72	Sequence 70, Appl	919	11	61.1	467	4	US-09-270-767-856	Sequence 856, Ap
C 846	11	61.1	223	4	US-09-493-795B-90	Sequence 72, Appl	C 920	11	61.1	467	4	US-09-270-767-1618	Sequence 1618, A
C 847	11	61.1	223	4	US-09-493-795B-134	Sequence 134, Appl	C 921	11	61.1	475	4	US-09-621-976-18640	Sequence 2, Appl1
C 848	11	61.1	223	4	US-09-493-795B-291	Sequence 291, Appl	C 922	11	61.1	475	4	US-09-312-283C-2	Sequence 2, Appl1
C 849	11	61.1	226	3	US-09-488-799-86	Sequence 86, Appl	C 923	11	61.1	477	4	US-09-282-991B-8503	Sequence 8503, Ap
C 850	11	61.1	226	3	US-09-488-799-88	Sequence 88, Appl	C 924	11	61.1	480	3	US-08-814-052-16	Sequence 16, Appl
C 851	11	61.1	226	3	US-09-488-799-94	Sequence 94, Appl	925	11	61.1	480	3	US-09-461-997-47	Sequence 47, Appl
C 852	11	61.1	226	4	US-09-493-795B-90	Sequence 90, Appl	C 926	11	61.1	487	4	US-09-270-767-30314	Sequence 30314, A
C 853	11	61.1	226	4	US-09-493-795B-92	Sequence 92, Appl	C 927	11	61.1	491	3	US-08-485-942A-94	Sequence 94, Appl
C 854	11	61.1	227	4	US-09-493-795B-58	Sequence 58, Appl	928	11	61.1	491	3	US-08-488-214A-94	Sequence 94, Appl
C 855	11	61.1	227	4	US-09-493-795B-76	Sequence 76, Appl	C 929	11	61.1	491	3	US-08-488-208A-94	Sequence 94, Appl
C 856	11	61.1	248	4	US-09-493-795B-104	Sequence 104, Appl	930	11	61.1	491	3	US-08-483-211A-94	Sequence 94, Appl
C 857	11	61.1	248	4	US-09-493-795B-112	Sequence 112, Appl	931	11	61.1	491	3	US-08-488-223A-94	Sequence 94, Appl
C 858	11	61.1	262	4	US-09-513-999C-32006	Sequence 32006, A	932	11	61.1	491	3	US-08-438-431A-94	Sequence 94, Appl
C 859	11	61.1	262	4	US-09-513-999C-34997	Sequence 34997, A	933	11	61.1	498	3	US-08-488-225A-94	Sequence 94, Appl
C 860	11	61.1	282	3	US-08-866-340-20	Sequence 20, Appl	C 934	11	61.1	502	4	US-09-195-106-8	Sequence 8, Appl1
C 861	11	61.1	282	3	US-09-103-875-26	Sequence 26, Appl	935	11	61.1	502	4	US-09-621-976-2291	Sequence 2291, Ap
C 862	11	61.1	285	4	US-09-513-999C-3436	Sequence 3436, Ap	C 936	11	61.1	504	3	US-09-889-595-9	Sequence 9, Appl1
C 863	11	61.1	302	4	US-09-902-540-9391	Sequence 9391, Ap	C 937	11	61.1	504	4	US-09-899-995-9	Sequence 9, Appl1
C 864	11	61.1	303	3	US-09-461-697-61	Sequence 61, Appl	938	11	61.1	511	4	US-09-621-976-9546	Sequence 9546, Ap
C 865	11	61.1	312	3	US-09-240-274-118	Sequence 118, Appl	C 939	11	61.1	513	1	US-08-031-143B-70	Sequence 70, Appl
C 866	11	61.1	314	4	US-09-313-294A-6075	Sequence 6075, Ap	C 940	11	61.1	518	4	US-09-902-540-1541	Sequence 1541, Ap
C 867	11	61.1	315	4	US-09-252-991A-16252	Sequence 16252, A	C 941	11	61.1	519	4	US-09-270-767-2671	Sequence 2671, Ap
C 868	11	61.1	318	3	US-09-240-274-116	Sequence 116, Appl	942	11	61.1	519	4	US-09-270-767-17953	Sequence 17953, A
C 869	11	61.1	318	3	US-09-240-274-117	Sequence 117, Appl	C 943	11	61.1	524	4	US-09-621-976-3553	Sequence 3553, Ap
C 870	11	61.1	318	3	US-09-240-274-119	Sequence 119, Appl	C 944	11	61.1	524	4	US-09-270-767-70297	Sequence 70297, Ap
C 871	11	61.1	319	4	US-09-513-999C-14106	Sequence 14106, A	C 945	11	61.1	525	4	US-09-621-976-22379	Sequence 22379, A
C 872	11	61.1	327	4	US-09-451-651-37	Sequence 30821, A	946	11	61.1	525	4	US-09-464-635-19	Sequence 19, Appl
C 873	11	61.1	331	4	US-09-621-976-7963	Sequence 7963, Ap	947	11	61.1	535	4	US-09-636-215-596	Sequence 596, Appl
C 874	11	61.1	334	4	US-09-513-999C-3421	Sequence 3421, Ap	948	11	61.1	535	4	US-09-685-166A-536	Sequence 536, Appl
C 875	11	61.1	336	4	US-09-902-540-8592	Sequence 8592, Ap	949	11	61.1	535	4	US-09-679-426-596	Sequence 596, Appl
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C 877	11	61.1	345	4	US-09-573-080A-316	Sequence 316, Appl	951	11	61.1	537	4	US-09-621-976-3109	Sequence 3109, Ap
C 878	11	61.1	348	3	US-09-461-697-57	Sequence 57, Appl	952	11	61.1	539	1	US-08-229-518A-11	Sequence 11, Appl
C 879	11	61.1	363	4	US-09-252-991A-8832	Sequence 8832, Ap	953	11	61.1	539	1	US-08-645-865-11	Sequence 11, Appl
C 880	11	61.1	365	4	US-08-905-223-180	Sequence 180, Appl	954	11	61.1	544	5	US-09-471-276-781	Sequence 781, Appl
C 881	11	61.1	367	3	US-09-513-999C-35117	Sequence 35117, A	955	11	61.1	545	4	US-09-640-211A-2056	Sequence 2056, Ap
C 882	11	61.1	383	4	US-09-370-838-88	Sequence 88, Appl	956	11	61.1	548	4	US-09-621-976-3559	Sequence 3559, Ap
C 883	11	61.1	387	3	US-09-854-133-88	Sequence 88, Appl	957	11	61.1	548	4	US-09-621-976-14602	Sequence 14602, A
C 884	11	61.1	387	3	US-09-854-133-88	Sequence 88, Appl	958	11	61.1	551	4	US-08-290-665A-116	Sequence 116, Appl
C 885	11	61.1	396	4	US-09-713-550-36	Sequence 36, Appl	959	11	61.1	551	2	US-08-290-665A-117	Sequence 117, Appl
C 886	11	61.1	396	4	US-09-825-294-36	Sequence 36, Appl	961	11	61.1	573	2	US-08-290-665A-118	Sequence 118, Appl
C 887	11	61.1	396	4	US-09-970-966-36	Sequence 36, Appl	962	11	61.1	573	2	US-08-290-665A-116	Sequence 116, Appl
C 888	11	61.1	396	4	US-09-970-966-36	Sequence 36, Appl	963	11	61.1	573	2	PCT-US95-10398-116	Sequence 116, Appl
C 889	11	61.1	398	1	US-08-118-101A-5	Sequence 5, Appl1	964	11	61.1	573	5	PCT-US95-10398-117	Sequence 117, Appl
C 890	11	61.1	399	3	US-09-461-697-53	Sequence 53, Appl	965	11	61.1	573	5	PCT-US95-10398-118	Sequence 118, Appl
C 891	11	61.1	407	4	US-09-621-976-18088	Sequence 18088, A	966	11	61.1	573	5	PCT-US95-10398-119	Sequence 119, Appl
C 892	11	61.1	413	4	US-09-513-999C-10717	Sequence 10717, A	967	11	61.1	579	3	PCT-US95-10398-126	Sequence 126, Appl
C 893	11	61.1	416	4	US-09-461-697-51	Sequence 51, Appl	968	11	61.1	579	4	US-08-836-075A-15	Sequence 15, Appl1
C 894	11	61.1	420	3	US-09-397-787-228	Sequence 228, Appl	969	11	61.1	579	4	US-09-673-429-2	Sequence 2, Appl1
C 895	11	61.1	428	3	US-09-327-138C-11	Sequence 11, Appl	C 970	11	61.1	601	4	US-09-949-016-18129	Sequence 18129, A
C 896	11	61.1	433	4	US-09-327-138C-39	Sequence 39, Appl	C 971	11	61.1	601	4	US-09-949-016-18381	Sequence 18381, A
C 897	11	61.1	433	4	US-09-679-185-1	Sequence 1, Appl1	C 972	11	61.1	601	4	US-09-949-016-19336	Sequence 19336, A
C 898	11	61.1	436	3	US-09-679-185-3	Sequence 3, Appl1	C 973	11	61.1	601	4	US-09-949-016-19963	Sequence 19963, A
C 899	11	61.1	437	4	US-09-621-976-1458	Sequence 1458, Ap	C 974	11	61.1	601	4	US-09-949-016-19964	Sequence 19964, A
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C 901	11	61.1	438	4	US-09-621-976-1458	Sequence 1458, Ap	976	11	61.1	601	4	US-09-949-016-20681	Sequence 20681, A



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C 977 11 61.1 601 4 US-09-949-016-21112 Sequence 21112, A
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C 979 11 61.1 601 4 US-09-949-016-21114 Sequence 21114, A
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C 981 11 61.1 601 4 US-09-949-016-21195 Sequence 21195, A
C 982 11 61.1 601 4 US-09-949-016-21195 Sequence 21195, A
C 983 11 61.1 601 4 US-09-949-016-21197 Sequence 21197, A
C 984 11 61.1 601 4 US-09-949-016-22265 Sequence 22265, A
C 985 11 61.1 601 4 US-09-949-016-22919 Sequence 22919, A
C 986 11 61.1 601 4 US-09-949-016-22920 Sequence 22920, A
C 987 11 61.1 601 4 US-09-949-016-22921 Sequence 22921, A
C 988 11 61.1 601 4 US-09-949-016-23001 Sequence 23001, A
C 989 11 61.1 601 4 US-09-949-016-23130 Sequence 23130, A
C 990 11 61.1 601 4 US-09-949-016-23131 Sequence 23131, A
C 991 11 61.1 601 4 US-09-949-016-23132 Sequence 23132, A
C 992 11 61.1 601 4 US-09-949-016-24638 Sequence 24638, A
C 993 11 61.1 601 4 US-09-949-016-26121 Sequence 26121, A
C 994 11 61.1 601 4 US-09-949-016-26267 Sequence 26267, A
C 995 11 61.1 601 4 US-09-949-016-27307 Sequence 27307, A
C 996 11 61.1 601 4 US-09-949-016-27476 Sequence 27476, A
C 997 11 61.1 601 4 US-09-949-016-27859 Sequence 27859, A
C 998 11 61.1 601 4 US-09-949-016-29148 Sequence 29148, A
C 999 11 61.1 601 4 US-09-949-016-29149 Sequence 29149, A
C 1000 11 61.1 601 4 US-09-949-016-32534 Sequence 32534, A
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## ALIGNMENTS

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RESULT 1
US-09-949-016-16910/c
; Sequence 16910, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 16910
; LENGTH: 59479
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(59479)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16910
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Query Match 72.2%; Score 13; DB 4; Length 59479;
Best Local Similarity 92.3%; Pred. No. 1.2e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 6 CCUGAGNNNNNN 18
DB 11936 CCGAGNNNNNN 11924
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RESULT 2
US-09-647-344A-43/c
; Sequence 43, Application US/09647344A
; Patent No. 6586180
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
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; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678 PCT US
; CURRENT APPLICATION NUMBER: US/09/647, 344A
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NO 43
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..6
; OTHER INFORMATION: A portion of an antisense library including a Bpm1 site.
US-09-647-344A-43
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Query Match 66.7%; Score 12; DB 4; Length 12;
Best Local Similarity 91.7%; Pred. No. 9.6e+02;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 7 CCUGAGNNNNNN 18
DB 12 CCGAGNNNNNN 1
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RESULT 3
US-08-650-093C-97/c
; Sequence 97, Application US/08650093C
; Patent No. 6391342
; GENERAL INFORMATION:
; APPLICANT: Kevin P. Anderson et al.
; TITLE OF INVENTION: Compositions And Methods For Treatment Of
; Hepatitis C Virus-Associated Diseases
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LICATA & TYRELL, P.C.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WORDPERFECT 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/650, 093C
; FILING DATE: 17-May-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/452, 841
; FILING DATE: May 30, 1995
; APPLICATION NUMBER: 08/397, 220
; FILING DATE: March 9, 1995
; APPLICATION NUMBER: 07/945, 289
; FILING DATE: September 10, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: 11PH-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
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ANTI-SENSE: No
SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-08-650-093C-97

Query Match      66.7%; Score 12; DB 3; Length 14;
Best Local Similarity 83.3%; Pred. No. 9.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGUCCUGAG 12
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Db      14 GGGGTCTTGAG 3

RESULT 4
US-08-954-210-39
Sequence 39, Application US/08954210
Patent No. 6043077
GENERAL INFORMATION:
APPLICANT: Barber, Jack R.
APPLICANT: Welch, Peter J.
APPLICANT: Tritz, Richard
APPLICANT: Yel, Soomin
TITLE OF INVENTION: HEPATITIS C VIRUS RIBOZYMES
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,210
FILING DATE: 20-OCT-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480124.403C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-954-210-39

Query Match      66.7%; Score 12; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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APPLICANT: Yel, Soomin
APPLICANT: Yu, Mang
TITLE OF INVENTION: HEPATITIS C VIRUS RIBOZYMES
FILE REFERENCE: 480124.403C3
CURRENT APPLICATION NUMBER: US/09/431,419A
CURRENT FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 39
LENGTH: 16
TYPE: DNA
ORGANISM: Hepatitis C Virus
US-09-431-419A-39

Query Match      66.7%; Score 12; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGUCCUGAG 12
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Db      3 GGGGUCCUGAG 14

RESULT 6
US-09-782-361-14
Sequence 14, Application US/09782361
Patent No. 6811974
GENERAL INFORMATION:
APPLICANT: Hu, Yu-Men
TITLE OF INVENTION: PRIMER-SPECIFIC AND MISPAIR EXTENSION ASSAY FOR IDENTIFYING GE
FILE REFERENCE: 2883-4257US
CURRENT APPLICATION NUMBER: US/09/782,361
CURRENT FILING DATE: 2001-02-13
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: primer for PSMEA
US-09-782-361-14

Query Match      66.7%; Score 12; DB 4; Length 19;
Best Local Similarity 83.3%; Pred. No. 9.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGUCCUGAG 12
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Db      2 GGGGTCTTGAG 13

RESULT 7
US-08-483-695-22/C
Sequence 22, Application US/08483695
Patent No. 5866139
GENERAL INFORMATION:
APPLICANT: Brecht, Christian
APPLICANT: Kremendorf, Dina
APPLICANT: Porchon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
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COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,695  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,285  
FILING DATE: 18-MAR-1993  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: DNA probe  
US-08-483-695-22

Query Match. 66.7%; Score 12; DB 2; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 19 GGGGTCCTGGAG 8

RESULT 8  
US-07-965-285-22/c  
Sequence 22, Application US/07965285  
Patent No. 5879904  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Krensdorf, Dina  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/965,285  
FILING DATE: 18-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: DNA probe  
US-07-965-285-22

NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
DESCRIPTION: DNA probe  
US-07-965-285-22

Query Match. 66.7%; Score 12; DB 2; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 19 GGGGTCCTGGAG 8

RESULT 9  
US-08-487-231-22/c  
Sequence 22, Application US/08487231  
Patent No. 5919454  
GENERAL INFORMATION:  
APPLICANT: Brechot, Christian  
APPLICANT: Krensdorf, Dina  
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESS: Dunner  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,231  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/965,285  
FILING DATE: 18-MAR-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91 06 882  
FILING DATE: 06-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 05286-0001-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

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;      TOPOLOGY:  linear
;      MOLECULE TYPE:  Other
;      DESCRIPTION:  DNA probe
US-08-487-231-22

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Query Match	66.7%	Score 12:	DB 2:	Length 20:
Best Local Similarity	83.3%	Pred. No.	9.1e+02:	
Matches 10:	Conservative	2:	Mismatches 0:	Indels 0:
				Gaps 0:

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QY      1 GGGGUCCTGGAG 12
         ||||:|||||
Db      19 GGGGTCCTGGAG  8

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RESULT 10
US-09-201-912-22/c
: Sequence 22, Application US/09201912
: Patent No. 6210962
: GENERAL INFORMATION:
: APPLICANT: Brechot, Christian
: APPLICANT: Krensdorf, Dina
: APPLICANT: Porchon, Colette
: TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
: TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
: TITLE OF INVENTION: Applications
: NUMBER OF SEQUENCES: 46
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
: ADDRESSEE: Dunner
: STREET: 1300 I Street, N.W.
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005-3315
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/201,912
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/965,285
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Meyers, Kenneth J.
: REGISTRATION NUMBER: 25,146
: REFERENCE/DOCKET NUMBER: 05286-0001-00000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-408-4000
: TELEFAX: 202-408-4400
: INFORMATION FOR SEQ ID NO: 22:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 20 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Other
: DESCRIPTION: DNA probe
US-09-201-912-22

Query Match 66.7%; Score 12; DB 3; Length 20;
Best Local Similarity 83.3%; Pred. No. 9.1e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGCGCCGAG 12
|||:|||||
Db 19 GGGCTCTGGAG 8

```

US-08-397-220B-38  
Sequence 38, Application US/08397220B  
Patent No. 6284458  
GENERAL INFORMATION:  
APPLICANT: Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment  
Of Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jane Massey Licata, Esq.  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM 486  
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,220B  
FILING DATE: 09-Mar-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/01293  
FILING DATE: 10-Sep-93  
APPLICATION NUMBER: JP 5-87195  
FILING DATE: 14-Apr-93  
APPLICATION NUMBER: 07/945,289  
FILING DATE: 10-Sep-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-08-397-220B-38  
Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
CY 1 GGGGUCCTGGAG 12  
|||:|:|:|:|  
DB 1 GGGGCTCTGGAG 12  
RESULT 12  
US-08-397-220B-39  
Sequence 39, Application US/08397220B  
Patent No. 6284458  
GENERAL INFORMATION:  
APPLICANT: Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment  
Of Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jane Massey Licata, Esq.  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM 486  
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,220B  
FILING DATE: 09-Mar-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/01293  
FILING DATE: 10-Sep-93  
APPLICATION NUMBER: JP 5-87195  
FILING DATE: 14-Apr-93  
APPLICATION NUMBER: 07/945,289  
FILING DATE: 10-Sep-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-08-397-220B-39

Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
Db 3 GGGGCTCTGGAG 14

RESULT 13  
US-08-397-220B-40  
Sequence 40, Application US/08397220B  
Patent No. 6284458  
GENERAL INFORMATION:  
APPLICANT: Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment  
Of Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jane Massey Licata, Esq.  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM 486  
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,220B  
FILING DATE: 09-Mar-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/01293  
FILING DATE: 10-Sep-93  
APPLICATION NUMBER: JP 5-87195  
FILING DATE: 14-Apr-93  
APPLICATION NUMBER: 07/945,289

FILING DATE: 10-Sep-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
US-08-397-220B-40

Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
Db 5 GGGGCTCTGGAG 16

RESULT 14  
US-08-397-220B-41  
Sequence 41, Application US/08397220B  
Patent No. 6284458  
GENERAL INFORMATION:  
APPLICANT: Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment  
Of Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jane Massey Licata, Esq.  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM 486  
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,220B  
FILING DATE: 09-Mar-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/01293  
FILING DATE: 10-Sep-93  
APPLICATION NUMBER: JP 5-87195  
FILING DATE: 14-Apr-93  
APPLICATION NUMBER: 07/945,289  
FILING DATE: 10-Sep-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes

SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-08-397-2208-41

Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
DB 7 GGGGCTCGAG 18

## RESULT 15

US-08-397-2208-44  
Sequence 44, Application US/083972208  
Patent No. 6284458  
GENERAL INFORMATION:  
APPLICANT: Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment Of Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jane Massey Licata, Esq.  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM 486  
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,2208  
FILING DATE: 09-Mar-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/01293  
FILING DATE: 10-Sep-93  
APPLICATION NUMBER: JP 5-87195  
FILING DATE: 14-Apr-93  
APPLICATION NUMBER: 07/945,289  
FILING DATE: 10-Sep-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 44:  
US-08-397-2208-44  
Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
DB 9 GGGGCTCGAG 20

## RESULT 16

US-08-650-093C-38  
Sequence 38, Application US/08650093C

Patent No. 6391542  
GENERAL INFORMATION:

APPLICANT: Kevin P. Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment Of Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 118  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LICATA & TYRRELL P.C.  
STREET: 66 E. Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08053

## COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WORDPERFECT 6.1 for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/650,093C  
FILING DATE: 17-May-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/452,841  
FILING DATE: May 30, 1995  
APPLICATION NUMBER: 08/397,220  
FILING DATE: March 9, 1995  
APPLICATION NUMBER: 07/945,289  
FILING DATE: September 10, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-08-650-093C-38  
Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
DB 1 GGGGCTCGAG 12

## RESULT 17

US-08-650-093C-39  
Sequence 39, Application US/08650093C  
Patent No. 6391542  
GENERAL INFORMATION:  
APPLICANT: Kevin P. Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment Of Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 118  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LICATA & TYRRELL P.C.  
STREET: 66 E. Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WORDPERFECT 6.1 for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/650,093C  
FILING DATE: 17-May-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/452,841  
FILING DATE: May 30, 1995  
APPLICATION NUMBER: 08/397,220  
FILING DATE: March 9, 1995  
APPLICATION NUMBER: 07/945,289  
FILING DATE: September 10, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-08-650-093C-39

Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
Db 3 GGGGTCCTGGAG 14

RESULT 18  
US-08-650-093C-40  
Sequence 40, Application US/08650093C  
Patent No. 6391542  
GENERAL INFORMATION:  
APPLICANT: Kevin P. Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment Of  
Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 118  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LICATA & TYRRELL P.C.  
STREET: 66 E. Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WORDPERFECT 6.1 for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/650,093C  
FILING DATE: 17-May-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/452,841  
FILING DATE: May 30, 1995  
APPLICATION NUMBER: 08/397,220  
FILING DATE: March 9, 1995  
APPLICATION NUMBER: 07/945,289  
FILING DATE: September 10, 1992  
ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
US-08-650-093C-40

Query Match 66.7%; Score 12; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
Db 5 GGGGTCCTGGAG 16

RESULT 19  
US-08-650-093C-41  
Sequence 41, Application US/08650093C  
Patent No. 6391542  
GENERAL INFORMATION:  
APPLICANT: Kevin P. Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment Of  
Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 118  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LICATA & TYRRELL P.C.  
STREET: 66 E. Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WORDPERFECT 6.1 for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/550,093C  
FILING DATE: 17-May-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/452,841  
FILING DATE: May 30, 1995  
APPLICATION NUMBER: 08/397,220  
FILING DATE: March 9, 1995  
APPLICATION NUMBER: 07/945,289  
FILING DATE: September 10, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
US-08-650-093C-41

Query Match 66.7%; Score 12; DB 3; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
 |||||:  
 Db 7 GGGGCTCGAG 18

RESULT 20  
 US-08-650-093C-44  
 ; Sequence 44, Application US/08650093C  
 ; Patent No. 6391542  
 ; GENERAL INFORMATION:

APPLICANT: Kevin P. Anderson et al.  
 TITLE OF INVENTION: Compositions And Methods For Treatment Of  
 Hepatitis C Virus-Associated Diseases  
 NUMBER OF SEQUENCES: 118  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LICATA & TYRRELL P.C.  
 STREET: 66 E. Main Street  
 CITY: Marlton  
 STATE: NJ  
 COUNTRY: USA  
 ZIP: 08053

COMPUTER READABLE FORM:  
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows 95  
 SOFTWARE: WORDPERFECT 6.1 for Windows

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/650,093C  
 FILING DATE: 17-May-1996  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/452,841  
 FILING DATE: May 30, 1995  
 APPLICATION NUMBER: 08/397,220  
 FILING DATE: March 9, 1995  
 APPLICATION NUMBER: 07/945,289  
 FILING DATE: September 10, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata  
 REGISTRATION NUMBER: 32,257  
 REFERENCE/DOCKET NUMBER: ISPH-  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (609) 779-2400  
 TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 44:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 20  
 TYPE: Nucleic Acid  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear

ANTI-SENSE: Yes  
 SEQUENCE DESCRIPTION: SEQ ID NO: 44:  
 US-08-650-093C-44

Query Match 66.7%; Score 12; DB 3; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 9.1e+02;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
 |||||:  
 Db 9 GGGGCTCGAG 20

RESULT 21  
 US-09-647-344A-49/c  
 ; Sequence 49, Application US/09647344A  
 ; Patent No. 6586180  
 ; GENERAL INFORMATION:

APPLICANT: Ruffner, Duane E.  
 APPLICANT: Pierce, Michael L.  
 APPLICANT: Chen, Zhidong  
 TITLE OF INVENTION: Directed Antisense Libraries  
 FILE REFERENCE: T6678.PCT.US  
 CURRENT APPLICATION NUMBER: US/09/647,344A  
 CURRENT FILING DATE: 2000-12-04  
 PRIOR APPLICATION NUMBER: PCT/US99/06742  
 PRIOR FILING DATE: 1999-03-28  
 NUMBER OF SEQ ID NOS: 50  
 SEQ ID NO 49  
 TYPE: DNA  
 LENGTH: 20  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 1..14  
 OTHER INFORMATION: Deletion fragment in a deletion fragment library, including a pc  
 US-09-647-344A-49

Query Match 66.7%; Score 12; DB 4; Length 20;  
 Best Local Similarity 91.7%; Pred. No. 9.1e+02;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGGAGNNNNN 18  
 |||||:  
 Db 20 CTGGAGNNNNN 9

RESULT 22  
 US/09/647/c  
 ; Sequence 38, Application US/09647344A  
 ; Patent No. 6586180  
 ; GENERAL INFORMATION:

APPLICANT: Ruffner, Duane E.  
 APPLICANT: Pierce, Michael L.  
 APPLICANT: Chen, Zhidong

TITLE OF INVENTION: Directed Antisense Libraries

FILE REFERENCE: T6678.PCT.US

CURRENT APPLICATION NUMBER: US/09/647,344A

PRIOR APPLICATION NUMBER: PCT/US99/06742

PRIOR FILING DATE: 1999-03-28

NUMBER OF SEQ ID NOS: 50

SEQ ID NO 38

LENGTH: 22

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 1..16

OTHER INFORMATION: Portion of an intermediate in the making of a deletion library,  
 US/09/647,344A-38

Query Match 66.7%; Score 12; DB 4; Length 22;  
 Best Local Similarity 91.7%; Pred. No. 9e+02;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGGAGNNNNN 18  
 |||||:  
 Db 22 CTGGAGNNNNN 11

RESULT 23  
 US-08-639-080-22  
 ; Sequence 22, Application US/08639080  
 ; Patent No. 5843651  
 ; GENERAL INFORMATION:  
 APPLICANT: Rothmund, Paul W.K.  
 TITLE OF INVENTION: METHOD FOR CONSTRUCTING UNIVERSAL DNA  
 NUMBER OF SEQUENCES: 31  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Ste 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION NUMBER: US/08/639,080  
FILING DATE: April 24, 1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Harris, Scott C.  
REGISTRATION NUMBER: 32,030  
REFERENCE/DOCKET NUMBER: 06618/129001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 678-5070  
TELEFAX: (619) 678-5099  
TELEX:  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: oligonucleotide  
FEATURE:  
LOCATION: 7-24  
OTHER INFORMATION: where N at positions 6-13 can be adenine,  
OTHER INFORMATION: guanine, cytosine, thymine or uracil  
US-08-639-080-22

Query Match 66.7%; Score 12; DB 2; Length 24;  
Best Local Similarity 91.7%; Pred. No. 9e+02;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGAGNNNNN 18  
DB 1 CTGAGAGNNNNN 12

RESULT 24  
US/09/647/c  
Sequence 39, Application US/09647344A  
Patent No. 6586180  
GENERAL INFORMATION:  
APPLICANT: Ruffner, Duane E.  
APPLICANT: Pierce, Michael L.  
APPLICANT: Chen, Zhidong  
TITLE OF INVENTION: Directed Antisense Libraries  
FILE REFERENCE: 16678.PCT.US  
CURRENT APPLICATION NUMBER: US/09/647,344A  
CURRENT FILING DATE: 2000-12-04  
PRIOR APPLICATION NUMBER: PCT/US99/06742  
PRIOR FILING DATE: 1999-03-28  
NUMBER OF SEQ ID NOS: 50  
SEQ ID NO 39  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 6..19  
OTHER INFORMATION: 14 bp variable sequence fragment of a deletion library including  
US/09/647,344A-39

Query Match 66.7%; Score 12; DB 4; Length 25;  
Best Local Similarity 91.7%; Pred. No. 8.9e+02;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGAGNNNNN 18  
DB 25 CTGAGAGNNNNN 14

RESULT 25  
US-09-647-344A-47/c  
Sequence 47, Application US/09647344A  
Patent No. 6586180  
GENERAL INFORMATION:  
APPLICANT: Ruffner, Duane E.  
APPLICANT: Pierce, Michael L.  
APPLICANT: Chen, Zhidong  
TITLE OF INVENTION: Directed Antisense Libraries  
FILE REFERENCE: 16678.PCT.US  
CURRENT APPLICATION NUMBER: US/09/647,344A  
CURRENT FILING DATE: 2000-12-04  
PRIOR APPLICATION NUMBER: PCT/US99/06742  
PRIOR FILING DATE: 1999-03-28  
NUMBER OF SEQ ID NOS: 50  
SEQ ID NO 47  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 14..19  
OTHER INFORMATION: Sequence flanking the chloramphenicol (CAT) gene after insertion  
US-09-647-344A-47

Query Match 66.7%; Score 12; DB 4; Length 25;  
Best Local Similarity 91.7%; Pred. No. 8.9e+02;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGAGNNNNN 18  
DB 25 CTGAGAGNNNNN 14

RESULT 26  
US-08-397-220B-98/c  
Sequence 98, Application US/08397220B  
Patent No. 6284458  
GENERAL INFORMATION:  
APPLICANT: Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment Of Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 98  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jane Massey Licata, Esq.  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM 486  
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,220B  
FILING DATE: 09-Mar-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/01293  
FILING DATE: 10-Sep-93  
APPLICATION NUMBER: JP 5-87195  
FILING DATE: 14-Apr-93  
APPLICATION NUMBER: 07/945,289



FILING DATE: 10-SEP-92  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 98:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26  
TYPE: nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 98:  
US-08-397-220B-98  
Query Match 66.7%; Score 12; DB 3; Length 26;  
Best Local Similarity 83.3%; Pred. No. 8.9e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGUCCUGAG 12  
|||:|:|:  
Db 20 GGGGTCTGAG 9  
RESULT 27  
US-08-650-093C-98/c  
Sequence 98, Application US/08650093C  
Patent No. 6391542  
GENERAL INFORMATION:  
APPLICANT: Kevin P. Anderson et al.  
TITLE OF INVENTION: Compositions And Methods For Treatment Of  
Hepatitis C Virus-Associated Diseases  
NUMBER OF SEQUENCES: 118  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LICATA & TYRRELL P.C.  
STREET: 66 E. Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WORDPERFECT 6.1 for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/650,093C  
FILING DATE: 17-May-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/452,841  
FILING DATE: May 30, 1995  
APPLICATION NUMBER: 08/397,220  
FILING DATE: March 9, 1995  
APPLICATION NUMBER: 07/945,289  
FILING DATE: September 10, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 98:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 98:  
US-08-650-093C-98  
Query Match 66.7%; Score 12; DB 3; Length 26;  
Best Local Similarity 83.3%; Pred. No. 8.9e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGUCCUGAG 12  
|||:|:|:  
Db 20 GGGGTCTGAG 9  
RESULT 28  
US-08-240-547-7/c  
Sequence 7, Application US/08240547  
Patent No. 5527669  
GENERAL INFORMATION:  
APPLICANT: Resnick, Robert M.  
APPLICANT: Young, Karen K.Y.  
TITLE OF INVENTION: Primers and Probes for Detection of  
Hepatitis C and No. 5527669el Variants  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingland Street  
CITY: Nutley  
STATE: NJ  
COUNTRY: U.S.A.  
ZIP: 07110-1199  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/240,547  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/918,844  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sias Ph.D., Stacey R.  
REGISTRATION NUMBER: 32,630  
REFERENCE/DOCKET NUMBER: 8586  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2863  
TELEFAX: (510) 814-2977  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-240-547-7  
Query Match 66.7%; Score 12; DB 1; Length 30;  
Best Local Similarity 83.3%; Pred. No. 8.8e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGUCCUGAG 12  
|||:|:|:  
Db 13 GGGGTCTGAG 2  
RESULT 29  
US-08-530-492-66/c  
Sequence 66, Application US/08530492  
Patent No. 5689052  
GENERAL INFORMATION:  
APPLICANT: Brown, Sherri M.  
APPLICANT: Dean, Duff A.

```

; APPLICANT: Fromm, Michael E.
; APPLICANT: Sanders, Patricia R.
; TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced
; TITLE OF INVENTION: Expression in Monocytledonous Plants and Method For
; TITLE OF INVENTION: Preparation Thereof
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. B94F
; STREET: 700 Chesterfield Parkway No. 5689052ch
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,492
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/172,333
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10605)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6047
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; US-08-530-492-66

Query Match      66.7%; Score 12; DB 1; Length 39;
Best Local Similarity 83.3%; Pred. No. 8.6e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCUCGAG 12
Db      20 GGGGCTCTGGAG 9

RESULT 30
US-08-906-517-66/c
; Sequence 66, Application US/08906517
; Patent No. 6180774
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Dean, Duff A.
; APPLICANT: Fromm, Michael E.
; APPLICANT: Sanders, Patricia R.
; TITLE OF INVENTION: Synthetic DNA Sequences Having Enhanced
; TITLE OF INVENTION: Expression in Monocytledonous Plants and Method For
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,517
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: MOBT:170
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-906-517-66

Query Match      66.7%; Score 12; DB 3; Length 39;
Best Local Similarity 83.3%; Pred. No. 8.6e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCUCGAG 12
Db      20 GGGGCTCTGGAG 9

RESULT 31
US-09-647-344A-48/c
; Sequence 48, Application US/09647344A
; Patent No. 6586180
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678.PCT.US
; CURRENT APPLICATION NUMBER: US/09/647,344A
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NO 48
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 6..12 and 35..40
; OTHER INFORMATION: Hammerhead ribozyme library with flanking sequences.
; US-09-647-344A-48

Query Match      66.7%; Score 12; DB 4; Length 46;
Best Local Similarity 91.7%; Pred. No. 8.4e+02;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      7 CUGAGNNNNNN 18
Db      46 CTGAGNNNNNN 35

RESULT 32
US-09-422-978-2597
; Sequence 2597, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

```

FILE REFERENCE: GENSET.020CP1  
CURRENT APPLICATION NUMBER: US/09/422,978  
CURRENT FILING DATE: 1999-10-20  
EARLIER APPLICATION NUMBER: US 09/298,850  
EARLIER FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 60/109,732  
EARLIER FILING DATE: 1998-11-23  
EARLIER APPLICATION NUMBER: US 60/082,614  
EARLIER FILING DATE: 1998-04-21  
NUMBER OF SEQ ID NOS: 11796  
SEQ ID NO 2597  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: allele  
LOCATION: 24  
OTHER INFORMATION: 99-1211-59 : polymorphic base C or T  
US-09-422-978-2597

Query Match 66.7%; Score 12; DB 4; Length 47;  
Best Local Similarity 83.3%; Pred. No. 8.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCUGAG 12  
|||:|||||  
Db 25 GGGGTCTGAG 36

RESULT 33  
US-09-621-976-10142  
Sequence 10142, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 10142  
LENGTH: 61  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 6  
OTHER INFORMATION: n=a, g, c or t  
US-09-621-976-10142

Query Match 66.7%; Score 12; DB 4; Length 61;  
Best Local Similarity 83.3%; Pred. No. 8.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCUGAG 12  
|||:|||||  
Db 29 GGGGTCTGAG 40

RESULT 34  
US-08-474-700B-41  
Sequence 41, Application US/08474700B  
Patent No. 6001990  
GENERAL INFORMATION:  
APPLICANT: Maeda, Jack  
APPLICANT: Makita, Takaji  
APPLICANT: Moradpour, Darius  
TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C  
TITLE OF INVENTION: VIRUS  
NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 555X  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,700B  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/240,382  
FILING DATE: 10 May 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00786/279001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 155 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-474-700B-41

Query Match 66.7%; Score 12; DB 3; Length 155;  
Best Local Similarity 83.3%; Pred. No. 7.5e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCUGAG 12  
|||:|||||  
Db 33 GGGGTCTGAG 44

RESULT 35  
US-08-256-568B-61/C  
Sequence 61, Application US/08256568B  
Patent No. 5846704  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,568B  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: bea2 (also referred to as be99)  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-08-256-568B-61

Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGAGUCCUGAG 12  
|||:|||||  
Db 26 GGAGTCTCGAG 15

RESULT 36  
US-08-256-568B-67/c  
Sequence 67, Application US/08256568B  
Patent No. 5846704  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWM, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,568B  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: 9B48  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-08-256-568B-67

Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGAGUCCUGAG 12  
|||:|||||  
Db 26 GGAGTCTCGAG 15

RESULT 37  
US-08-256-568B-68/c  
Sequence 68, Application US/08256568B  
Patent No. 5846704  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWM, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,568B  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:  
CLONE: gb116  
POSITION IN GENOME:  
MAP POSITION: 5', untranslated region  
US-08-256-568B-68

Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCTGGAG 15

## RESULT 38

US-08-256-568B-69/c  
Sequence 69, Application US/08256568B  
Patent No. 5846704  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,568B  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8002  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:  
CLONE: gb569  
POSITION IN GENOME:  
MAP POSITION: 5', untranslated region  
US-08-256-568B-69

Query Match 66.7%; Score 12; DB 2; Length 177;

Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCTGGAG 15

## RESULT 39

US-08-256-568B-70/c  
Sequence 70, Application US/08256568B  
Patent No. 5846704  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,568B  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8002  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:  
CLONE: gb358  
POSITION IN GENOME:  
MAP POSITION: 5', untranslated region  
US-08-256-568B-70

Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCTGGAG 15

## RESULT 40

US-08-256-568B-72/c  
; Sequence 72, Application US/08256568B  
; Patent No. 5846704  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,568B  
; FILING DATE: 18-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410,004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 72:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: Cam600  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
US-08-256-568B-72  
Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGUGAG 12  
DB 26 GGGGTCCTGGAG 15  
RESULT 41  
US-08-256-568B-73/c  
; Sequence 73, Application US/08256568B  
; Patent No. 5846704  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,568B  
; FILING DATE: 18-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410,004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: Cam736  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
US-08-256-568B-73  
Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGUGAG 12  
DB 26 GGGGTCCTGGAG 15  
RESULT 42  
US-08-256-568B-74/c  
; Sequence 74, Application US/08256568B  
; Patent No. 5846704  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,568B
FILING DATE: 18-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: gpb809
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-08-256-568B-74

Query Match      66.7%; Score 12; DB 2; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCGCGAG 12
        |||:|:|:|:|
Db      26 GGGGTCTCGAG 15

RESULT 43
US-08-256-568B-75/c
; Sequence 75, Application US/08256568B
; Patent No. 5846704
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWM, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,568B
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03325
```

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FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: gpb487
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-08-256-568B-75

Query Match      66.7%; Score 12; DB 2; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCGCGAG 12
        |||:|:|:|:|
Db      26 GGGGTCTCGAG 15

RESULT 44
US-08-256-568B-76/c
; Sequence 76, Application US/08256568B
; Patent No. 5846704
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWM, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,568B
; FILING DATE: 18-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
```

REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb724  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-08-256-568B-76

Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
|||:|||||  
Db 26 GGGGTCTGAG 15

RESULT 45  
US-08-256-568B-77/c  
Sequence 77, Application US/08256568B  
Patent No. 5846704  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,568B  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid

STANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: be97  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-08-256-568B-77

Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
|||:|||||  
Db 26 GGGGTCTGAG 15

RESULT 46  
US-08-256-568B-78/c  
Sequence 78, Application US/08256568B  
Patent No. 5846704  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,568B  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be95  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-08-256-568B-78



Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 26 GGGGTCTGGAG 15

RESULT 47  
US-08-256-568B-79/c  
; Sequence 79, Application US/08256568B  
; Patent No. 5846704  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256.568B  
; FILING DATE: 18-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402.129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403.222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 79:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: be96  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; US-08-256-568B-79

Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 26 GGGGTCTGGAG 15

RESULT 48  
US-08-256-568B-80/c  
; Sequence 80, Application US/08256568B  
; Patent No. 5846704  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256.568B  
; FILING DATE: 18-JUL-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402.129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403.222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 80:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: be98  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; US-08-256-568B-80

Query Match 66.7%; Score 12; DB 2; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 26 GGGGTCTGGAG 15

RESULT 49  
US-09-038-369B-61/c  
; Sequence 61, Application US/09038369B  
; Patent No. 6171784  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; ISOLATES

```

NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,369B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: be82 (also referred to as be99)
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-09-038-369B-61

Query Match          66.7%; Score 12; DB 3; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12
    |||:|||||
DB 26 GGGGTCTGTGAG 15

RESULT 50
US-09-038-369B-67/c
; Sequence 67, Application US/09038369B
; Patent No. 6171784
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
```

```

ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,369B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: 9b48
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-09-038-369B-67

Query Match          66.7%; Score 12; DB 3; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12
    |||:|||||
DB 26 GGGGTCTGTGAG 15

RESULT 51
US-09-038-369B-68/c
; Sequence 68, Application US/09038369B
; Patent No. 6171784
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb116  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-68

Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 26 GGGGTCTCTGGAG 15

RESULT 52  
US-09-038-369B-69/c  
Sequence 69, Application US/09038369B  
Patent No. 6171784  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325

FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb569  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-69

Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 26 GGGGTCTCTGGAG 15

RESULT 53  
US-09-038-369B-70/c  
Sequence 70, Application US/09038369B  
Patent No. 6171784  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: g9358  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-70

Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
Db 26 GGGGCTCTGGAG 15

RESULT 54  
US-09-038-369B-72/c  
Sequence 72, Application US/09038369B  
Patent No. 6171784  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: cam600  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-72

Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
Db 26 GGGGCTCTGGAG 15

RESULT 55  
US-09-038-369B-73/c  
Sequence 73, Application US/09038369B  
Patent No. 6171784  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:  
CLONE: cam736  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-73

Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 26 GGGGTCCTGGAG 15

RESULT 56  
US-09-038-369B-74/c  
Sequence 74, Application US/09038369B  
Patent No. 6171784  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: gp809  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-74

Query Match 66.7%; Score 12; DB 3; Length 177;

Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 26 GGGGTCCTGGAG 15

RESULT 57  
US-09-038-369B-75/c  
Sequence 75, Application US/09038369B  
Patent No. 6171784  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: gp487  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-75

Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 26 GGGGTCCTGGAG 15

RESULT 58  
US-09-038-369B-76/C  
; Sequence 76, Application US/09038369B  
; Patent No. 6171784  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/038,369B  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 76:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: gp724  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; US-09-038-369B-76  
Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
Db 26 GGGGTCCTGAG 15  
RESULT 59  
US-09-038-369B-77/C  
; Sequence 77, Application US/09038369B  
; Patent No. 6171784  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;

; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/038,369B  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 77:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; LIBRARY: be97  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; US-09-038-369B-77  
Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
Db 26 GGGGTCCTGAG 15  
RESULT 60  
US-09-038-369B-78/C  
; Sequence 78, Application US/09038369B  
; Patent No. 6171784  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE

CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
FILING DATE: US/09/038,369B  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: be95  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-78  
Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
Db 26 GGGGTCTCTGAG 15  
RESULT 61  
US-09-038-369B-79/c  
Sequence 79; Application US/09038369B  
Patent No. 6171784  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: be96  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-79  
Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
Db 26 GGGGTCTCTGAG 15  
RESULT 62  
US-09-038-369B-80/c  
Sequence 80; Application US/09038369B  
Patent No. 6171784  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: be98  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369b-80

Query Match 66.7%; Score 12; DB 3; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCGUCCUGAG 12  
||||:|||||  
Db 26 GGCGTCTCGAG 15

RESULT 63  
US-09-378-900A-61/c  
Sequence 61, Application US/09378900A  
Patent No. 6495670  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: be82 (also referred to as be99)  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-378-900A-61

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCGUCCUGAG 12  
||||:|||||  
Db 26 GGCGTCTCGAG 15

RESULT 64  
US-09-378-900A-67/c  
Sequence 67, Application US/09378900A  
Patent No. 6495670  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004



```
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:
; CLONE: gb48
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
US-09-378-900A-67

Query Match      66.7%; Score 12; DB 4; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCUUGAG 12
        |||:|||||
Db      26 GGGGTCCTGGAG 15

RESULT 65
US-09-378-900A-68/c
; Sequence 68, Application US/093789900A
; Patent No. 6495670
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; NUMBER OF SEQUENCES: 97
; ADDRESS: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410,004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
```

```
STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:
; CLONE: gb116
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
US-09-378-900A-68

Query Match      66.7%; Score 12; DB 4; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCUUGAG 12
        |||:|||||
Db      26 GGGGTCCTGGAG 15

RESULT 66
US-09-378-900A-69/c
; Sequence 69, Application US/093789900A
; Patent No. 6495670
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; NUMBER OF SEQUENCES: 97
; ADDRESS: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410,004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; IMMEDIATE SOURCE:
; CLONE: gb569
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
```

US-09-378-900A-69

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 26 GGGGCTCTGGAG 15

RESULT 67

US-09-378-900A-70/c  
; Sequence 70, Application US/09378900A  
; Patent No. 6495670

; GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97

; CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/378,900A

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/256,568

; FILING DATE: 18-JUL-1994

; APPLICATION NUMBER: PCT/EP93/03325

; FILING DATE: 26-NOV-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP/93/402,123.6

; FILING DATE: 31-AUG-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP/92/403,222.0

; FILING DATE: 27-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: CHARLES A. MUSERLIAN

; REGISTRATION NUMBER: 19,683

; REFERENCE/DOCKET NUMBER: 410,004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 661-8000

; TELEFAX: (212) 661-8002

; INFORMATION FOR SEQ ID NO: 70:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 177 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; IMMEDIATE SOURCE:

; CLONE: GP358

; POSITION IN GENOME:

; MAP POSITION: 5' untranslated region

; US-09-378-900A-70

OY 1 GGGGUCCTGGAG 12

Db 26 GGGGCTCTGGAG 15  
||||:|||||

RESULT 68

US-09-378-900A-72/c  
; Sequence 72, Application US/09378900A  
; Patent No. 6495670

; GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97

; CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/378,900A

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/256,568

; FILING DATE: 18-JUL-1994

; APPLICATION NUMBER: PCT/EP93/03325

; FILING DATE: 26-NOV-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP/93/402,123.6

; FILING DATE: 31-AUG-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP/92/403,222.0

; FILING DATE: 27-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: CHARLES A. MUSERLIAN

; REGISTRATION NUMBER: 19,683

; REFERENCE/DOCKET NUMBER: 410,004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 661-8000

; TELEFAX: (212) 661-8002

; INFORMATION FOR SEQ ID NO: 72:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 177 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; IMMEDIATE SOURCE:

; CLONE: cam600

; POSITION IN GENOME:

; MAP POSITION: 5' untranslated region

; US-09-378-900A-72

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
||||:|||||

Db 26 GGGGCTCTGGAG 15

RESULT 69

US-09-378-900A-73/c  
; Sequence 73, Application US/09378900A

```
; Patent No. 6495670
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; CLONE: cam736
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
;
; US-09-378-900A-73
;
; Query Match          66.7%; Score 12; DB 4; Length 177;
; Best Local Similarity 83.3%; Pred. No. 7.4e+02;
; Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; CLONE: gb809
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
;
; US-09-378-900A-74
;
; Query Match          66.7%; Score 12; DB 4; Length 177;
; Best Local Similarity 83.3%; Pred. No. 7.4e+02;
; Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,900A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: 9b487
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-09-378-900A-75

Query Match      66.7%; Score 12; DB 4; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
        |||||:|||||
        26 GGGGTCCTGGAG 15

Db

RESULT 72
US-09-378-900A-76/C
Sequence 76, Application US/09378900A
Patent No. 6495670
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT, STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,900A
```

```
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: 9b724
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-09-378-900A-76

Query Match      66.7%; Score 12; DB 4; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
        |||||:|||||
        26 GGGGTCCTGGAG 15

Db

RESULT 73
US-09-378-900A-77/C
Sequence 77, Application US/09378900A
Patent No. 6495670
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT, STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,900A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
```

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: be97  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-378-900A-77

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 26 GGGTCTCTGGAG 15

RESULT 74  
US-09-378-900A-78/c  
Sequence 78, Application US/093789900A  
Patent No. 6495670  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be95  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-378-900A-78

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 26 GGGTCTCTGGAG 15

RESULT 75  
US-09-378-900A-79/c  
Sequence 79, Application US/093789900A  
Patent No. 6495670  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 79:

SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be96  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-378-900A-79

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
Db 26 GGGGTCCTGGAG 15

RESULT 76  
US-09-378-900A-80/c  
Sequence 80, Application US/09378900A  
Patent No. 6495670  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:

CLONE: be98  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-378-900A-80

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
Db 26 GGGGTCCTGGAG 15

RESULT 77  
US-09-899-044-61/c  
Sequence 61, Application US/09899044  
Patent No. 6548244  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-JUL-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be82 (also referred to as be99)  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 61:  
US-09-899-044-61

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCGAG 12  
| | | | : | | : | | | |  
Db 26 GGGGTCTGAG 15

## RESULT 78

US-09-899-044-67/c  
; Sequence 67, Application US/09899044  
; Patent No. 6548244  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899,044  
; FILING DATE: 06-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/378,900  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 67:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; IMMEDIATE SOURCE:  
; CLONE: gb48  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-899-044-67

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 GGGGUCGAG 12  
| | | | : | | : | | | |  
Db 26 GGGGTCTGAG 15

RESULT 79  
US-09-899-044-68/c

; Sequence 68, Application US/09899044  
; Patent No. 6548244  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899,044  
; FILING DATE: 06-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/378,900  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 68:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; IMMEDIATE SOURCE:  
; CLONE: gb116  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; SEQUENCE DESCRIPTION: SEQ ID NO: 68:  
US-09-899-044-68

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 GGGGUCGAG 12  
| | | | : | | : | | | |  
Db 26 GGGGTCTGAG 15

RESULT 80  
US-09-899-044-69/c  
; Sequence 69, Application US/09899044  
; Patent No. 6548244  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; ISOLATES  
; NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: 9b569  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-899-044-69  
Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
Db 26 GGGGTCTGTGAG 15  
RESULT 81  
US-09-899-044-70/c  
Sequence 70; Application US/09899044  
Patent No. 6548244  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: 9b358  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 70:  
US-09-899-044-70  
Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
Db 26 GGGGTCTGTGAG 15  
RESULT 82  
US-09-899-044-72/c  
Sequence 72; Application US/09899044  
Patent No. 6548244  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>



PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: cam600  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 72:  
US-09-899-044-72

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGCGAG 12  
|||:|||||  
Db 26 GGGGTCTCGAG 15

RESULT 83  
US-09-899-044-73/c  
Sequence 73, Application US/09899044  
Patent No. 6548244  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0

FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: cam736  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 73:  
US-09-899-044-73

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGCGAG 12  
|||:|||||  
Db 26 GGGGTCTCGAG 15

RESULT 84  
US-09-899-044-74/c  
Sequence 74, Application US/09899044  
Patent No. 6548244  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb809  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 74:  
US-09-899-044-74

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGCGCUGAG 12  
Db 26 GGGGCTCTGAG 15

RESULT 85  
US-09-899-044-75/c  
Sequence 75, Application US/09899044  
Patent No. 6548244  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:

CLONE: gb487  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 75:  
US-09-899-044-75

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGCGCUGAG 12  
Db 26 GGGGCTCTGAG 15

RESULT 86  
US-09-899-044-76/c  
Sequence 76, Application US/09899044  
Patent No. 6548244  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/399,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb724  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 76:  
US-09-899-044-76

Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 26 GGGGTCTCGAG 15

## RESULT 87

US-09-899-044-77/c

; Sequence 77, Application US/09899044  
; Patent No. 6548244

GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWM, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES

NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/378,900

FILING DATE: &lt;Unknown&gt;

APPLICATION NUMBER: PCT/EP93/03325

FILING DATE: 26-NOV-1993

APPLICATION NUMBER: EP/93/402,129.6

FILING DATE: 31-AUG-1993

APPLICATION NUMBER: EP/92/403,222.0

FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:

LENGTH: 177 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

LIBRARY: be97

POSITION IN GENOME:

MAP POSITION: 5' untranslated region

SEQUENCE DESCRIPTION: SEQ ID NO: 77:

US-09-899-044-77

Query Match

Best Local Similarity 83.3%; Score 12; DB 4; Length 177;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 26 GGGGTCTCGAG 15

## RESULT 88

US-09-899-044-78/c

; Sequence 78, Application US/09899044  
; Patent No. 6548244

GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWM, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES

NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/378,900

FILING DATE: &lt;Unknown&gt;

APPLICATION NUMBER: PCT/EP93/03325

FILING DATE: 26-NOV-1993

APPLICATION NUMBER: EP/93/402,129.6

FILING DATE: 31-AUG-1993

APPLICATION NUMBER: EP/92/403,222.0

FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 78:

SEQUENCE CHARACTERISTICS:

LENGTH: 177 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

CLONE: be95

POSITION IN GENOME:

MAP POSITION: 5' untranslated region

SEQUENCE DESCRIPTION: SEQ ID NO: 78:

US-09-899-044-78

Query Match

Best Local Similarity 83.3%; Score 12; DB 4; Length 177;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 26 GGGGTCTCGAG 15

## RESULT 89

US-09-899-044-79/c

; Sequence 79, Application US/09899044  
; Patent No. 6548244

GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWM, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES

NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-JUL-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be96  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 79:  
US-09-899-044-79  
Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 26 GGGGTCCTGGAG 15  
RESULT 90  
US-09-899-044-80/c  
Sequence 80, Application US/09899044  
Patent No. 6548244  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT, STUYVER, LIEVEN,  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,568B  
FILING DATE: 18-JUL-1994

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-JUL-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be98  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 80:  
US-09-899-044-80  
Query Match 66.7%; Score 12; DB 4; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 26 GGGGTCCTGGAG 15  
RESULT 91  
US-08-256-568B-59/c  
Sequence 59, Application US/08256568B  
Patent No. 5846704  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT, STUYVER, LIEVEN,  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,568B  
FILING DATE: 18-JUL-1994

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: hu74  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-08-256-568B-59

Query Match 66.7%; Score 12; DB 2; Length 178;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 26 GGGGTCTCTGGAG 15

RESULT 92  
US-08-256-568B-71/c  
Sequence 71, Application US/08256568B  
Patent No. 5846704  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,568B  
FILING DATE: 18-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0

FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gbs49  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-08-256-568B-71

Query Match 66.7%; Score 12; DB 2; Length 178;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 26 GGGGTCTCTGGAG 15

RESULT 93  
US-09-038-369B-59/c  
Sequence 59, Application US/09038369B.  
Patent No. 6171784  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: bu74  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-59

Query Match 66.7%; Score 12; DB 3; Length 178;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCCTGGAG 15

RESULT 94  
US-09-038-369B-71/c  
Sequence 71, Application US/09038369B  
Patent No. 6171784  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,369B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: pb549  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-038-369B-71

Query Match 66.7%; Score 12; DB 3; Length 178;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCCTGGAG 15

RESULT 95  
US-09-378-900A-59/c  
Sequence 59, Application US/09378900A  
Patent No. 6495670  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: bu74  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-378-900A-59

Query Match 66.7%: Score 12; DB 4; Length 178;  
Best Local Similarity 83.3%: Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 26 GGGGTCCTGGAG 15

RESULT 96  
US-09-378-900A-71/c  
; Sequence 71, Application US/09378900A  
; Patent No. 6495670  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWIN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; TITLE OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/378, 900A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/256, 568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402, 129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403, 222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8002  
; TELEFAX: (212) 661-8000  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 178 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: gbs49  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; US-09-378-900A-71

Query Match 66.7%: Score 12; DB 4; Length 178;  
Best Local Similarity 83.3%: Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 26 GGGGTCCTGGAG 15

RESULT 97  
US-09-899-044-59/c  
; Sequence 59, Application US/09899044  
; Patent No. 6548244  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWIN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; TITLE OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899, 044  
; FILING DATE: 06-JUL-2001  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/378, 900  
; FILING DATE: <unknown>  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; APPLICATION NUMBER: EP/93/402, 129.6  
; FILING DATE: 31-AUG-1993  
; APPLICATION NUMBER: EP/92/403, 222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 59:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 178 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: bu74  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
; US-09-899-044-59

Query Match 66.7%: Score 12; DB 4; Length 178;  
Best Local Similarity 83.3%: Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
|||:|||||  
Db 26 GGGGTCCTGGAG 15

RESULT 98  
US-09-899-044-71/c  
; Sequence 71, Application US/09899044  
; Patent No. 6548244  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;

ROSSAU, RUDI; VAN HEUVERSWM, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gds49  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 71:  
US-09-899-044-71  
Query Match 66.7%; Score 12; DB 4; Length 178;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
DB 26 GGGGTCCTGGAG 15  
RESULT 99  
US-08-441-971-50/c  
Sequence 50, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts

COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE: US/07/881,528  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TEXT: EZEKIEL  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 180 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: sa3  
US-08-441-971-50  
Query Match 66.7%; Score 12; DB 3; Length 180;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
DB 34 GGGGTCCTGGAG 23  
RESULT 100  
US-08-441-971-51/c  
Sequence 51, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653



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: FILING DATE:
: APPLICATION NUMBER: US/07/881,528
: FILING DATE: 07/697,326
: APPLICATION NUMBER: 07/697,326
: FILING DATE: 8 May 1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Janluk, Anthony J.
: REGISTRATION NUMBER: 29,809
: REFERENCE/DOCKET NUMBER: C0772/7000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 720-3500
: TELEFAX: (617) 720-2441
: TELEX: EZEKIEL
: INFORMATION FOR SEQ ID NO: 51:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 180 nucleotides
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: sa4
: US-08-441-971-51

Query Match      66.7%; Score 12; DB 3; Length 180;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCUGAG 12
Db      34 GGGGCTCTGAG 23

RESULT 101
US-08-221-653-50/c
: Sequence 50, Application US/08221653
: Patent No. 6190864
: GENERAL INFORMATION:
: APPLICANT: Tai-An Cha
: TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
: NUMBER OF SEQUENCES: 147
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
: STREET: 600 Atlantic Avenue
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 5.25 inch
: OPERATING SYSTEM: MS-DOS Version 3.3
: SOFTWARE: Wordperfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/221,653
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/881,528
: FILING DATE:
: APPLICATION NUMBER: 07/697,326
: FILING DATE: 8 May 1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Janluk, Anthony J.
: REGISTRATION NUMBER: 29,809
: REFERENCE/DOCKET NUMBER: C0772/7000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 720-3500
: TELEFAX: (617) 720-2441
: TELEX: EZEKIEL
: INFORMATION FOR SEQ ID NO: 50:
: SEQUENCE CHARACTERISTICS:
```

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: LENGTH: 180 nucleotides
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: sa3
: US-08-221-653-50

Query Match      66.7%; Score 12; DB 3; Length 180;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCUGAG 12
Db      34 GGGGCTCTGAG 23

RESULT 102
US-08-221-653-51/c
: Sequence 51, Application US/08221653
: Patent No. 6190864
: GENERAL INFORMATION:
: APPLICANT: Tai-An Cha
: TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
: NUMBER OF SEQUENCES: 147
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
: STREET: 600 Atlantic Avenue
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 5.25 inch
: OPERATING SYSTEM: MS-DOS Version 3.3
: SOFTWARE: Wordperfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/221,653
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/881,528
: FILING DATE:
: APPLICATION NUMBER: 07/697,326
: FILING DATE: 8 May 1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Janluk, Anthony J.
: REGISTRATION NUMBER: 29,809
: REFERENCE/DOCKET NUMBER: C0772/7000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 720-3500
: TELEFAX: (617) 720-2441
: TELEX: EZEKIEL
: INFORMATION FOR SEQ ID NO: 51:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 180 nucleotides
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: sa4
: US-08-221-653-51

Query Match      66.7%; Score 12; DB 3; Length 180;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCUGAG 12
Db      34 GGGGCTCTGAG 23
```

Db 34 GGGGCTCTGGAG 23

```
RESULT 103
US-08-442-144A-50/c
; Sequence 50, Application US/08442144A
; Patent No. 6214583
; GENERAL INFORMATION:
; APPLICANT: Tai-An Cha
; APPLICANT: Eileen Beall
; APPLICANT: Bruce Irvine
; APPLICANT: Michael Kolberg
; APPLICANT: Michael S. Urdea
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 Inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,144A
; FILING DATE: MAY 16, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/221,653
; FILING DATE: APRIL 1, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Doreen Yacko Trujillo
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CHIR-0121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; TELEX:
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 Nucleotides
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: sa3
; US-08-442-144A-50

Query Match 66.7%; Score 12; DB 3; Length 180;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCTCTGGAG 12
Db 34 GGGGCTCTGGAG 23

RESULT 104
US-08-442-144A-51/c
; Sequence 51, Application US/08442144A
; Patent No. 6214583
; GENERAL INFORMATION:
; APPLICANT: Tai-An Cha
; APPLICANT: Eileen Beall
; APPLICANT: Bruce Irvine
; APPLICANT: Michael Kolberg
; APPLICANT: Michael S. Urdea
```

```
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 Inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows NT
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,144A
; FILING DATE: MAY 16, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/221,653
; FILING DATE: APRIL 1, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Doreen Yacko Trujillo
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CHIR-0121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; TELEX:
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 Nucleotides
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: sa4
; US-08-442-144A-51

Query Match 66.7%; Score 12; DB 3; Length 180;
Best Local Similarity 83.3%; Pred. No. 7.4e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCTCTGGAG 12
Db 34 GGGGCTCTGGAG 23

RESULT 105
US-08-441-970-50/c
; Sequence 50, Application US/08441970
; Patent No. 6297370
; GENERAL INFORMATION:
; APPLICANT: Tai-An Cha
; TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS Version 3.3
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,970
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FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 MAY 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 180 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: sa3  
US-08-441-970-50

Query Match 66.7%; Score 12; DB 3; Length 180;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCUGAG 12  
Db 34 GGGGTCTCGAG 23

RESULT 106  
US-08-441-970-51/c  
Sequence 51, Application US/08441970  
Patent No. 6297370  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,970  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/881,528  
FILING DATE: 08-MAY-1992  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL

INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 180 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: sa4  
US-08-441-970-51

Query Match 66.7%; Score 12; DB 3; Length 180;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCUGAG 12  
Db 34 GGGGTCTCGAG 23

RESULT 107  
US-08-634-797-46/c  
Sequence 46, Application US/08634797  
Patent No. 5851759  
GENERAL INFORMATION:  
APPLICANT: WEINER, AMY J.  
TITLE OF INVENTION: HETEROIDUPLEX TRACKING ASSAY (HTA) FOR  
TITLE OF INVENTION: GENOTYPING HCV  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street - R440  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608-2916  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/634,797  
FILING DATE: 19-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hardin, Alisha A.  
REGISTRATION NUMBER: 33,895  
REFERENCE/DOCKET NUMBER: 1226,001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-3274  
TELEFAX: (510) 655-3542  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 194 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-634-797-46

Query Match 66.7%; Score 12; DB 2; Length 194;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCUGAG 12  
Db 56 GGGGTCTCGAG 45

RESULT 108  
US-08-634-797-47/c

```
; Sequence 47, Application US/08634797
; Patent No. 5851759
; GENERAL INFORMATION:
; APPLICANT: WEINER, AMY J.
; TITLE OF INVENTION: HETERODUPLEX TRACKING ASSAY (HTA) FOR
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street - R440
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,797
; FILING DATE: 19-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hardin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 1226.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-3274
; TELEFAX: (510) 655-3542
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-634-797-47

Query Match          66.7%; Score 12; DB 2; Length 194;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGGUCCUGAG 12
      |||:|:|:|
Db      56 GGGGTCTCGAG 45
```

```
RESULT 109
US-08-634-797-48/C
; Sequence 48, Application US/08634797
; Patent No. 5851759
; GENERAL INFORMATION:
; APPLICANT: WEINER, AMY J.
; TITLE OF INVENTION: HETERODUPLEX TRACKING ASSAY (HTA) FOR
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street - R440
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,797
; FILING DATE: 19-APR-1996
```

```
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hardin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 1226.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-3274
; TELEFAX: (510) 655-3542
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-634-797-48
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```
Query Match          66.7%; Score 12; DB 2; Length 194;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 GGGGUCCUGAG 12
      |||:|:|:|
Db      56 GGGGTCTCGAG 45
```

```
RESULT 110
US-09-270-767-28457/C
; Sequence 28457, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 28457
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; US-09-270-767-28457
```

```
Query Match          66.7%; Score 12; DB 4; Length 201;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGGUCCUGAG 12
      |||:|:|:|
Db      102 GGGGTCTCGAG 91
```

```
RESULT 111
US-09-513-999C-29549
; Sequence 29549, Application US/0951399C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513, 999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,407
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.ppm
; SEQ ID NO 29549
; LENGTH: 221
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-29549

Query Match      66.7%; Score 12; DB 4; Length 221;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
       |||:|||||
Db      15 GGGGTCTCTGGAG 26

RESULT 112
US-09-034-205-37/c
; Sequence 37, Application US/09034205
; Patent No. 6194149
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
; TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,205
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-03268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-09-034-205-37

Query Match      66.7%; Score 12; DB 3; Length 222;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
       |||:|||||
Db      47 GGGGTCTCTGGAG 36

RESULT 113
US-08-934-097A-37/c
; Sequence 37, Application US/08934097A
; Patent No. 6210880
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
```

```
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neil, Bruce P.
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
; TITLE OF INVENTION: Structure Probing With Structure-Bridging
; TITLE OF INVENTION: Oligonucleotides.
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,097A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-02980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-934-097A-37

Query Match      66.7%; Score 12; DB 3; Length 222;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
       |||:|||||
Db      47 GGGGTCTCTGGAG 36

RESULT 114
US-08-851-588-37/c
; Sequence 37, Application US/08851588
; Patent No. 6214545
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Prudent, James R.
; APPLICANT: Dahlberg, James E.
; APPLICANT: Fors, Lance
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
; TITLE OF INVENTION: Structure Probing
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-37

Query Match 66.7%; Score 12; DB 3; Length 232;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
Db 47 GGGGTCCTGGAG 36

RESULT 115  
US-09-677-218B-37/C  
Sequence 37, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamachev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neil, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-677-218B-37

Query Match 66.7%; Score 12; DB 3; Length 232;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
Db 47 GGGGTCCTGGAG 36

RESULT 116  
US-09-677-192-37/C  
Sequence 37, Application US/09677192  
Patent No. 6358691  
GENERAL INFORMATION:  
APPLICANT: Lyamachev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neil, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
FILE REFERENCE: FORS-04708  
CURRENT APPLICATION NUMBER: US/09/677,192  
CURRENT FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 09/034,205  
PRIOR FILING DATE: 1998-03-03  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 37  
LENGTH: 232  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-677-192-37

Query Match 66.7%; Score 12; DB 3; Length 232;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
Db 47 GGGGTCCTGGAG 36

RESULT 117  
US-09-402-618B-37/C  
Sequence 37, Application US/09402618B  
Patent No. 6709815  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamachev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance  
APPLICANT: Neil, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot:  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/09/402,618B  
CURRENT FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 37  
LENGTH: 232  
TYPE: DNA

ORGANISM: Hepatitis C virus  
US-09-402-618B-37

Query Match 66.7% Score 12; DB 4; Length 232;  
Best Local Similarity 83.3% Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
DB 47 GGGGCTCTGGAG 36

## RESULT 118

US-09-825-574-37/C  
Sequence 37, Application US/09825574  
Patent No. 6709819

## GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

For, Mary Ann D.

For, Bruce P.

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825.574

FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-02980

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 232 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 37:

US-09-825-574-37

Query Match 66.7% Score 12; DB 4; Length 232;  
Best Local Similarity 83.3% Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
DB 47 GGGGCTCTGGAG 36

RESULT 119  
US-09-676-768-37/C

Sequence 37, Application US/09676768  
Patent No. 6780585

## GENERAL INFORMATION:

APPLICANT: Dong, Fang

Lyamichev, Victor I.

Prudent, James R.

Dahlberg, James E.

For, Lance

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/676,768

FILING DATE: 02-Oct-2000

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/851,588

FILING DATE: 05-May-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: FORS-02777

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 232 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 37:

US-09-676-768-37

Query Match 66.7% Score 12; DB 4; Length 232;  
Best Local Similarity 83.3% Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
DB 47 GGGGCTCTGGAG 36

## RESULT 120

US-09-034-205-32/C  
Sequence 32, Application US/09034205  
Patent No. 6194149

## GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

APPLICANT: Brow, Mary Ann D.

APPLICANT: For, Lance

APPLICANT: Neil, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

```
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/034,205
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-09-034-205-32

Query Match      66.7% Score 12; DB 3; Length 239;
Best Local Similarity 83.3% Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12
    |||:|:|:|
Db 54 GGGGTCTGGAG 43

RESULT 121
US-09-034-205-36/c
Sequence 36, Application US/09034205
Patent No. 6194149
GENERAL INFORMATION:
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
APPLICANT: Fors, Lance P.
APPLICANT: Neri, Bruce P.
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
STRUCTURE-BRIDGING OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/034,205
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
```

```
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-09-034-205-36
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Query Match      66.7% Score 12; DB 3; Length 239;
Best Local Similarity 83.3% Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GGGGUCCUGAG 12
    |||:|:|:|
Db 54 GGGGTCTGGAG 43
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RESULT 122
US-08-934-097A-32/c
Sequence 32, Application US/08934097A
Patent No. 6210880
GENERAL INFORMATION:
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
APPLICANT: Fors, Lance P.
APPLICANT: Neri, Bruce P.
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
STRUCTURE PROBING WITH STRUCTURE-BRIDGING
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,097A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: FORS-02980
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-934-097A-32
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Query Match      66.7% Score 12; DB 3; Length 239;
Best Local Similarity 83.3% Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GGGGUCCUGAG 12
    |||:|:|:|
Db 54 GGGGTCTGGAG 43
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RESULT 123  
US-08-934-097A-36/c  
; Sequence 36, Application US/08934097A  
; Patent No. 6210680  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Neil, Bruce P.  
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
; TITLE OF INVENTION: Structure Probing With Structure-Bridging  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk.  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/934,097A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: FORS-02980  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 239 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
; US-08-934-097A-36  
Query Match 66.7%; Score 12; DB 3; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGCGAG 12  
Db 54 GGGGTCTCGAG 43  
RESULT 124  
US-08-851-588-32/c  
; Sequence 32, Application US/08851588  
; Patent No. 6214545  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Prudent, James R.  
; APPLICANT: Dahlberg, James E.  
; APPLICANT: Fors, Lance  
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
; TITLE OF INVENTION: Structure Probing  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco

STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-32  
Query Match 66.7%; Score 12; DB 3; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGCGAG 12  
Db 54 GGGGTCTCGAG 43  
RESULT 125  
US-08-851-588-36/c  
; Sequence 36, Application US/08851588  
; Patent No. 6214545  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Prudent, James R.  
; APPLICANT: Dahlberg, James E.  
; APPLICANT: Fors, Lance  
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
; TITLE OF INVENTION: Structure Probing  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/851,588  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ingolia, Diane E.  
; REGISTRATION NUMBER: 40,027  
; REFERENCE/DOCKET NUMBER: FORS-02777  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-36

Query Match 66.7%; Score 12; DB 3; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGAG 12  
DB 54 GGGGTCCTGAG 43

RESULT 126  
US-09-677-218B-32/c  
Sequence 32, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Fors, Lance  
Neil, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-677-218B-32

Query Match 66.7%; Score 12; DB 3; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGAG 12  
DB 54 GGGGTCCTGAG 43

RESULT 127  
US-09-677-218B-36/c  
Sequence 36, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Fors, Lance  
Neil, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-09-677-218B-36

Query Match 66.7%; Score 12; DB 3; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGAG 12  
DB 54 GGGGTCCTGAG 43

RESULT 128  
US-09-677-192-32/c  
Sequence 32, Application US/09677192  
Patent No. 6358691  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Fors, Lance  
Neil, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING

TITLE OF INVENTION: OLIGONUCLEOTIDES  
FILE REFERENCE: FORS-04708  
CURRENT APPLICATION NUMBER: US/09/677,192  
CURRENT FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 09/034,205  
PRIOR FILING DATE: 1998-03-03  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 32  
LENGTH: 239  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-677-192-32

Query Match 66.7%; Score 12; DB 3; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
DB 54 GGGGTCTCGAG 43

RESULT 129  
US-09-677-192-36/c  
Sequence 36, Application US/09677192  
Patent No. 6358691  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
FILE REFERENCE: FORS-04708  
CURRENT APPLICATION NUMBER: US/09/677,192  
CURRENT FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: 09/034,205  
PRIOR FILING DATE: 1998-03-03  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 36  
LENGTH: 239  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-677-192-36

Query Match 66.7%; Score 12; DB 3; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
DB 54 GGGGTCTCGAG 43

RESULT 130  
US-09-402-618B-32/c  
Sequence 32, Application US/09402618B  
Patent No. 6709815  
GENERAL INFORMATION:  
APPLICANT: Dong, Pang  
APPLICANT: Lyamichev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/09/402,618B  
CURRENT FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 32  
LENGTH: 239  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-402-618B-32

Query Match 66.7%; Score 12; DB 4; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
DB 54 GGGGTCTCGAG 43

RESULT 131  
US-09-402-618B-36/c  
Sequence 36, Application US/09402618B  
Patent No. 6709815  
GENERAL INFORMATION:  
APPLICANT: Dong, Pang  
APPLICANT: Lyamichev, Victor  
APPLICANT: Prudent, James  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/09/402,618B  
CURRENT FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 36  
LENGTH: 239  
TYPE: DNA  
ORGANISM: Hepatitis C virus  
US-09-402-618B-36

Query Match 66.7%; Score 12; DB 4; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
DB 54 GGGGTCTCGAG 43

RESULT 132  
US-09-825-574-32/c  
Sequence 32, Application US/09825574  
Patent No. 6709819  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA

COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-825-574-32  
Query Match 66.7%; Score 12; DB 4; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
Db 54 GGGGTCCTGGAG 43  
RESULT 133  
US-09-825-574-36/C  
Sequence 36, Application US/09825574  
Patent No. 6709819  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-09-825-574-36  
Query Match 66.7%; Score 12; DB 4; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
Db 54 GGGGTCCTGGAG 43  
RESULT 134  
US-09-676-768-32/C  
Sequence 32, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 32;  
US-09-676-768-32

Query Match 66.7%; Score 12; DB 4; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGCGAG 12  
||||:|||||  
DB 54 GGGGTCCTGGAG 43

## RESULT 135

US-09-676-768-36/C  
Sequence 36, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:

APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Danberg, James E.  
Fors, Lance

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco

STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 239 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 36;  
US-09-676-768-36

Query Match 66.7%; Score 12; DB 4; Length 239;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGCGAG 12  
||||:|||||  
DB 54 GGGGTCCTGGAG 43

## RESULT 136

US-09-034-205-33/C  
Sequence 33, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco

STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/034,205  
FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

US-09-034-205-33

Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGCGAG 12  
||||:|||||  
DB 55 GGGGTCCTGGAG 44

## RESULT 137

US-09-034-205-38/C  
Sequence 38, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco

STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-38

Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
||||:|||||  
Db 56 GGGGTCTGGAG 45

RESULT 138  
US-08-934-097A-33/c  
Sequence 33, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs

TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-33

Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
||||:|||||  
Db 55 GGGGTCTGGAG 44

RESULT 139  
US-08-934-097A-38/c  
Sequence 38, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-38

Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
||||:|||||  
Db 56 GGGGTCTGGAG 45

RESULT 140  
US-08-851-588-33/c

Sequence 33, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-33  
Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGUCGUGAG 12  
Db 55 GGGGTCCTGGAG 44  
RESULT 141  
US-08-851-588-38/C  
Sequence 38, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-38  
Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGUCGUGAG 12  
Db 56 GGGGTCCTGGAG 45  
RESULT 142  
US-09-677-218B-33/C  
Sequence 33, Application US/09677218B  
Patent No. 6353437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Neri, Bruce P.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-677-218B-33

Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 55 GGGGTCTCGAG 44

## RESULT 143

US-09-677-218B-38/c  
Sequence 38, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Brow, Mary Ann D.

Fors, Lance

Neil, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING

STRUCTURE-BRIDGING OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/677,218B

FILING DATE: 02-Oct-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/034,205

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Karmin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-03268

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 240 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-677-218B-38

Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 56 GGGGTCTCGAG 45

## RESULT 144

US-09-677-192-33/c  
Sequence 33, Application US/09677192  
Patent No. 6358691  
GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Brow, Mary Ann D.

Fors, Lance

Neil, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING

FILE REFERENCE: FORS-04708

CURRENT APPLICATION NUMBER: US/09/677,192

CURRENT FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: 09/034,205

PRIOR FILING DATE: 1998-03-03

NUMBER OF SEQ ID NOS: 68

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 33

LENGTH: 240

TYPE: DNA

ORGANISM: Hepatitis C virus

US-09-677-192-33

Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 55 GGGGTCTCGAG 44

## RESULT 145

US-09-677-192-38/c  
Sequence 38, Application US/09677192  
Patent No. 6358691  
GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

Brow, Mary Ann D.

Fors, Lance

Neil, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING

FILE REFERENCE: FORS-04708

CURRENT APPLICATION NUMBER: US/09/677,192

CURRENT FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: 09/034,205

PRIOR FILING DATE: 1998-03-03

NUMBER OF SEQ ID NOS: 68

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 38

LENGTH: 240

TYPE: DNA

ORGANISM: Hepatitis C virus

US-09-677-192-38

Query Match 66.7%; Score 12; DB 3; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:|||||  
Db 56 GGGGTCTCGAG 45

## RESULT 146

US-09-402-618B-33/c



```
; Sequence 33, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-402-618B-33

Query Match      66.7%; Score 12; DB 4; Length 240;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCUCGAG 12
        ||||:|||||
Db      55 GGGGTCTCGAG 44

RESULT 147
US-09-402-618B-38/c
; Sequence 38, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-402-618B-38

Query Match      66.7%; Score 12; DB 4; Length 240;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCUCGAG 12
        ||||:|||||
Db      56 GGGGTCTCGAG 45

RESULT 148
US-09-825-574-33/c
; Sequence 33, Application US/09825574
```

```
; Patent No. 6709819
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
; Structure Probing with Structure-Bridging
; Oligonucleotides.
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/825,574
; FILING DATE: 03-Apr-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/934,097
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-02980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 base pairs
; TYPE: nucleic acid
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-825-574-33

Query Match      66.7%; Score 12; DB 4; Length 240;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCUCGAG 12
        ||||:|||||
Db      55 GGGGTCTCGAG 44

RESULT 149
US-09-825-574-38/c
; Sequence 38, Application US/09825574
; Patent No. 6709819
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
; Structure Probing with Structure-Bridging
; Oligonucleotides.
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
```

STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-825-574-38

Query Match 66.7%; Score 12; DB 4; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
Db 56 GGGGCTCGAG 45

RESULT 150  
US-09-676-768-33/C  
Sequence 33, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588

FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-676-768-33

Query Match 66.7%; Score 12; DB 4; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
Db 55 GGGGCTCGAG 44

RESULT 151  
US-09-676-768-38/C  
Sequence 38, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/576,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/351,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-676-768-38

Query Match 66.7%; Score 12; DB 4; Length 240;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
|||:||||  
Db 56 GGGGTCTCGAG 45

RESULT 152  
US-08-335-595-1/c  
Sequence 1, Application US/08335595  
Patent No. 5914228  
GENERAL INFORMATION:  
APPLICANT: VIERLING, JOHN M  
APPLICANT: HU, KE-QIN  
TITLE OF INVENTION: DIRECT DETECTION OF HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LYON & LYON  
STREET: 611 WEST 6TH STREET  
CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335.595  
FILING DATE: 08-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/175.473  
FILING DATE:  
APPLICATION NUMBER: US/07/758.862  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: SCHNEIDER, CAROL A  
REGISTRATION NUMBER: 34,923  
REFERENCE/DOCKET NUMBER: 194/285  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 213-489-1600  
TELEFAX: 213-955-0440  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 242 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-335-595-1

Query Match 66.7%; Score 12; DB 2; Length 242;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
|||:||||  
Db 100 GGGGTCTCGAG 89

RESULT 153  
US-09-034-205-26/c  
Sequence 26, Application US/09034205  
Patent No. 6194149

GENERAL INFORMATION:  
APPLICANT: Lyamchev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neel, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034.205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-26

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
|||:||||  
Db 56 GGGGTCTCGAG 45

RESULT 154  
US-09-034-205-29/c  
Sequence 29, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lyamchev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neel, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-09-034-205-29

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGAG 12  
|||:|:|:|:|  
Db 56 GGGGTCCTGAG 45

#### RESULT 155

US-09-034-205-31/C  
Sequence 31, Application US/09034205  
Patent No. 6194149  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,205  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"  
US-09-034-205-31

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGAG 12  
|||:|:|:|:|  
Db 55 GGGGTCCTGAG 44

#### RESULT 156

US-08-934-097A-26/C  
Sequence 26, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-26

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGAG 12  
|||:|:~|:|:|  
Db 56 GGGGTCCTGAG 45

#### RESULT 157

US-08-934-097A-29/C  
Sequence 29, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.

APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-29

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
|||||:  
Db 56 GGGGTCTCTGGAG 45

RESULT 158  
US-08-934-097A-31/c  
Sequence 31, Application US/08934097A  
Patent No. 6210880  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Brow, Mary Ann D.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing With Structure-Bridging  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,097A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-934-097A-31

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
|||||:  
Db 55 GGGGTCTCTGGAG 44

RESULT 159  
US-08-851-588-26/c  
Sequence 26, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-26

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGAG 12  
DB 56 GGGGTCCTGAG 45

RESULT 160  
US-08-851-588-29/C  
Sequence 29, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-29

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGAG 12  
DB 56 GGGGTCCTGAG 45

RESULT 161  
US-08-851-588-31/C  
Sequence 31, Application US/08851588  
Patent No. 6214545  
GENERAL INFORMATION:

APPLICANT: Dong, Fang  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Prudent, James R.  
APPLICANT: Dahlberg, James E.  
APPLICANT: Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
TITLE OF INVENTION: Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-851-588-31

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGAG 12  
DB 55 GGGGTCCTGAG 44

RESULT 162  
US-09-677-218B-26/C  
Sequence 26, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
APPLICANT: Fors, Mary Ann D.  
APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA

COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-09-677-218B-26  
Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGCUCCGAG 12  
Db 56 GGGGTCTCTGGAG 45  
RESULT 163  
US-09-677-218B-29/c  
Sequence 29, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-677-218B-29  
Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGCUCCGAG 12  
Db 56 GGGGTCTCTGGAG 45  
RESULT 164  
US-09-677-218B-31/c  
Sequence 31, Application US/09677218B  
Patent No. 6355437  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Fors, Lance  
Neri, Bruce P.  
TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING  
STRUCTURE-BRIDGING OLIGONUCLEOTIDES  
NUMBER OF SEQUENCES: 68  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/677,218B  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/034,205  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-03268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-677-218B-31  
Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
| | | | | | | | | |  
Db 55 GGGGTCTCGAG 44

RESULT 165  
US-09-677-192-26/C  
; Sequence 26, Application US/09677192  
; Patent No. 6358691  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
; FILE REFERENCE: FORS-04708  
; CURRENT APPLICATION NUMBER: US/09/677,192  
; CURRENT FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 09/034,205  
; PRIOR FILING DATE: 1998-03-03  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 244  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-09-677-192-26

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
| | | | | | | | | |  
Db 56 GGGGTCTCGAG 45

RESULT 166  
US-09-677-192-29/C  
; Sequence 29, Application US/09677192  
; Patent No. 6358691  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
; FILE REFERENCE: FORS-04708  
; CURRENT APPLICATION NUMBER: US/09/677,192  
; CURRENT FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 09/034,205  
; PRIOR FILING DATE: 1998-03-03  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 29  
; LENGTH: 244  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-09-677-192-29

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
| | | | | | | | | |  
Db 56 GGGGTCTCGAG 45

RESULT 167  
US-09-677-192-31/C

; Sequence 31, Application US/09677192  
; Patent No. 6358691  
; GENERAL INFORMATION:  
; APPLICANT: Lyamichev, Victor I.  
; APPLICANT: Brow, Mary Ann D.  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce P.  
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING  
; FILE REFERENCE: FORS-04708  
; CURRENT APPLICATION NUMBER: US/09/677,192  
; CURRENT FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 09/034,205  
; PRIOR FILING DATE: 1998-03-03  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 244  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-09-677-192-31

Query Match 66.7%; Score 12; DB 3; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
| | | | | | | | | |  
Db 55 GGGGTCTCGAG 44

RESULT 168  
US-09-402-618B-26/C  
; Sequence 26, Application US/09402618B  
; Patent No. 6709815  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Prudent, James  
; APPLICANT: Fors, Lance  
; APPLICANT: Neri, Bruce  
; APPLICANT: Brow, Mary Ann  
; APPLICANT: Anderson, Todd  
; APPLICANT: Dahlberg, James  
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot  
; FILE REFERENCE: FORS-04012  
; CURRENT APPLICATION NUMBER: US/09/402,618B  
; CURRENT FILING DATE: 2000-07-18  
; PRIOR APPLICATION NUMBER: PCT/US98/03194  
; PRIOR FILING DATE: 1998-05-05  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 26  
; LENGTH: 244  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-09-402-618B-26

Query Match 66.7%; Score 12; DB 4; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
| | | | | | | | | |  
Db 56 GGGGTCTCGAG 45

RESULT 169  
US-09-402-618B-29/C  
; Sequence 29, Application US/09402618B  
; Patent No. 6709815  
; GENERAL INFORMATION:  
; APPLICANT: Dong, Fang



```
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-402-618B-29
```

```
Query Match 66.7%; Score 12; DB 4; Length 244;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 GGGGUCCTGGAG 12
Db 56 GGGGTCTCTGGAG 45
```

```
RESULT 170
US-09-402-618B-31/C
; Sequence 31, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-402-618B-31
```

```
Query Match 66.7%; Score 12; DB 4; Length 244;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GGGGUCCTGGAG 12
Db 55 GGGGTCTCTGGAG 44
```

```
RESULT 171
US-09-402-618B-124
; Sequence 124, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
```

```
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 124
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-402-618B-124
```

```
Query Match 66.7%; Score 12; DB 4; Length 244;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 GGGGUCCTGGAG 12
Db 189 GGGGTCTCTGGAG 200
```

```
RESULT 172
US-09-402-618B-127
; Sequence 127, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleot
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 127
; LENGTH: 244
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-09-402-618B-127
```

```
Query Match 66.7%; Score 12; DB 4; Length 244;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GGGGUCCTGGAG 12
Db 189 GGGGTCTCTGGAG 200
```

```
RESULT 173
US-09-402-618B-128
; Sequence 128, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
```

APPLICANT: Fors, Lance  
APPLICANT: Neri, Bruce  
APPLICANT: Brow, Mary Ann  
APPLICANT: Anderson, Todd  
APPLICANT: Dahlberg, James  
TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides  
FILE REFERENCE: FORS-04012  
CURRENT APPLICATION NUMBER: US/09/402,618B  
CURRENT FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: PCT/US98/03194  
PRIOR FILING DATE: 1998-05-05  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 128  
LENGTH: 244  
TYPE: DNA  
US-09-402-618B-128

Query Match 66.7%; Score 12; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 189 GGGGUCCTGGAG 200

## RESULT 174

US-09-825-574-26/c  
Sequence 26, Application US/09825574  
Patent No. 6709819

## GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Neri, Bruce P.  
Fors, Lance

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 26;  
US-09-825-574-26

Query Match 66.7%; Score 12; DB 4; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 56 GGGGUCCTGGAG 45

## RESULT 175

US-09-825-574-29/c  
Sequence 29, Application US/09825574  
Patent No. 6709819

## GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
Neri, Bruce P.  
Fors, Lance

TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESSES:

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/825,574

FILING DATE: 03-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/934,097

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 244 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 29;

US-09-825-574-29

Query Match 66.7%; Score 12; DB 4; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 56 GGGGUCCTGGAG 45

RESULT 176  
US-09-825-574-31/C  
Sequence 31, Application US/09825574  
Patent No. 6709819  
GENERAL INFORMATION:  
APPLICANT: Lyamichev, Victor I.  
Brow, Mary Ann D.  
For, Lance  
Neri, Bruce P.  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing With Structure-Bridging  
Oligonucleotides.  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/825,574  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/934,097  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: FORS-02980  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-825-574-31

Query Match 66.7%; Score 12; DB 4; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
||||:|||||  
DB 55 GGGGTCTTGAG 44

RESULT 177  
US-09-676-768-26/C  
Sequence 26, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
For, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-09-676-768-26

ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-09-676-768-26

Query Match 66.7%; Score 12; DB 4; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
||||:|||||  
DB 56 GGGGTCTTGAG 45

RESULT 178  
US-09-676-768-29/C  
Sequence 29, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
For, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
US-09-676-768-29

Query Match 66.7%; Score 12; DB 4; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
||||:|||||  
Db 56 GGGGCTCGAG 45

RESULT 179  
US-09-676-768-31/C  
Sequence 31, Application US/09676768  
Patent No. 6780585  
GENERAL INFORMATION:  
APPLICANT: Dong, Fang  
Lyamichev, Victor I.  
Prudent, James R.  
Dahlberg, James E.  
Fors, Lance  
TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid  
Structure Probing  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/676,768  
FILING DATE: 02-Oct-2000  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,588  
FILING DATE: 05-May-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ingolia, Diane E.  
REGISTRATION NUMBER: 40,027  
REFERENCE/DOCKET NUMBER: FORS-02777  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs

TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-676-768-31

Query Match 66.7%; Score 12; DB 4; Length 244;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
||||:|||||  
Db 55 GGGGCTCGAG 44

RESULT 180  
US-08-441-971-33/C  
Sequence 33, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-May-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,523  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiak, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE: (ATCC # 40394)  
INDIVIDUAL ISOLATE: hcv1  
US-08-441-971-33

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12

Db 34 GGGGTCTGTGAG 23

||||:|||||

RESULT 181

US-08-441-971-34/c  
Sequence 34, Application US/08441971

Patent No. 6071693

GENERAL INFORMATION:

APPLICANT: Tai-An Cha

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS Version 3.3

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,971

FILING DATE: 16-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/221,653

FILING DATE:

APPLICATION NUMBER: US/07/881,528

FILING DATE:

APPLICATION NUMBER: 07/697,326

FILING DATE: 8 May 1991

ATTORNEY/AGENT INFORMATION:

NAME: Janiuk, Anthony J.

REGISTRATION NUMBER: 29,809

REFERENCE/DOCKET NUMBER: C0772/7000

TELEPHONE: (617) 720-3500

TELEFAX: (617) 720-2441

TELEX: EZEKIEL

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 252 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: u85

US-08-441-971-34

Query Match 66.7%; Score 12; DB 3; Length 252;

Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 34 GGGGTCTGTGAG 23

||||:|||||

RESULT 182

US-08-441-971-35/c

Sequence 35, Application US/08441971

Patent No. 6071693

GENERAL INFORMATION:

APPLICANT: Tai-An Cha

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS Version 3.3

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,971

FILING DATE: 16-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/221,653

FILING DATE:

APPLICATION NUMBER: US/07/881,528

FILING DATE:

APPLICATION NUMBER: 07/697,326

FILING DATE: 8 May 1991

ATTORNEY/AGENT INFORMATION:

NAME: Janiuk, Anthony J.

REGISTRATION NUMBER: 29,809

REFERENCE/DOCKET NUMBER: C0772/7000

TELEPHONE: (617) 720-3500

TELEFAX: (617) 720-2441

TELEX: EZEKIEL

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 252 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: aue1

US-08-441-971-35

Query Match 66.7%; Score 12; DB 3; Length 252;

Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 34 GGGGTCTGTGAG 23

||||:|||||

RESULT 183

US-08-441-971-36/c

Sequence 36, Application US/08441971

Patent No. 6071693

GENERAL INFORMATION:

APPLICANT: Tai-An Cha

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS Version 3.3

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: sp2  
US-08-441-971-36

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUGAG 12  
|||:|:|:|  
Db 34 GGGGTCTGAG 23

RESULT 184  
US-08-441-971-37/c  
Sequence 37, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809

REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: gm2  
US-08-441-971-37

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCUGAG 12  
|||:|:|:|  
Db 34 GGGGTCTGAG 23

RESULT 185  
US-08-441-971-38/c  
Sequence 38, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: 121  
US-08-441-971-38

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
||||:|||||  
DB 34 GGGGTCCTGGAG 23

## RESULT 186

US-08-441-971-39/C  
Sequence 39, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441.971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221.653  
FILING DATE:  
APPLICATION NUMBER: US/07/881.528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: us4  
US-08-441-971-39

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
||||:|||||  
DB 34 GGGGTCCTGGAG 23

RESULT 187

US-08-441-971-40/C  
Sequence 40, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441.971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221.653  
FILING DATE:  
APPLICATION NUMBER: US/07/881.528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: jh1  
US-08-441-971-40

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
||||:|||||  
DB 34 GGGGTCCTGGAG 23

## RESULT 188

US-08-441-971-41/C  
Sequence 41, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts

COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE: US/07/881,528  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKTEL  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: nacs  
US-08-441-971-41

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
Db 34 GGGGCTCTGGAG 23

RESULT 189  
US-08-441-971-42/c  
Sequence 42, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653

FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKTEL  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: arg2  
US-08-441-971-42

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
Db 34 GGGGCTCTGGAG 23

RESULT 190  
US-08-441-971-43/c  
Sequence 43, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE: US/07/881,528  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKTEL



INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: spl  
US-08-441-971-43

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 34 GGGGTCTCGAG 23

RESULT 191  
US-08-441-971-44/c  
Sequence 44, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: ghl  
US-08-441-971-44  
Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 34 GGGGTCTCGAG 23

RESULT 192  
US-08-441-971-45/c  
Sequence 45, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: i15  
US-08-441-971-45  
Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 34 GGGGTCTCGAG 23  
RESULT 193  
US-08-441-971-49/c  
Sequence 49, Application US/08441971  
Patent No. 6071693  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,971  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE: US/07/881,528  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE: DNA  
INDIVIDUAL ISOLATE: 9161329  
US-08-441-971-49  
Query Match 66.7%; Score 12; DB 3; Length 252;  
Best local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
Db 34 GGGGTCCTGGAG 23  
RESULT 194  
US-08-221-653-33/c  
Sequence 33, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE: (ATCC # 40394)  
INDIVIDUAL ISOLATE: hcv1  
US-08-221-653-33

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
Db 34 GGGGTCCTGGAG 23

RESULT 195  
US-08-221-653-34/c  
Sequence 34, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: us5  
US-08-221-653-34

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|:|:|:|  
Db 34 GGGGTCTCGAG 23

RESULT 196  
US-08-221-653-35/C  
Sequence 35, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221.653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881.528  
FILING DATE:  
APPLICATION NUMBER: 07/697.326  
FILING DATE: 8 MAY 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: aus1  
US-08-221-653-35

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|:|:|:|  
Db 34 GGGGTCTCGAG 23

RESULT 197  
US-08-221-653-36/C  
Sequence 36, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
NUMBER OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221.653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881.528  
FILING DATE:  
APPLICATION NUMBER: 07/697.326  
FILING DATE: 8 MAY 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janluk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKIEL  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: sp2  
US-08-221-653-36

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|:~|:|:|  
Db 34 GGGGTCTCGAG 23

RESULT 198  
US-08-221-653-37/C  
Sequence 37, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKTEL  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: gm2  
US-08-221-653-37

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 34 GGGGTCCTGGAG 23

RESULT 199  
US-08-221-653-38/c  
Sequence 38, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500  
TELEFAX: (617) 720-2441  
TELEX: EZEKTEL  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 252 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: 121  
US-08-221-653-38

Query Match 66.7%; Score 12; DB 3; Length 252;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 34 GGGGTCCTGGAG 23

RESULT 200  
US-08-221-653-39/c  
Sequence 39, Application US/08221653  
Patent No. 6190864  
GENERAL INFORMATION:  
APPLICANT: Tai-An Cha  
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR  
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 147  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS Version 3.3  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,653  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/881,528  
FILING DATE:  
APPLICATION NUMBER: 07/697,326  
FILING DATE: 8 May 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janiuk, Anthony J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: C0772/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 720-3500

TELEFAX: (617) 720-2441  
 TELETYPE: EZEKIEL  
 INFORMATION FOR SEQ ID NO: 39:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 252 nucleotides  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 ORIGINAL SOURCE:  
 INDIVIDUAL ISOLATE: us4  
 US-08-221-653-39

Query Match 66.7%; Score 12; DB 3; Length 252;  
 Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GGGGUCUCGAG 12  
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 Db 34 GGGGTCCTCGAG 23

Search completed: April 25, 2005, 13:47:54  
 Job time : 83.6842 secs

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OM nucleic - nucleic search, using sw model

Run on: April 25, 2005, 13:45:46 ; Search time 252.474 Seconds  
(without alignments)  
432.833 Million cell updates/sec

Title: US-08-887-505B-38

Perfect score: 18

Sequence: 1 GGGGUCGAGGAGNNNNN 18

Scoring table:

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Gapop 60.0 , Gapext 60.0

Searched: 563728 seqs, 3035525691 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11267456

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	15	83.3	29	US-10-053-883-11	Sequence 11, Appl
5	13	72.2	20	US-10-008-1408-30	Sequence 30, Appl
6	13	72.2	3286	US-10-723-860-5700	Sequence 5700, Ap
7	13	72.2	5132	US-10-723-860-5700	Sequence 5700, Ap
8	13	72.2	92726	US-09-997-722-193	Sequence 193, App
9	13	72.2	165221	US-10-087-192-1015	Sequence 1015, Ap
10	13	72.2	167163	US-10-394-948-31	Sequence 31, Appl
11	12	66.7	12	US-08-887-505-47	Sequence 47, Appl

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238	12	66.7	201	19	US-10-741-600-58311	Sequence 58311, A	C 311	12	66.7	289	19	US-10-655-362-23	Sequence 20, Appl
239	12	66.7	217	16	US-10-029-386-16443	Sequence 16443, A	C 312	12	66.7	297	9	US-09-864-761-26956	Sequence 26956, A
240	12	66.7	226	17	US-10-688-272-19	Sequence 19, Appl	C 313	12	66.7	298	9	US-09-345-761-7	Sequence 7, Appl
241	12	66.7	227	9	US-09-783-590-523	Sequence 523, Appl	C 314	12	66.7	298	18	US-10-687-588-7	Sequence 7, Appl
242	12	66.7	230	16	US-10-029-386-21951	Sequence 21951, A	C 315	12	66.7	299	9	US-09-983-965-5881	Sequence 5881, Ap
243	12	66.7	230	17	US-10-688-272-22	Sequence 22, Appl	C 316	12	66.7	299	16	US-10-230-381-1	Sequence 1, Appl
244	12	66.7	230	17	US-10-688-272-23	Sequence 23, Appl	C 317	12	66.7	302	9	US-09-786-682-9227	Sequence 9227, Ap
245	12	66.7	232	9	US-09-825-574-37	Sequence 37, Appl	C 318	12	66.7	302	14	US-10-040-862-9227	Sequence 9227, Ap
246	12	66.7	232	10	US-09-882-945A-37	Sequence 37, Appl	C 319	12	66.7	302	17	US-10-057-4755-9227	Sequence 9227, Ap
247	12	66.7	232	18	US-10-807-114-37	Sequence 37, Appl	C 320	12	66.7	302	17	US-10-154-884A-9227	Sequence 9227, Ap
248	12	66.7	232	19	US-10-655-362-37	Sequence 37, Appl	C 321	12	66.7	302	18	US-10-764-324-9227	Sequence 9227, Ap
249	12	66.7	239	9	US-09-825-574-32	Sequence 32, Appl	C 322	12	66.7	306	18	US-10-425-115-171472	Sequence 171472, A
250	12	66.7	239	9	US-09-825-574-36	Sequence 36, Appl	C 323	12	66.7	315	9	US-09-345-761-6	Sequence 6, Appl
251	12	66.7	239	10	US-09-882-945A-32	Sequence 32, Appl	C 324	12	66.7	315	18	US-10-687-588-6	Sequence 6, Appl
252	12	66.7	239	10	US-09-882-945A-36	Sequence 36, Appl	C 325	12	66.7	319	18	US-10-425-115-12017	Sequence 12017, A
253	12	66.7	239	18	US-10-807-114-32	Sequence 36, Appl	C 326	12	66.7	328	10	US-09-882-945A-240	Sequence 240, Appl
254	12	66.7	239	18	US-10-807-114-36	Sequence 36, Appl	C 327	12	66.7	328	10	US-09-882-945A-242	Sequence 242, Appl
255	12	66.7	239	19	US-10-655-362-32	Sequence 36, Appl	C 328	12	66.7	328	18	US-10-475-024-18	Sequence 18, Appl
256	12	66.7	239	19	US-10-655-362-36	Sequence 36, Appl	C 329	12	66.7	328	18	US-10-807-114-240	Sequence 240, Appl
257	12	66.7	239	19	US-10-927-520-9	Sequence 9, Appl	C 330	12	66.7	328	18	US-10-807-114-242	Sequence 242, Appl
258	12	66.7	239	19	US-10-927-520-10	Sequence 10, Appl	C 331	12	66.7	330	18	US-10-425-115-112799	Sequence 112799, A
259	12	66.7	240	9	US-09-825-574-33	Sequence 33, Appl	C 332	12	66.7	337	10	US-09-940-244-45	Sequence 45, Appl
260	12	66.7	240	9	US-09-825-574-38	Sequence 38, Appl	C 333	12	66.7	337	10	US-09-982-667-56	Sequence 56, Appl
261	12	66.7	240	10	US-09-882-945A-33	Sequence 33, Appl	C 334	12	66.7	337	13	US-10-083-297-45	Sequence 45, Appl
262	12	66.7	240	10	US-09-882-945A-38	Sequence 38, Appl	C 335	12	66.7	337	13	US-10-081-806-56	Sequence 56, Appl
263	12	66.7	240	18	US-10-807-114-33	Sequence 33, Appl	C 336	12	66.7	337	16	US-10-442-283-136	Sequence 136, Appl
264	12	66.7	240	18	US-10-807-114-38	Sequence 38, Appl	C 337	12	66.7	337	16	US-10-290-386-45	Sequence 45, Appl
265	12	66.7	240	19	US-10-655-362-33	Sequence 33, Appl	C 338	12	66.7	337	17	US-10-356-861-45	Sequence 45, Appl
266	12	66.7	240	19	US-10-655-362-38	Sequence 38, Appl	C 339	12	66.7	337	18	US-10-309-584-45	Sequence 45, Appl
267	12	66.7	241	14	US-10-087-631B-10	Sequence 10, Appl	C 340	12	66.7	337	18	US-10-897-793-45	Sequence 45, Appl
268	12	66.7	241	16	US-10-419-022-10	Sequence 10, Appl	C 341	12	66.7	337	19	US-10-783-557-45	Sequence 45, Appl
269	12	66.7	244	9	US-09-825-574-26	Sequence 26, Appl	C 342	12	66.7	341	9	US-09-814-292-44	Sequence 44, Appl
270	12	66.7	244	9	US-09-825-574-29	Sequence 29, Appl	C 343	12	66.7	341	10	US-09-814-357-3	Sequence 3, Appl
271	12	66.7	244	9	US-09-825-574-31	Sequence 31, Appl	C 344	12	66.7	341	10	US-09-814-357-13	Sequence 3, Appl
272	12	66.7	244	10	US-09-882-945A-26	Sequence 26, Appl	C 345	12	66.7	341	15	US-10-259-275-35	Sequence 35, Appl
273	12	66.7	244	10	US-09-882-945A-29	Sequence 29, Appl	C 346	12	66.7	347	10	US-09-814-353-1497	Sequence 1497, Ap
274	12	66.7	244	10	US-09-882-945A-31	Sequence 31, Appl	C 347	12	66.7	347	10	US-09-814-353-7856	Sequence 7856, Ap
275	12	66.7	244	17	US-10-688-272-16	Sequence 16, Appl	C 348	12	66.7	347	15	US-10-132-293-1	Sequence 1, Appl
276	12	66.7	244	18	US-10-807-114-26	Sequence 26, Appl	C 349	12	66.7	366	9	US-09-877-526A-48	Sequence 48, Appl
277	12	66.7	244	18	US-10-807-114-29	Sequence 29, Appl	C 350	12	66.7	366	9	US-09-992-160-48	Sequence 48, Appl
278	12	66.7	244	18	US-10-807-114-31	Sequence 31, Appl	C 351	12	66.7	366	10	US-09-740-332-9701	Sequence 9701, Ap
279	12	66.7	244	19	US-10-655-362-26	Sequence 26, Appl	C 352	12	66.7	366	10	US-09-817-879-9701	Sequence 9701, Ap
280	12	66.7	244	19	US-10-655-362-29	Sequence 29, Appl	C 353	12	66.7	366	14	US-10-056-761-48	Sequence 48, Appl
281	12	66.7	244	19	US-10-655-362-31	Sequence 31, Appl	C 354	12	66.7	366	17	US-10-422-050-48	Sequence 48, Appl
282	12	66.7	244	19	US-10-655-362-124	Sequence 124, Appl	C 355	12	66.7	366	18	US-10-669-841-16198	Sequence 16198, A
283	12	66.7	244	19	US-10-655-362-127	Sequence 127, Appl	C 356	12	66.7	368	13	US-09-960-352-12725	Sequence 12725, A
284	12	66.7	244	19	US-10-655-362-128	Sequence 128, Appl	C 357	12	66.7	368	13	US-10-027-632-278770	Sequence 278770, A
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286	12	66.7	278	9	US-09-294-093B-1960	Sequence 1960, Ap	C 359	12	66.7	368	13	US-10-027-632-278772	Sequence 278772, A
287	12	66.7	278	9	US-09-294-093B-2729	Sequence 2729, Ap	C 360	12	66.7	368	13	US-10-027-632-278770	Sequence 278770, A
288	12	66.7	278	18	US-10-653-047-3593	Sequence 3593, Ap	C 361	12	66.7	368	17	US-10-027-632-278771	Sequence 278771, A
289	12	66.7	281	10	US-09-940-925A-121	Sequence 121, Appl	C 362	12	66.7	368	17	US-10-027-632-278772	Sequence 278772, A
290	12	66.7	281	10	US-09-940-925A-126	Sequence 126, Appl	C 363	12	66.7	374	17	US-10-324-408B-32	Sequence 32, Appl
291	12	66.7	281	10	US-09-940-925A-127	Sequence 127, Appl	C 364	12	66.7	374	17	US-10-324-408B-30	Sequence 730, Ap
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293	12	66.7	281	10	US-09-940-925A-132	Sequence 132, Appl	C 366	12	66.7	374	19	US-10-332-626-1	Sequence 1, Appl
294	12	66.7	281	10	US-09-941-193A-121	Sequence 121, Appl	C 367	12	66.7	386	10	US-09-940-925A-122	Sequence 122, Appl
295	12	66.7	281	10	US-09-941-193A-126	Sequence 126, Appl	C 368	12	66.7	386	10	US-09-941-193A-122	Sequence 122, Appl
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297	12	66.7	281	10	US-09-941-193A-128	Sequence 128, Appl	C 370	12	66.7	393	18	US-10-363-829-168	Sequence 168, Appl
298	12	66.7	281	10	US-09-941-193A-132	Sequence 132, Appl	C 371	12	66.7	393	15	US-10-376-513-5	Sequence 5, Appl
299	12	66.7	282	10	US-09-940-925A-124	Sequence 124, Appl	C 372	12	66.7	394	9	US-09-867-701-6178	Sequence 6178, Ap
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302	12	66.7	282	10	US-09-941-193A-130	Sequence 130, Appl	C 375	12	66.7	397	18	US-10-357-930-1963	Sequence 1963, Ap
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C 379	12	66.7	400	13	US-10-027-632-292329	Sequence 292329, A	C 452	12	66.7	552	17	US-10-027-632-138522	Sequence 138522, A
C 380	12	66.7	400	17	US-10-027-632-292328	Sequence 292328, A	C 453	12	66.7	552	17	US-10-027-632-138523	Sequence 138523, A
C 381	12	66.7	400	17	US-10-027-632-292329	Sequence 292329, A	C 454	12	66.7	552	17	US-10-027-632-138524	Sequence 138524, A
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C 385	12	66.7	401	14	US-10-007-700-264	Sequence 264, App	C 458	12	66.7	560	17	US-10-027-632-90602	Sequence 90602, A
C 386	12	66.7	401	15	US-10-117-982-264	Sequence 264, App	C 459	12	66.7	562	16	US-10-029-386-1350	Sequence 1350, App
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C 388	12	66.7	404	18	US-10-775-972-264	Sequence 264, App	C 461	12	66.7	569	16	US-10-029-386-1176	Sequence 1176, App
C 389	12	66.7	404	9	US-09-867-701-5163	Sequence 5163, App	C 462	12	66.7	571	16	US-10-027-632-129745	Sequence 129745, A
C 390	12	66.7	407	18	US-10-437-963-81717	Sequence 81717, A	C 463	12	66.7	582	13	US-10-027-632-129745	Sequence 129745, A
C 391	12	66.7	410	10	US-09-814-353-14240	Sequence 14240, A	C 464	12	66.7	584	9	US-09-854-761-9831	Sequence 9831, App
C 392	12	66.7	411	10	US-09-918-995-14240	Sequence 14240, A	C 465	12	66.7	584	9	US-09-854-761-9831	Sequence 9831, App
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C 394	12	66.7	414	13	US-10-027-632-46928	Sequence 46928, A	C 467	12	66.7	591	11	US-09-369-034-2265	Sequence 2265, App
C 395	12	66.7	414	17	US-10-027-632-46928	Sequence 46928, A	C 468	12	66.7	591	18	US-10-425-115-67445	Sequence 67445, A
C 396	12	66.7	418	9	US-09-960-352-588	Sequence 588, App	C 469	12	66.7	599	18	US-10-767-701-29289	Sequence 29289, A
C 397	12	66.7	431	18	US-10-357-930-32305	Sequence 32305, A	C 470	12	66.7	600	14	US-10-198-846-13916	Sequence 13916, A
C 398	12	66.7	433	18	US-10-357-930-7216	Sequence 7216, App	C 471	12	66.7	610	13	US-10-027-632-269815	Sequence 269815, A
C 399	12	66.7	434	15	US-10-102-524-1040	Sequence 1040, App	C 472	12	66.7	610	13	US-10-027-632-269815	Sequence 269815, A
C 400	12	66.7	437	17	US-10-424-599-88199	Sequence 88199, A	C 473	12	66.7	610	17	US-10-027-632-269815	Sequence 269815, A
C 401	12	66.7	440	18	US-10-357-930-32267	Sequence 32267, A	C 474	12	66.7	610	17	US-10-027-632-269815	Sequence 269815, A
C 402	12	66.7	440	18	US-10-357-930-41199	Sequence 41199, A	C 475	12	66.7	610	18	US-10-357-930-41197	Sequence 41197, A
C 403	12	66.7	440	18	US-10-357-930-41237	Sequence 41237, A	C 476	12	66.7	610	18	US-10-357-930-41229	Sequence 41229, A
C 404	12	66.7	441	18	US-10-425-115-37975	Sequence 37975, A	C 477	12	66.7	610	18	US-10-357-930-47041	Sequence 27041, A
C 405	12	66.7	446	10	US-09-918-995-28661	Sequence 28661, A	C 478	12	66.7	610	18	US-10-357-930-47073	Sequence 27073, A
C 406	12	66.7	448	18	US-10-437-963-88979	Sequence 88979, A	C 479	12	66.7	613	13	US-10-027-632-99472	Sequence 99472, A
C 407	12	66.7	454	17	US-10-027-632-136999	Sequence 136999, A	C 480	12	66.7	613	17	US-10-027-632-99472	Sequence 99472, A
C 408	12	66.7	454	17	US-10-027-632-136999	Sequence 136999, A	C 481	12	66.7	615	18	US-10-425-115-40181	Sequence 40181, A
C 409	12	66.7	455	13	US-10-027-632-195949	Sequence 195949, A	C 482	12	66.7	623	13	US-10-027-632-47265	Sequence 247265, A
C 410	12	66.7	455	17	US-10-027-632-195949	Sequence 195949, A	C 483	12	66.7	623	17	US-10-027-632-47265	Sequence 247265, A
C 411	12	66.7	457	10	US-09-918-995-28679	Sequence 28679, A	C 484	12	66.7	623	17	US-10-027-632-47265	Sequence 247265, A
C 412	12	66.7	458	18	US-10-357-930-37184	Sequence 37184, A	C 485	12	66.7	625	17	US-10-027-632-47266	Sequence 247266, A
C 413	12	66.7	461	9	US-09-851-138-103	Sequence 103, App	C 486	12	66.7	625	17	US-10-276-774-429	Sequence 429, App
C 414	12	66.7	463	18	US-10-425-115-162307	Sequence 162307, A	C 487	12	66.7	626	13	US-10-027-632-282944	Sequence 282944, A
C 415	12	66.7	469	10	US-09-984-130-95	Sequence 95, App1	C 488	12	66.7	626	17	US-10-027-632-282944	Sequence 282944, A
C 416	12	66.7	469	10	US-09-836-353A-95	Sequence 95, App1	C 489	12	66.7	631	13	US-10-027-632-88162	Sequence 88162, A
C 417	12	66.7	474	10	US-09-918-995-15614	Sequence 15614, A	C 490	12	66.7	631	13	US-10-027-632-107161	Sequence 107161, A
C 418	12	66.7	475	9	US-09-864-761-10323	Sequence 10323, A	C 491	12	66.7	631	13	US-10-027-632-139050	Sequence 139050, A
C 419	12	66.7	475	18	US-10-758-846-21	Sequence 21, App1	C 492	12	66.7	631	13	US-10-027-632-294984	Sequence 294984, A
C 420	12	66.7	477	10	US-09-918-995-22114	Sequence 22114, A	C 493	12	66.7	631	16	US-10-029-386-20805	Sequence 20805, A
C 421	12	66.7	478	16	US-10-029-386-20547	Sequence 20547, A	C 494	12	66.7	631	17	US-10-027-632-68162	Sequence 68162, A
C 422	12	66.7	480	9	US-09-771-209-35	Sequence 35, App1	C 495	12	66.7	631	17	US-10-027-632-107161	Sequence 107161, A
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C 425	12	66.7	482	17	US-10-240-425-487	Sequence 487, App	C 498	12	66.7	642	18	US-10-767-701-19385	Sequence 19385, A
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C 432	12	66.7	493	9	US-09-783-590-6626	Sequence 6626, App	C 505	12	66.7	657	17	US-10-027-632-239167	Sequence 239167, A
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C 438	12	66.7	506	16	US-10-029-386-8251	Sequence 8251, App	C 511	12	66.7	672	18	US-10-425-115-169941	Sequence 169941, A
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C 442	12	66.7	519	19	US-10-660-811A-110	Sequence 110, App	C 515	12	66.7	673	17	US-10-027-632-138772	Sequence 138772, A
C 443	12	66.7	531	18	US-10-437-963-78326	Sequence 78326, A	C 516	12	66.7	681	13	US-10-027-632-283518	Sequence 283518, A
C 444	12	66.7	532	16	US-10-029-386-2743	Sequence 2743, App	C 517	12	66.7	681	17	US-10-027-632-284925	Sequence 284925, A
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C 446	12	66.7	542	13	US-10-027-632-230493	Sequence 230493, A	C 519	12	66.7	685	17	US-10-457-304-37	Sequence 37, App1
C 447	12	66.7	542	17	US-10-027-632-220493	Sequence 220493, A	C 520	12	66.7	691	18	US-10-454-293-37	Sequence 37, App1
C 448	12	66.7	543	15	US-10-156-761-4088	Sequence 4088, App	C 521	12	66.7	691	18	US-10-767-701-10176	Sequence 10176, A
C 449	12	66.7	552	13	US-10-027-632-138522	Sequence 138522, A	C 522	12	66.7	692	13	US-10-027-632-32098	Sequence 32098, A

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C 568	12	66.7	819	9	US-09-896-913A-3	Sequence 3, App
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C 571	12	66.7	822	16	US-10-041-319-5	Sequence 5, App
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C 577	12	66.7	829	17	US-10-027-632-158595	Sequence 158595, A
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C 581	12	66.7	834	13	US-10-027-632-137821	Sequence 137821, A
C 582	12	66.7	834	17	US-10-027-632-137821	Sequence 137821, A
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C 593	12	66.7	842	9	US-09-875-338-90	Sequence 90, App
C 594	12	66.7	842	14	US-10-077-023-20	Sequence 20, App
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C 599	12	66.7	911	13	US-10-027-632-9547	Sequence 9547, App
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C 601	12	66.7	911	17	US-10-027-632-9546	Sequence 9547, App
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C 604	12	66.7	950	17	US-10-114-270-103	Sequence 103, App
C 605	12	66.7	951	15	US-10-156-761-719	Sequence 719, App
C 606	12	66.7	961	9	US-09-864-761-1566	Sequence 1566, App
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C 611	12	66.7	995	17	US-10-425-114-27811	Sequence 27811, A
C 612	12	66.7	1005	15	US-10-156-761-1982	Sequence 1982, App
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C 615	12	66.7	1021	17	US-10-425-114-16806	Sequence 16806, A
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C 618	12	66.7	1024	15	US-10-212-677-275	Sequence 275, App
C 619	12	66.7	1024	17	US-10-361-811-274	Sequence 274, App
C 620	12	66.7	1024	17	US-10-361-811-275	Sequence 275, App
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C 627	12	66.7	1031	17	US-10-027-632-10588	Sequence 10588, A
C 628	12	66.7	1031	17	US-10-027-632-10589	Sequence 10589, A
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C 630	12	66.7	1057	14	US-10-004-860-204	Sequence 204, App
C 631	12	66.7	1057	14	US-10-023-282-204	Sequence 204, App
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C 636	12	66.7	1105	17	US-10-369-022-23	Sequence 23, App
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C 638	12	66.7	1111	10	US-09-903-190-146	Sequence 146, App
C 639	12	66.7	1111	11	US-09-978-360A-337	Sequence 337, App
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C 645	12	66.7	1157	13	US-10-027-632-124052	Sequence 124052, A
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C 647	12	66.7	1157	17	US-10-027-632-118118	Sequence 118118, A
C 648	12	66.7	1157	17	US-10-027-632-118118	Sequence 118118, A
C 649	12	66.7	1181	13	US-09-729-658B-14	Sequence 14, App
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C 653	12	66.7	1183	17	US-10-641-643-600	Sequence 600, App
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C 655	12	66.7	1204	17	US-10-425-114-1211	Sequence 1211, App
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C 658	12	66.7	1210	17	US-10-158-057-29	Sequence 29, App
C 659	12	66.7	1223	9	US-09-895-837-1	Sequence 1, App
C 660	12	66.7	1223	9	US-09-896-913A-1	Sequence 1, App
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C 662	12	66.7	1237	9	US-09-925-100-478	Sequence 478, App
C 663	12	66.7	1258	17	US-10-302-117-844	Sequence 844, App
C 664	12	66.7	1261	9	US-09-755-100-6	Sequence 6, App
C 665	12	66.7	1261	17	US-10-298-965-6	Sequence 6, App
C 666	12	66.7	1261	17	US-10-800-665-6	Sequence 6, App
C 667	12	66.7	1261	18	US-10-800-665-6	Sequence 6, App
C 668	12	66.7	1264	9	US-09-764-868-198	Sequence 198, App
C 669	12	66.7	1264	11	US-09-764-868-198	Sequence 198, App
C 670	12	66.7	1264	11	US-09-764-868-198	Sequence 198, App
C 671	12	66.7	1264	11	US-09-764-868-198	Sequence 198, App
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C 673	12	66.7	1264	11	US-09-764-868-198	Sequence 198, App
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C 675	12	66.7	1264	11	US-09-764-868-198	Sequence 198, App
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679	12	66.7	1410	17	US-10-369-493-34362	Sequence 34362, A	752	12	66.7	1998	18	US-10-128-558-120	Sequence 120, App
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681	12	66.7	1455	17	US-10-425-114-28938	Sequence 28938, A	754	12	66.7	2019	15	US-10-156-761-4549	Sequence 4549, Ap
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686	12	66.7	1511	19	US-10-764-503-20	Sequence 20, Appl	759	12	66.7	2058	14	US-10-158-238-1	Sequence 31, Appl
687	12	66.7	1547	9	US-09-764-887-525	Sequence 525, App	760	12	66.7	2061	17	US-10-451-168-15	Sequence 15, Appl
688	12	66.7	1547	14	US-10-073-961-525	Sequence 525, App	761	12	66.7	2091	15	US-10-142-174-4	Sequence 4, Appl
689	12	66.7	1548	18	US-10-437-963-26804	Sequence 26804, App	762	12	66.7	2091	18	US-10-381-820A-7	Sequence 7, Appl
690	12	66.7	1549	17	US-10-398-221-3152	Sequence 3152, Ap	763	12	66.7	2098	15	US-10-142-174-13	Sequence 13, Appl
691	12	66.7	1551	14	US-10-197-666A-17	Sequence 17, Appl	764	12	66.7	2098	15	US-10-142-174-13	Sequence 41, Appl
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693	12	66.7	1551	16	US-10-132-089-1	Sequence 1, Appl	766	12	66.7	2098	15	US-10-008-960-1	Sequence 1, Appl
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696	12	66.7	1551	18	US-10-024-298A-72	Sequence 72, Appl	769	12	66.7	2116	18	US-10-723-860-6981	Sequence 6981, Ap
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704	12	66.7	1602	18	US-10-128-558-50	Sequence 50, Appl	777	12	66.7	2127	15	US-10-252-157-123	Sequence 423, App
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711	12	66.7	1678	9	US-09-925-300-153	Sequence 153, App	784	12	66.7	2163	17	US-10-132-072-234	Sequence 234, App
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713	12	66.7	1691	17	US-10-425-114-15801	Sequence 15801, A	786	12	66.7	2170	17	US-10-264-237-1398	Sequence 1398, App
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715	12	66.7	1707	15	US-10-267-255-68	Sequence 68, Appl	788	12	66.7	2176	10	US-10-104-047-731	Sequence 731, App
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## ALIGNMENTS

RESULT 1  
US-08-887-505-38  
; Sequence 38, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,505  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/471,968  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerner, Ann-Louise  
; REGISTRATION/DOCKET NUMBER: 33,523  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 526-6000  
; TELEFAX: (617) 526-5000  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA/RNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
US-08-887-505-38  
Query Match 100.0%; Score 18; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
US-08-887-505-67  
; Sequence 67, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
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; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,505  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/471,968  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerner, Ann-Louise  
; REGISTRATION/DOCKET NUMBER: 33,523  
; REFERENCE/DOCKET NUMBER: HYZ-040CIP

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-67

Query Match 100.0%; Score 18; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.32;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUGAGNNNNN 18  
Db 1 GGGGUCUGAGNNNNN 18

RESULT 3  
US-10-053-883-10  
Sequence 10, Application US/10053883  
Publication No. US20030113737A1  
GENERAL INFORMATION:  
APPLICANT: PEDERSEN, Morten Lorentz  
TITLE OF INVENTION: ASSAY AND KIT FOR ANALYZING GENE EXPRESSION  
FILE REFERENCE: PEDERSEN-1A  
CURRENT APPLICATION NUMBER: US/10/053,883  
CURRENT FILING DATE: 2002-01-02  
PRIOR APPLICATION NUMBER: PA 2001 00126  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: US 60/267,704  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 148  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 29  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic  
NAME/KEY: misc feature  
LOCATION: (12)-(29)  
OTHER INFORMATION: n is a, c, g or t  
US-10-053-883-10

Query Match 83.3%; Score 15; DB 15; Length 29;  
Best Local Similarity 86.7%; Pred. No. 19;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 GUCCUGAGNNNNN 18  
Db 3 GTCTGGAGNNNNN 17

RESULT 4  
US-10-053-883-11/c  
Sequence 11, Application US/10053883  
Publication No. US20030113737A1  
GENERAL INFORMATION:  
APPLICANT: PEDERSEN, Morten Lorentz  
TITLE OF INVENTION: ASSAY AND KIT FOR ANALYZING GENE EXPRESSION  
FILE REFERENCE: PEDERSEN-1A  
CURRENT APPLICATION NUMBER: US/10/053,883  
CURRENT FILING DATE: 2002-01-02  
PRIOR APPLICATION NUMBER: PA 2001 00126  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: US 60/267,704

PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 148  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 11  
LENGTH: 29  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic  
NAME/KEY: misc feature  
LOCATION: (1)-(18)  
OTHER INFORMATION: n is a, c, g or t  
US-10-053-883-11

Query Match 83.3%; Score 15; DB 15; Length 29;  
Best Local Similarity 86.7%; Pred. No. 19;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 GUCCUGAGNNNNN 18  
Db 27 GTCTGGAGNNNNN 13

RESULT 5  
US-10-008-140B-30/c  
Sequence 30, Application US/10008140B  
Publication No. US20030124512A1  
GENERAL INFORMATION:  
APPLICANT: Stuyver, Lieven  
TITLE OF INVENTION: Simultaneous Quantification of Nucleic Acids in Diseased Cells  
FILE REFERENCE: 08841, 105021  
CURRENT APPLICATION NUMBER: US/10/008,140B  
CURRENT FILING DATE: 2001-10-18  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 30  
LENGTH: 20  
TYPE: DNA  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: labelled oligonucleotide (probe) used to detect HCV viral load  
NAME/KEY: misc\_feature  
LOCATION: (1)-(1)  
OTHER INFORMATION: n=FAM modified cytosine  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (20)-(20)  
OTHER INFORMATION: n=TAMRA modified cytosine  
US-10-008-140B-30

Query Match 72.2%; Score 13; DB 15; Length 20;  
Best Local Similarity 84.6%; Pred. No. 3.2e+02;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUGAGN 13  
Db 13 GGGGUCUGAGN 1

RESULT 6  
US-10-723-860-5790/c  
Sequence 5790, Application US/10723860  
Publication No. US20040253606A1  
GENERAL INFORMATION:  
APPLICANT: Azizi, Natascha  
APPLICANT: Ginsburg, Wendy M.  
APPLICANT: Zlotnik, Albert  
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
FILE REFERENCE: 05882, 0193, NPUS01



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; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5790
; LENGTH: 3286
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (248)..(271)
; OTHER INFORMATION: "n" is a, c, g, or t
; US-10-723-860-5790

Query Match      72.2% Score 13; DB 18; Length 3286;
Best Local Similarity 92.3%; Pred. No. 88;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      6 CCUGAGNNNNNN 18
Db      278 CCTGAGNNNNNN 266

RESULT 7
; US-10-723-860-5700/c
; Sequence 5700, Application US/10723860
; Publication No. US2004025606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natacha
; APPLICANT: Ginzburg, Wendy M.
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882, 0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5700
; LENGTH: 5132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (974)..(1005)
; OTHER INFORMATION: "n" is a, c, g, or t
; US-10-723-860-5700

Query Match      72.2% Score 13; DB 18; Length 5132;
Best Local Similarity 92.3%; Pred. No. 78;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      6 CCUGAGNNNNNN 18
Db      1012 CCTGAGNNNNNN 1000

RESULT 8
; US-09-997-722-193/c
; Sequence 193, Application US/09997722
; Publication No. US2004007215A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/997,722
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
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; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 193
; LENGTH: 92726
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (122)..(148)
; OTHER INFORMATION: "n" at positions 122 through 148 can be any base.
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (7485)..(8927)
; OTHER INFORMATION: "n" at positions 7485 through 8927 can be any base.
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (24884)..(25439)
; OTHER INFORMATION: "n" at positions 24884 through 25439 can be any base.
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (36036)..(36055)
; OTHER INFORMATION: "n" at positions 36036 through 36055 can be any base.
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (46607)..(46729)
; OTHER INFORMATION: "n" at positions 46607 through 46729 can be any base.
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (77651)..(77670)
; OTHER INFORMATION: "n" at positions 77651 through 77670 can be any base.
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (81264)..(81462)
; OTHER INFORMATION: "n" at positions 81264 through 81462 can be any base.
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (89156)..(89175)
; OTHER INFORMATION: "n" at positions 89156 through 89175 can be any base.
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (90342)..(90361)
; OTHER INFORMATION: "n" at positions 90342 through 90361 can be any base.
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (91379)..(91398)
; OTHER INFORMATION: "n" at positions 91379 through 91398 can be any base.
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (92723)..(92726)
; OTHER INFORMATION: "n" at positions 92723 through 92726 can be any base.
; US-09-997-722-193

Query Match      72.2% Score 13; DB 11; Length 92726;
Best Local Similarity 92.3%; Pred. No. 38;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      6 CCUGAGNNNNNN 18
Db      155 CCTGAGNNNNNN 143

RESULT 9
; US-10-087-192-1015
; Sequence 1015, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
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; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1015
; LENGTH: 165221
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(165221)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1015

Query Match      72.2%; Score 13; DB 13; Length 165221;
Best Local Similarity 92.3%; Pred. No. 33;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      6 CCUGAGNNNNNN 18
      ||:|||||
Db      59475 CCTGAGNNNNNN 59487

RESULT 10
US-10-394-948-31
; Sequence 31, Application US/10394948
; Publication No. US20040023267A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NO. US20040023267A1 Compositions and Methods in Cancer
; FILE REFERENCE: 529452000900
; CURRENT APPLICATION NUMBER: US/10/394,948
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US 60/367,025
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 167163
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(167163)
; OTHER INFORMATION: n = A,T,C or G
US-10-394-948-31

Query Match      72.2%; Score 13; DB 17; Length 167163;
Best Local Similarity 92.3%; Pred. No. 32;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      6 CCUGAGNNNNNN 18
      ||:|||||
Db      62041 CCTGAGNNNNNN 62053

RESULT 11
US-08-887-505-47
; Sequence 47, Application US/08887505
; Publication No. US20020081577A1
; GENERAL INFORMATION:
; APPLICANT: Kiluskie, Robert E.
; APPLICANT: Frank, Bruce L.
; APPLICANT: Goodchild, John
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; APPLICANT: Wolfe, Jia L.
; APPLICANT: Roberts, Peter C.
; APPLICANT: Hamlin, Jr., Henry A.
; APPLICANT: Roberts, No. US20020081577A1 A.
; APPLICANT: Walcher, Debra M.
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR
; TITLE OF INVENTION: HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 172
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,505
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/471,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-040CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-887-505-47

Query Match      66.7%; Score 12; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 GGGGUCCTUGAG 12
      |||||||
Db      1 GGGGUCCTUGAG 12

RESULT 12
US-10-291-230-43/c
; Sequence 43, Application US/10291230
; Publication No. US20030108939A1
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: 76678.US.A
; CURRENT APPLICATION NUMBER: US/10/291,230
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 09/647,344
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; PRIOR APPLICATION NUMBER: US 60/079,792
; PRIOR FILING DATE: 1998-03-28
; PRIOR APPLICATION NUMBER: US 60/107,504
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; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A portion of an antisense library including a Bpm1 site.
; NAME/KEY: misc_feature
; LOCATION: (1)..(6)
; OTHER INFORMATION: The "n" in the sequence means a or g or c or t.
US-10-291-230-43

Query Match
Best Local Similarity 66.7%; Score 12; DB 15; Length 12;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGNNNNNN 18
Db 12 CTGAGNNNNNN 1

RESULT 13
US-10-291-249-43/c
; Sequence 43, Application US/10291249
; Publication No. US20030119041A1
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678 US B
; CURRENT APPLICATION NUMBER: US/10/291,249
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 09/647,344
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; PRIOR APPLICATION NUMBER: US 60/079,792
; PRIOR FILING DATE: 1998-03-28
; PRIOR APPLICATION NUMBER: US 60/107,504
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A portion of an antisense library including a Bpm1 site.
; NAME/KEY: misc_feature
; LOCATION: (1)..(6)
; OTHER INFORMATION: The "n" in the sequence means a or g or c or t.
US-10-291-249-43

Query Match
Best Local Similarity 66.7%; Score 12; DB 15; Length 12;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGNNNNNN 18
Db 12 CTGAGNNNNNN 1

RESULT 14
US-10-322-138-5/c
; Sequence 5, Application US/10322138
; Publication No. US20030175765A1
; GENERAL INFORMATION:
; APPLICANT: Kessler, Christoph
```

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; APPLICANT: Haberkusen, Gerd
; APPLICANT: Bartl, Knut
; APPLICANT: Orum, Henrik
; TITLE OF INVENTION: SPECIFIC AND SENSITIVE METHOD FOR DETECTING NUCLEIC ACIDS
; FILE REFERENCE: 4817/OO
; CURRENT APPLICATION NUMBER: US/10/322,138
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US/09/530,746B
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 5
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: probe
US-10-322-138-5

Query Match
Best Local Similarity 66.7%; Score 12; DB 16; Length 12;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGAG 12
Db 12 GGGGTCCTGAG 1

RESULT 15
US-09-504-231A-1587/c
; Sequence 1587, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Maceljak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT-
; FILE REFERENCE: TP1 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1587
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-1587

Query Match
Best Local Similarity 66.7%; Score 12; DB 9; Length 15;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGAG 12
Db 15 GGGGTCCTGAG 4

RESULT 16
US-09-274-553D-1587/c
; Sequence 1587, Application US/09274553D
```

Patent No. US20020082225A1  
GENERAL INFORMATION:  
APPLICANT: Blatt, Lawrence  
APPLICANT: McSwiggen, James  
APPLICANT: Roberts, Beth  
APPLICANT: Pavco, Pamela  
APPLICANT: Macejak, Dennis  
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION  
FILE REFERENCE: rpl 247/282  
CURRENT APPLICATION NUMBER: US/09/274,553D  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 09/257,608  
PRIOR FILING DATE: 1999-02-24  
PRIOR APPLICATION NUMBER: 60/100,842  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/083,217  
PRIOR FILING DATE: 1998-04-27  
NUMBER OF SEQ ID NOS: 3148  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1587  
LENGTH: 15  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-274-553D-1587

Query Match 66.7%; Score 12; DB 9; Length 15;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 15 GGGGTCTCTGGAG 4

RESULT 17  
US-09-740-332-26/c  
Sequence 26, Application US/09740332  
Publication No. US20030125270A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals Inc.  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate  
TITLE OF INVENTION: Hepatitis C Virus Infection  
FILE REFERENCE: RPI 400/003  
CURRENT APPLICATION NUMBER: US/09/740,332  
CURRENT FILING DATE: 2001-03-26  
NUMBER OF SEQ ID NOS: 9704  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 26  
LENGTH: 17  
TYPE: RNA  
ORGANISM: artificial sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION:  
OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-26

Query Match 66.7%; Score 12; DB 10; Length 17;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 13 GGGGTCTCTGGAG 2

RESULT 18  
US-09-740-332-4529  
Sequence 4529, Application US/09740332  
Publication No. US20030125270A1

GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals Inc.  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
TITLE OF INVENTION: Hepatitis C Virus Infection  
FILE REFERENCE: RPI 400/003  
CURRENT APPLICATION NUMBER: US/09/740,332  
CURRENT FILING DATE: 2001-03-26  
NUMBER OF SEQ ID NOS: 9704  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4529  
LENGTH: 17  
TYPE: RNA  
ORGANISM: artificial sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION:  
OTHER INFORMATION: oligonucleotide substrate  
US-09-740-332-4529

Query Match 66.7%; Score 12; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 6 GGGGUCCTGGAG 17

RESULT 19  
US-09-817-879-26/c  
Sequence 26, Application US/09817879  
Publication No. US20030171311A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals Inc.  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
TITLE OF INVENTION: Hepatitis C Virus Infection  
FILE REFERENCE: MBH00-801-F  
CURRENT APPLICATION NUMBER: US/09/817,879  
CURRENT FILING DATE: 2001-03-26  
NUMBER OF SEQ ID NOS: 9703  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 26  
LENGTH: 17  
TYPE: RNA  
ORGANISM: artificial sequence  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION:  
OTHER INFORMATION: oligonucleotide substrate  
US-09-817-879-26

Query Match 66.7%; Score 12; DB 10; Length 17;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
||||:|||||  
Db 13 GGGGTCTCTGGAG 2

RESULT 20  
US-09-817-879-4529  
Sequence 4529, Application US/09817879  
Publication No. US20030171311A1  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals Inc.  
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relat  
TITLE OF INVENTION: Hepatitis C Virus Infection  
FILE REFERENCE: MBH00-801-F  
CURRENT APPLICATION NUMBER: US/09/817,879  
CURRENT FILING DATE: 2001-03-26  
NUMBER OF SEQ ID NOS: 9703  
SOFTWARE: PatentIn version 3.0

```

; SEQ ID NO 4529
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-4529

Query Match      66.7%; Score 12; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGUCUCUGAG 12
Db      6 GGGGUCUCUGAG 17

RESULT 21
US-10-298-255-4/c
; Sequence 4, Application US/10298255
; Publication No. US20030134312A1
; GENERAL INFORMATION:
; APPLICANT: BURGOME, LEIGH A.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR DETECTING GENETIC MATERIAL
; FILE REFERENCE: 45858-56064
; CURRENT APPLICATION NUMBER: US/10/298,255
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/336,005
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-298-255-4

Query Match      66.7%; Score 12; DB 15; Length 17;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGUCUCUGAG 12
Db      16 GGGGUCUCUGAG 5

RESULT 22
US-10-669-841-2619/c
; Sequence 2619, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blact
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; TITLE OF INVENTION: VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBH02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
```

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; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2619
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-2619

Query Match      66.7%; Score 12; DB 18; Length 17;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGUCUCUGAG 12
Db      13 GGGGUCUCUGAG 2

RESULT 23
US-10-669-841-7122
; Sequence 7122, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blact
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
; TITLE OF INVENTION: VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MBH02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
```

```

; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7122
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
; US-10-669-841-7122

Query Match      66.7%; Score 12; DB 18; Length 17;
Best Local Similarity 100.0%; Pred.No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGUCCUGAG 12
Db      6 GGGGUCCUGAG 17

RESULT 24
US-08-887-505-39
; Sequence 39, Application US/08887505
; Publication No. US20020081577A1
; GENERAL INFORMATION:
; APPLICANT: Kilukkie, Robert E.
; APPLICANT: Frank, Bruce L.
; APPLICANT: Goodchild, John
; APPLICANT: Wolfe, Jia L.
; APPLICANT: Roberts, Peter C.
; APPLICANT: Hamlin, Jr., Henry A.
; APPLICANT: Roberts, No. US20020081577A1 A.
; APPLICANT: Walther, Debra M.
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR
; TITLE OF INVENTION: HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 172
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,505
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/471,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-040CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 39:
```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA/RNA
; HYPOTHEICAL: NO
; ANTI-SENSE: YES
; US-08-887-505-39

Query Match      66.7%; Score 12; DB 8; Length 18;
Best Local Similarity 100.0%; Pred.No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGUCCUGAG 12
Db      1 GGGGUCCUGAG 12

RESULT 25
US-08-887-505-40
; Sequence 40, Application US/08887505
; Publication No. US20020081577A1
; GENERAL INFORMATION:
; APPLICANT: Kilukkie, Robert E.
; APPLICANT: Frank, Bruce L.
; APPLICANT: Goodchild, John
; APPLICANT: Wolfe, Jia L.
; APPLICANT: Roberts, Peter C.
; APPLICANT: Hamlin, Jr., Henry A.
; APPLICANT: Roberts, No. US20020081577A1 A.
; APPLICANT: Walther, Debra M.
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR
; TITLE OF INVENTION: HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 172
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,505
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/471,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-040CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA/RNA
; HYPOTHEICAL: NO
; ANTI-SENSE: YES
; US-08-887-505-40

Query Match      66.7%; Score 12; DB 8; Length 18;
```

Best Local Similarity 100.0%; Pred. No. 1.3e+03; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0;

QY 1 GGGGUCUGAG 12  
Db 7 GGGGUCUGAG 18

## RESULT 26

US-08-887-505-41

; Sequence 41, Application US/08887505  
; Publication No. US20020081577A1

GENERAL INFORMATION:

APPLICANT: Kilkuskie, Robert E.

APPLICANT: Frank, Bruce L.

APPLICANT: Goodchild, John

APPLICANT: Wolfe, Jia L.

APPLICANT: Roberts, Peter C.

APPLICANT: Hamlin, Jr., Henry A.

APPLICANT: Roberts, No. US20020081577A1 A.

TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR

NUMBER OF SEQUENCES: 172

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hale and Dorr LLP

STREET: 60 State Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,505

FILING DATE:

CLASSIFICATION: 514

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/471,968

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523

REFERENCE/DOCKET NUMBER: HYZ-040CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 526-5000

TELEFAX: (617) 526-5000

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA/RNA

HYPOTHETICAL: NO

ANTI-SENSE: YES

US-08-887-505-41

Query Match 66.7%; Score 12; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
Db 1 GGGGUCUGAG 12

## RESULT 27

US-08-887-505-42  
; Sequence 42, Application US/08887505

; Publication No. US20020081577A1

GENERAL INFORMATION:

APPLICANT: Kilkuskie, Robert E.

APPLICANT: Frank, Bruce L.

APPLICANT: Goodchild, John

APPLICANT: Wolfe, Jia L.

APPLICANT: Roberts, Peter C.

APPLICANT: Hamlin, Jr., Henry A.

APPLICANT: Roberts, No. US20020081577A1 A.

TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR

NUMBER OF SEQUENCES: 172

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hale and Dorr LLP

STREET: 60 State Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,505

FILING DATE:

CLASSIFICATION: 514

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/471,968

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523

REFERENCE/DOCKET NUMBER: HYZ-040CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 526-6000

TELEFAX: (617) 526-5000

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA/RNA

HYPOTHETICAL: NO

ANTI-SENSE: YES

US-08-887-505-42

Query Match 66.7%; Score 12; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGAG 12  
Db 7 GGGGUCUGAG 18

## RESULT 28

US-08-887-505-43

; Sequence 43, Application US/08887505  
; Publication No. US20020081577A1

GENERAL INFORMATION:

APPLICANT: Kilkuskie, Robert E.

APPLICANT: Frank, Bruce L.

APPLICANT: Goodchild, John

APPLICANT: Wolfe, Jia L.

APPLICANT: Roberts, Peter C.

APPLICANT: Hamlin, Jr., Henry A.

APPLICANT: Roberts, No. US20020081577A1 A.

APPLICANT: Walther, Debra M.

TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR

TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Keirner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-43

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
DB 1 GGGGUCCUGAG 12

RESULT 29  
US-08-887-505-44  
Sequence 44, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilukkie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Keirner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-44

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
DB 7 GGGGUCCUGAG 18

RESULT 30  
US-08-887-505-45  
Sequence 45, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilukkie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-6000  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-45

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
Db 1 GGGGUCCUGAG 12

## RESULT 31

US-08-887-505-46  
Sequence 46, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kiluskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walcher, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-46

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
Db 7 GGGGUCCUGAG 18

## RESULT 32

US-08-887-505-49  
Sequence 49, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kiluskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walcher, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-49

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12



Db 1 GGGGUCGAG 12

## RESULT 33

US-08-887-505-50  
; Sequence 50, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; APPLICANT: Walther, Debra M.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887, 505  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/471,968  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerner, Ann-Louise  
; REGISTRATION NUMBER: 33,523  
; REFERENCE/DOCKET NUMBER: HYZ-040CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 526-6000  
; TELEFAX: (617) 526-5000  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA/RNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; US-08-887-505-50

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
Db 7 GGGGUCGAG 18

RESULT 34  
US-08-887-505-51  
; Sequence 51, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.

APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; APPLICANT: Walther, Debra M.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887, 505  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/471,968  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerner, Ann-Louise  
; REGISTRATION NUMBER: 33,523  
; REFERENCE/DOCKET NUMBER: HYZ-040CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 526-6000  
; TELEFAX: (617) 526-5000  
; INFORMATION FOR SEQ ID NO: 51:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA/RNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; US-08-887-505-51

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
Db 1 GGGGUCGAG 12

RESULT 35  
US-08-887-505-52  
; Sequence 52, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; APPLICANT: Walther, Debra M.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP

STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-52

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
Db 7 GGGGCTCTGGAG 18

RESULT 36  
US-08-887-505-53  
Sequence 53, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuiskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-53

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
Db 1 GGGGUCCUGAG 12

RESULT 37  
US-08-887-505-54  
Sequence 54, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuiskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 54:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-54

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
DB 7 GGGGUCGAG 18

RESULT 38  
US-08-887-505-141  
Sequence 141, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kiluskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 141:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES

US-08-887-505-141

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
DB 7 GGGGUCGAG 18

RESULT 39  
US-08-887-505-142

Sequence 142, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kiluskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 142:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-142

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
DB 7 GGGGUCGAG 18

RESULT 40  
US-08-887-505-143  
; Sequence 143, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,505  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/471,968  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerner, Ann-Louise  
; REGISTRATION NUMBER: 33,523  
; REFERENCE/DOCKET NUMBER: HYZ-040CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 526-6000  
; TELEFAX: (617) 526-5000  
; INFORMATION FOR SEQ ID NO: 143:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA/RNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; US-08-887-505-143

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGGAG 12  
Db 7 GGGGUCUGGAG 18

RESULT 41  
US-08-887-505-144  
; Sequence 144, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.

APPLICANT: Roberts, No. US20020081577A1 A.  
; APPLICANT: Walthers, Debra M.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,505  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/471,968  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kerner, Ann-Louise  
; REGISTRATION NUMBER: 33,523  
; REFERENCE/DOCKET NUMBER: HYZ-040CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 526-6000  
; TELEFAX: (617) 526-5000  
; INFORMATION FOR SEQ ID NO: 144:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA/RNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES  
; US-08-887-505-144

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGGAG 12  
Db 7 GGGGUCUGGAG 18

RESULT 42  
US-08-887-505-145  
; Sequence 145, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA

ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 145:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-145

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGCGAG 12  
Db 1 GGGGUCGCGAG 12

RESULT 43  
US-08-887-505-146  
Sequence 146, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 146:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-146

Query Match 66.7%; Score 12; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGCGAG 12  
Db 1 GGGGUCGCGAG 12

RESULT 44  
US-08-887-505-147  
Sequence 147, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 147:  
SEQUENCE CHARACTERISTICS:

```

; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA/RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; US-08-887-505-147

Query Match          66.7%; Score 12; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGGAG 12
Db 1 GGGGUCCUGGAG 12

RESULT 45
US-09-782-361-14
; Sequence 14, Application US/09782361
; Patent No. US20020064778A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yu-Wen
; TITLE OF INVENTION: PRIMER-SPECIFIC AND MISPAIR EXTENSION ASSAY FOR IDENTIFYING GEN
; FILE REFERENCE: 2883-4757US
; CURRENT APPLICATION NUMBER: US/09/782,361
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: primer for PSMEA
; US-09-782-361-14

Query Match          66.7%; Score 12; DB 9; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGGAG 12
Db 2 GGGGTCTCTGGAG 13

RESULT 46
US-10-461-790-121/C
; Sequence 121, Application US/10461790
; Publication No. US2004002911A1
; GENERAL INFORMATION:
; APPLICANT: Lannen, Jeffery M.
; APPLICANT: Kolik, Daniel P.
; APPLICANT: Dockter, Daniel M.
; APPLICANT: Getman, Damon K.
; APPLICANT: Yoshimura, Tadashi
; APPLICANT: Ho-Sing-Loy, Marcy
; APPLICANT: Stringfellow, Leslie A.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP134-02.UT
; CURRENT APPLICATION NUMBER: US/10/461,790
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: 60/389,393
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 121
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Hepatitis C Virus
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US-10-461-790-121

Query Match          66.7%; Score 12; DB 17; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGGAG 12
Db 15 GGGGTCTCTGGAG 4

RESULT 47
US-10-667-271-466/C
; Sequence 466, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwigen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 466
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r

US-10-667-271-466

Query Match          66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGGAG 12
Db 13 GGGGTCTCTGGAG 2

RESULT 48
US-10-667-271-467/C
; Sequence 467, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwigen, James
```

```
APPLICANT: Macejak, Dennis
APPLICANT: Belgelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE REFERENCE: 400/129 (MBH02-763B)
CURRENT FILING DATE: 2003-09-15
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USSN 60/401,104
PRIOR FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: USSN 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: USSN 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: USSN 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: USSN 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: USSN 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: USSN 60/409,293
PRIOR FILING DATE: 2002-09-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2
SEQ ID NO 467
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-467

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
Db      12 GGGGTCTCTGGAG 1

RESULT 49
US-10-667-271-498/c
Sequence 498, Application US/10667271
Publication No. US20040209831A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: McSwigen, James
APPLICANT: Macejak, Dennis
APPLICANT: Belgelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE REFERENCE: 400/129 (MBH02-763B)
CURRENT APPLICATION NUMBER: US/10/667,271
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USSN 60/401,104
PRIOR FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: USSN 60/358,580
PRIOR FILING DATE: 2002-02-20
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PRIOR APPLICATION NUMBER: USSN 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: USSN 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: USSN 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: USSN 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: USSN 60/409,293
PRIOR FILING DATE: 2002-09-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2
SEQ ID NO 498
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-667-271-498

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
Db      16 GGGGTCTCTGGAG 5

RESULT 50
US-10-667-271-500/c
Sequence 500, Application US/10667271
Publication No. US20040209831A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics
APPLICANT: McSwigen, James
APPLICANT: Macejak, Dennis
APPLICANT: Belgelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE REFERENCE: 400/129 (MBH02-763B)
CURRENT APPLICATION NUMBER: US/10/667,271
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USSN 60/401,104
PRIOR FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: USSN 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: USSN 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: USSN 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: USSN 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: USSN 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: USSN 60/409,293
PRIOR FILING DATE: 2002-09-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2
SEQ ID NO 500
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-500

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCUGAG 12
      |||:|:|:|
Db      14 GGGGTCTGAG 3

RESULT 51
US-10-667-271-502/c
; Sequence 502, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics
; APPLICANT: Macejak, Dennis
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 502
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-502

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCUGAG 12
      |||:|:|:|
Db      15 GGGGTCTGAG 4

RESULT 52
US-10-667-271-538/c
; Sequence 538, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics
; APPLICANT: Macejak, Dennis
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-544/c
; Sequence 544, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics
; APPLICANT: Macejak, Dennis
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-578

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCUGAG 12
      |||:|:|:|
Db      18 GGGGTCTGAG 7

RESULT 53
US-10-667-271-578/c
; Sequence 578, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics
; APPLICANT: Macejak, Dennis
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-578
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; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 544
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-544

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGAG 12
        |||||
Db      19 GGGGTCTGAG 8

RESULT 54
US-10-667-271-545/c
; Sequence 545, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics
; APPLICANT: McSwigen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 545
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-667-271-545

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGAG 12
        |||||
Db      17 GGGGTCTGAG 6

RESULT 55
US-10-667-271-1162
; Sequence 1162, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirta Therapeutics
; APPLICANT: McSwigen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1162
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1162

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGAG 12
        |||||
Db      7 GGGGUCCTGAG 18

RESULT 56
US-10-667-271-1163
; Sequence 1163, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
```

```
APPLICANT: Sirna Therapeutics
APPLICANT: McSwiggen, James
APPLICANT: Macejak, Dennis
APPLICANT: Beigelman, Leonid
APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE REFERENCE: 400/129 (MBH02-763B)
CURRENT APPLICATION NUMBER: US/10/667,271
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USSN 60/401,104
PRIOR FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: USSN 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: USSN 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: USSN 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: USSN 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: USSN 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: USSN 60/409,293
PRIOR FILING DATE: 2002-09-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1163
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: sirna antisense region
US-10-667-271-1163

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCUCUGAG 12
Db      8 GGGGUCUCUGAG 19

RESULT 57
US-10-667-271-1194
; Sequence 1194, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE REFERENCE: 400/129 (MBH02-763B)
CURRENT APPLICATION NUMBER: US/10/667,271
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USSN 60/401,104
PRIOR FILING DATE: 2002-08-05
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PRIOR APPLICATION NUMBER: USSN 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: USSN 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: USSN 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: USSN 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: USSN 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: USSN 60/409,293
PRIOR FILING DATE: 2002-09-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1194
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: sirna antisense region
US-10-667-271-1194

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCUCUGAG 12
Db      4 GGGGUCUCUGAG 15

RESULT 58
US-10-667-271-1196
; Sequence 1196, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
FILE REFERENCE: 400/129 (MBH02-763B)
CURRENT APPLICATION NUMBER: US/10/667,271
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: US 10/444,853
PRIOR FILING DATE: 2003-05-23
PRIOR APPLICATION NUMBER: PCT / US03/05043
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: PCT / US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: USSN 60/401,104
PRIOR FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: USSN 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: USSN 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: USSN 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: USSN 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: USSN 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: USSN 60/409,293
PRIOR FILING DATE: 2002-09-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1196
LENGTH: 19
TYPE: RNA
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1198

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCGAG 12
        |||||
Db      6 GGGGUCGAG 17

RESULT 59
US-10-667-271-1198
; Sequence 1198, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Mesiugen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT FILING DATE: US/10/667,271
; PRIOR APPLICATION NUMBER: US/10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1198
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1198

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCGAG 12
        |||||
Db      5 GGGGUCGAG 16

RESULT 60
US-10-667-271-1234
; Sequence 1234, Application US/10667271
; Publication No. US20040209831A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: Mesiugen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT FILING DATE: US/10/667,271
; PRIOR APPLICATION NUMBER: US/10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1234
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-1234

Query Match      66.7%; Score 12; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCGAG 12
        |||||
Db      2 GGGGUCGAG 13

RESULT 61
US-10-667-271-1240
; Sequence 1240, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: Mesiugen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT FILING DATE: US/10/667,271
; PRIOR APPLICATION NUMBER: US/10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
```

PRIOR FILING DATE: 2002-08-05  
PRIOR APPLICATION NUMBER: USSN 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: USSN 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: USSN 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: USSN 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: USSN 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: USSN 60/409,293  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1705  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1240  
LENGTH: 19  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region  
US-10-667-271-1240

Query Match 66.7%; Score 12; DB 18; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUGGAG 12  
1 GGGGUCUGGAG 12

RESULT 62  
US-10-667-271-1241  
Sequence 1241, Application US/10667271  
Publication No. US20040209831A1  
GENERAL INFORMATION:  
APPLICANT: Sirna Therapeutics  
APPLICANT: McSwigen, James  
APPLICANT: Macejak, Dennis  
APPLICANT: Beigelman, Leonid  
APPLICANT: Morrissey, David  
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)  
TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)  
FILE REFERENCE: 400/129 (MHH02-763B)  
CURRENT APPLICATION NUMBER: US/10/667,271  
FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: US 10/444,853  
PRIOR FILING DATE: 2003-05-23  
PRIOR APPLICATION NUMBER: PCT / US03/05043  
PRIOR FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: PCT / US02/09187  
PRIOR FILING DATE: 2002-03-26  
PRIOR APPLICATION NUMBER: USSN 60/401,104  
PRIOR FILING DATE: 2002-08-05  
PRIOR APPLICATION NUMBER: USSN 60/358,580  
PRIOR FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: USSN 60/363,124  
PRIOR FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: USSN 60/386,782  
PRIOR FILING DATE: 2002-06-06  
PRIOR APPLICATION NUMBER: USSN 60/406,784  
PRIOR FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: USSN 60/408,378  
PRIOR FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: USSN 60/409,293  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1705  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1241  
LENGTH: 19

TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region  
US-10-667-271-1241

Query Match 66.7%; Score 12; DB 18; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUGGAG 12  
3 GGGGUCUGGAG 14

RESULT 63  
US-08-887-505-19  
Sequence 19, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilukie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-19

Query Match 66.7%; Score 12; DB 8; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUGGAG 12

Db 2 GGGCTCTGGAG 13

## RESULT 64

US-08-887-505-20  
 ; Sequence 20, Application US/08887505  
 ; Publication No. US20020081577A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kilkuskie, Robert E.  
 ; APPLICANT: Frank, Bruce L.  
 ; APPLICANT: Goodchild, John  
 ; APPLICANT: Wolfe, Jia L.  
 ; APPLICANT: Roberts, Peter C.  
 ; APPLICANT: Hamlin, Jr., Henry A.  
 ; APPLICANT: Roberts, No. US20020081577A1 A.  
 ; APPLICANT: Walther, Debra M.  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
 ; TITLE OF INVENTION: HEPATITIS C VIRUS  
 ; NUMBER OF SEQUENCES: 172  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Hale and Dorr LLP  
 ; STREET: 60 State Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/887,505  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/471,968  
 ; FILING DATE: 06-JUN-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kerner, Ann-Louise  
 ; REGISTRATION NUMBER: 33,523  
 ; REFERENCE/DOCKET NUMBER: HY2-040CIP  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (617) 526-6000  
 ; TELEFAX: (617) 526-5000  
 ; INFORMATION FOR SEQ ID NO: 20:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 20 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: YES  
 ; US-08-887-505-20

Query Match 66.7%; Score 12; DB 8; Length 20;  
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
 |||||:  
 Db 6 GGGGTCTGGAG 17

## RESULT 65

US-10-291-230-49/c  
 ; Sequence 49, Application US/10291230  
 ; Publication No. US20030108939A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruffner, Duane B.  
 ; APPLICANT: Pierce, Michael L.

APPLICANT: Chen, Zhidong  
 ; TITLE OF INVENTION: Directed Antisense Libraries  
 ; FILE REFERENCE: T6678.US.A  
 ; CURRENT APPLICATION NUMBER: US/10/291,230  
 ; CURRENT FILING DATE: 2002-11-07  
 ; PRIOR APPLICATION NUMBER: US 09/647,344  
 ; PRIOR FILING DATE: 2000-12-04  
 ; PRIOR APPLICATION NUMBER: PCT/US99/06742  
 ; PRIOR FILING DATE: 1999-03-28  
 ; PRIOR APPLICATION NUMBER: US 60/079,792  
 ; PRIOR FILING DATE: 1998-03-28  
 ; PRIOR APPLICATION NUMBER: US 60/107,504  
 ; PRIOR FILING DATE: 1998-11-06  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 49  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Deletion fragment in a deletion fragment library, including a po  
 ; FEATURE:  
 ; OTHER INFORMATION: tion of a multiple cloning site.  
 ; NAME/KEY: misc.feature  
 ; LOCATION: (1)-(14)  
 ; OTHER INFORMATION: The "n" in the sequence means a or g or c or t.  
 ; US-10-291-230-49

Query Match 66.7%; Score 12; DB 15; Length 20;  
 Best Local Similarity 91.7%; Pred. No. 1.3e+03;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGNNNNNN 18  
 |||||:  
 Db 20 CTGGAGNNNNNN 9

RESULT 66  
 US-10-291-249-49/c  
 ; Sequence 49, Application US/10291249  
 ; Publication No. US20030119041A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruffner, Duane B.  
 ; APPLICANT: Pierce, Michael L.  
 ; APPLICANT: Chen, Zhidong  
 ; TITLE OF INVENTION: Directed Antisense Libraries  
 ; FILE REFERENCE: T6678.US.B  
 ; CURRENT APPLICATION NUMBER: US/10/291,249  
 ; CURRENT FILING DATE: 2002-11-07  
 ; PRIOR APPLICATION NUMBER: US 09/647,344  
 ; PRIOR FILING DATE: 2000-12-04  
 ; PRIOR APPLICATION NUMBER: PCT/US99/06742  
 ; PRIOR FILING DATE: 1999-03-28  
 ; PRIOR APPLICATION NUMBER: US 60/079,792  
 ; PRIOR FILING DATE: 1998-03-28  
 ; PRIOR APPLICATION NUMBER: US 60/107,504  
 ; PRIOR FILING DATE: 1998-11-06  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 49  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Deletion fragment in a deletion fragment library, including a po  
 ; OTHER INFORMATION: tion of a multiple cloning site.  
 ; NAME/KEY: misc.feature  
 ; LOCATION: (1)-(14)  
 ; OTHER INFORMATION: The "n" in the sequence means a or g or c or t.  
 ; US-10-291-249-49

Query Match 66.7%; Score 12; DB 15; Length 20;

Best Local Similarity 91.7%; Pred. No. 1.3e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CUGAGAGNNNNNN 18  
Db 20 CTGAGAGNNNNNN 9

## RESULT 67

US-10-008-140B-12/c  
Sequence 12, Application US/10008140B  
Publication No. US20030124512A1  
GENERAL INFORMATION:  
APPLICANT: Pharmasset, Ltd.  
TITLE OF INVENTION: Simultaneous Quantification of Nucleic Acids in Diseased Cells  
FILE REFERENCE: 08841. 105021  
CURRENT APPLICATION NUMBER: US/10/008.140B  
CURRENT FILING DATE: 2001-10-18  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 12  
LENGTH: 20  
TYPE: DNA  
ORGANISM: artificial sequence  
FEATURE:  
OTHER INFORMATION: oligonucleotide (probe) used to detect HCV viral load  
US-10-008-140B-12

Query Match 66.7%; Score 12; DB 15; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUCUGAG 12  
Db 13 GGGGTCTCTGAG 2

## RESULT 68

US-10-169-371-48/c  
Sequence 48, Application US/10169371  
Publication No. US20030175729A1  
GENERAL INFORMATION:  
APPLICANT: VAN ELK, Michael Josephus Theresia  
APPLICANT: HOGERS, Rene Cornelis Josephus  
APPLICANT: HEIJNEN, Leo  
TITLE OF INVENTION: Method for generating oligonucleotides, in particular for the  
FILE REFERENCE: VAN ELK-2  
CURRENT APPLICATION NUMBER: US/10/169.371  
CURRENT FILING DATE: 2002-07-01  
PRIOR APPLICATION NUMBER: EPC 99204614.4  
PRIOR FILING DATE: 1999-12-29  
PRIOR APPLICATION NUMBER: PCT/NL00/00963  
PRIOR FILING DATE: 2000-12-28  
NUMBER OF SEQ ID NOS: 95  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 48  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: synthetic  
NAME/KEY: misc\_feature  
LOCATION: (1)-(14)  
OTHER INFORMATION: n is a, c, g, or t  
US-10-169-371-48

Query Match 66.7%; Score 12; DB 16; Length 20;  
Best Local Similarity 91.7%; Pred. No. 1.3e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CUGAGAGNNNNNN 18  
Db 20 CTGAGAGNNNNNN 9

## RESULT 69

US-09-747-419-7/c  
Sequence 7, Application US/09747419  
Patent No. US20020155582A1  
GENERAL INFORMATION:  
APPLICANT: Lemon, Stanley  
APPLICANT: Yi, Minkyung  
TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE  
FILE REFERENCE: 265.0007 0101  
CURRENT APPLICATION NUMBER: US/09/747.419  
CURRENT FILING DATE: 2000-12-23  
PRIOR APPLICATION NUMBER: US 60/171.909  
PRIOR FILING DATE: 1999-12-23  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 7  
LENGTH: 21  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Red probe  
NAME/KEY: misc\_difference  
LOCATION: (1)-(1)  
OTHER INFORMATION: LC640 labeled  
US-09-747-419-7

Query Match 66.7%; Score 12; DB 9; Length 21;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCUCUGAG 12  
Db 21 GGGGTCTCTGAG 10

## RESULT 70

US-10-259-275-7/c  
Sequence 7, Application US/10259275  
Publication No. US20030125541A1  
GENERAL INFORMATION:  
APPLICANT: Lemon, Stanley M.  
APPLICANT: Yi, Minkyung  
TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE  
FILE REFERENCE: 265.0007 0120  
CURRENT APPLICATION NUMBER: US/10/259.275  
CURRENT FILING DATE: 2003-01-13  
PRIOR APPLICATION NUMBER: US 60/171.909  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: US 09/747.419  
PRIOR FILING DATE: 2000-12-23  
PRIOR APPLICATION NUMBER: US 60/325.236  
PRIOR FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: US 60/338.123  
NUMBER OF SEQ ID NOS: 73  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 7  
LENGTH: 21  
TYPE: DNA  
ORGANISM: artificial  
FEATURE:  
OTHER INFORMATION: Red probe  
NAME/KEY: misc\_difference  
LOCATION: (1)-(1)  
OTHER INFORMATION: LC640 labeled  
US-10-259-275-7

Query Match 66.7%; Score 12; DB 15; Length 21;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
DB 21 GGGGTCTGTGAG 10

## RESULT 71

US-10-291-230-38/c  
; Sequence 38, Application US/10291230  
; Publication No. US20030108939A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruffner, Duane E.  
; APPLICANT: Pierce, Michael L.  
; TITLE OF INVENTION: Directed Antisense Libraries  
; FILE REFERENCE: T6678, US A  
; CURRENT APPLICATION NUMBER: US/10/291,230  
; PRIOR FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 09/647,344  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: PCT/US99/06742  
; PRIOR FILING DATE: 1999-03-28  
; PRIOR APPLICATION NUMBER: US 60/079,792  
; PRIOR FILING DATE: 1998-03-28  
; PRIOR APPLICATION NUMBER: US 60/107,504  
; PRIOR FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Portion of an intermediate in the making of a deletion library,  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(16)  
; OTHER INFORMATION: The "n" in the sequence means a or g or c or t/u.  
US-10-291-230-38

Query Match 66.7%; Score 12; DB 15; Length 22;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGNNNNNN 18  
DB 22 CTGAGNNNNNN 11

## RESULT 72

US-10-291-249-38/c  
; Sequence 38, Application US/10291249  
; Publication No. US20030119041A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruffner, Duane E.  
; APPLICANT: Pierce, Michael L.  
; TITLE OF INVENTION: Directed Antisense Libraries  
; FILE REFERENCE: T6678, US B  
; CURRENT APPLICATION NUMBER: US/10/291,249  
; PRIOR FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 09/647,344  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: PCT/US99/06742  
; PRIOR FILING DATE: 1999-03-28  
; PRIOR APPLICATION NUMBER: US 60/079,792  
; PRIOR FILING DATE: 1998-03-28  
; PRIOR APPLICATION NUMBER: US 60/107,504  
; PRIOR FILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Portion of an intermediate in the making of a deletion library,  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(16)  
; OTHER INFORMATION: The "n" in the sequence means a or g or c or t/u.  
US-10-291-249-38

Query Match 66.7%; Score 12; DB 15; Length 22;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGNNNNNN 18  
DB 22 CTGAGNNNNNN 11

## RESULT 73

US-10-169-371-47  
; Sequence 47, Application US/10169371  
; Publication No. US20030175729A1  
; GENERAL INFORMATION:  
; APPLICANT: VAN EIJK, Michael Josephus Theresia  
; APPLICANT: HOGERS, Rene Cornelis Josephus  
; APPLICANT: HEIJNEN, Leo  
; TITLE OF INVENTION: Method for generating oligonucleotides, in particular for the  
; FILE REFERENCE: VAN EIJK-2  
; CURRENT APPLICATION NUMBER: US/10/169,371  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: ERC 99204614.4  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: PCT/NL00/00963  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 47  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic  
; NAME/KEY: misc\_feature  
; LOCATION: (7)..(22)  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-169-371-47

Query Match 66.7%; Score 12; DB 16; Length 22;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 CUGAGNNNNNN 18  
DB 1 CTGAGNNNNNN 12

## RESULT 74

US-10-092-885-59  
; Sequence 59, Application US/10092885  
; Publication No. US20030190618A1  
; GENERAL INFORMATION:  
; APPLICANT: SAMAL, BABRU  
; APPLICANT: LI, YUAN  
; APPLICANT: HERMIDA, LEANDRO C.  
; APPLICANT: HOPPA, NANCY L.

```

APPLICANT: JOHE, KARL K.
TITLE OF INVENTION: METHOD FOR GENERATING FIVE PRIME BIASED TANDEM TAG
FILE REFERENCE: 0109015/026
CURRENT APPLICATION NUMBER: US/10/092,885
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 59
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified base
LOCATION: (7)..(22)
OTHER INFORMATION: a, t, c, g, other or unknown
US-10-092-885-59

```

```

Query Match      66.7%; Score 12; DB 16; Length 22;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 CUGAGANNNNNN 18
      1 CUGAGANNNNNN 12

```

```

RESULT 75
US-10-045-674-375

```

```

Sequence 375, Application US/10045674
Publication No. US2003023233A1
GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
APPLICANT: HOET, RENE
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: US/10/045,674
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 375
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide
FEATURE:
NAME/KEY: modified base
LOCATION: (7)..(22)
OTHER INFORMATION: A, T, C, G, other or unknown
US-10-045-674-375

```

```

Query Match      66.7%; Score 12; DB 17; Length 22;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 CUGAGANNNNNN 18
      1 CUGAGANNNNNN 12

```

```

RESULT 76
US-10-399-843-4
Sequence 4, Application US/10399843
Publication No. US20040053284A1
GENERAL INFORMATION:
APPLICANT: Andrus, Linda
APPLICANT: Nichols, Carmen Nicola
TITLE OF INVENTION: Universal Multi-Variant Detection System
FILE REFERENCE: 454-30 PCT/US
CURRENT APPLICATION NUMBER: US/10/399,843
CURRENT FILING DATE: 2003-04-22
PRIOR APPLICATION NUMBER: PCT/US02/12035
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/284,334
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(22)
OTHER INFORMATION: Nucleotide sequence encoding a primer
US-10-399-843-4

```

```

Query Match      66.7%; Score 12; DB 17; Length 22;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GGGGCTCUGGAG 12
      11 GGGGCTCUGGAG 22

```

```

RESULT 77
US-10-678-961B-22

```

```

Sequence 22, Application US/10678961B
Publication No. US2005007483A1
GENERAL INFORMATION:
APPLICANT: Slater, Michael R.
APPLICANT: Straus, Ethan Edward
APPLICANT: Wood, Keith V.
APPLICANT: Hartnett, James Robert
APPLICANT: Promega Corporation
TITLE OF INVENTION: Vectors for Directional Cloning
FILE REFERENCE: 341.023US1
CURRENT APPLICATION NUMBER: US/10/678,961B
CURRENT FILING DATE: 2003-10-03
NUMBER OF SEQ ID NOS: 91
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: A synthetic DNA fragment
FEATURE:
NAME/KEY: misc feature
LOCATION: 7-22
OTHER INFORMATION: n = A, T, G, or C
US-10-678-961B-22

```

```

Query Match      66.7%; Score 12; DB 19; Length 22;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 CUGAGANNNNNN 18
      1 CUGAGANNNNNN 12

```



RESULT 78  
US-10-702-228A-22  
Sequence 22, Application US/10702228A  
Publication No. US20050074785A1  
GENERAL INFORMATION:  
APPLICANT: Slater, Michael R.  
APPLICANT: Wood, Keith V.  
APPLICANT: Hartnett, James Robert  
APPLICANT: Promega Corporation  
TITLE OF INVENTION: Vectors for Directional Cloning  
FILE REFERENCE: 341.030US1  
CURRENT APPLICATION NUMBER: US/10/702,228A  
PRIOR FILING DATE: 2003-11-05  
PRIOR APPLICATION NUMBER: 10/678,961  
PRIOR FILING DATE: 2003-10-03  
NUMBER OF SEQ ID NOS: 92  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 22  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: A synthetic DNA fragment  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: 7-22  
OTHER INFORMATION: n = A, T, G, or C  
US-10-702-228A-22

Query Match 66.7%; Score 12; DB 19; Length 22;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CUGAGNNNNNN 18  
|:|||||  
Db 1 CTGAGNNNNNN 12

RESULT 79  
US-10-053-883-111  
Sequence 111, Application US/10053883  
Publication No. US20030113737A1  
GENERAL INFORMATION:  
APPLICANT: PEDERSEN, Morten Lorentz  
TITLE OF INVENTION: ASSAY AND KIT FOR ANALYZING GENE EXPRESSION  
FILE REFERENCE: PEDERSEN-1A  
CURRENT APPLICATION NUMBER: US/10/053,883  
CURRENT FILING DATE: 2002-01-02  
PRIOR APPLICATION NUMBER: PA 2001 00126  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: US 60/267,704  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 148  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 111  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: (7)..(23)  
OTHER INFORMATION: n is a, c, g or t  
US-10-053-883-111

Query Match 66.7%; Score 12; DB 15; Length 23;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CUGAGNNNNNN 18

Db 1 CTGAGNNNNNN 12

RESULT 80  
US-10-053-883-112/c  
Sequence 112, Application US/10053883  
Publication No. US20030113737A1  
GENERAL INFORMATION:  
APPLICANT: PEDERSEN, Morten Lorentz  
TITLE OF INVENTION: ASSAY AND KIT FOR ANALYZING GENE EXPRESSION  
FILE REFERENCE: PEDERSEN-1A  
CURRENT APPLICATION NUMBER: US/10/053,883  
CURRENT FILING DATE: 2002-01-02  
PRIOR APPLICATION NUMBER: PA 2001 00126  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: US 60/267,704  
PRIOR FILING DATE: 2001-02-12  
NUMBER OF SEQ ID NOS: 148  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 112  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: (1)..(17)  
OTHER INFORMATION: n is a, c, g or t  
US-10-053-883-112

Query Match 66.7%; Score 12; DB 15; Length 23;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CUGAGNNNNNN 18  
|:|||||  
Db 23 CTGAGNNNNNN 12

RESULT 81  
US-08-887-505-48  
Sequence 48, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kiluskie, Robert E.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-48

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
Db 1 GGGGTCTCGAG 12

RESULT 82  
US-08-887-505-55  
Sequence 55, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilnuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 55:

SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-55

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
Db 1 GGGGTCTCGAG 12

RESULT 83  
US-08-887-505-56  
Sequence 56, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilnuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-56

Query Match 66.7%; Score 12; DB 8; Length 24;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
Db 1 GGGGUCCTGGAG 12

## RESULT 84

US-08-887-505-57

; Sequence 57, Application US/08887505  
; Publication No. US20020081577A1

## GENERAL INFORMATION:

APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,505

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/471,968

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523

REFERENCE/DOCKET NUMBER: HYZ-040CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 526-6000

TELEFAX: (617) 526-5000

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

MOLECULE TYPE: linear

TOPOLOGY: linear

HYPOTHETICAL: NO

ANTI-SENSE: YES

US-08-887-505-57

Query Match

Best Local Similarity 83.3%; Pred. No. 1.2e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12

Db 13 GGGGUCCTGGAG 24

## RESULT 85

US-08-887-505-58

; Sequence 58, Application US/08887505

; Publication No. US20020081577A1  
; GENERAL INFORMATION:

APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,505

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/471,968

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523

REFERENCE/DOCKET NUMBER: HYZ-040CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 526-6000

TELEFAX: (617) 526-5000

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

MOLECULE TYPE: linear

TOPOLOGY: linear

HYPOTHETICAL: NO

ANTI-SENSE: YES

US-08-887-505-58

Query Match

Best Local Similarity 83.3%; Pred. No. 1.2e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12

Db 13 GGGGUCCTGGAG 24

Query Match

Best Local Similarity 83.3%; Pred. No. 1.2e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12

Db 13 GGGGUCCTGGAG 24

Query Match

Best Local Similarity 83.3%; Pred. No. 1.2e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12

Db 13 GGGGUCCTGGAG 24

Query Match

Best Local Similarity 83.3%; Pred. No. 1.2e+03;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12

Db 13 GGGGUCCTGGAG 24

TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-59

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
DB 13 GGGGTCCTGGAG 24

RESULT 87  
US-08-887-505-60  
Sequence 60, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilhuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A11 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-60

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
DB 1 GGGGTCCTGGAG 12

RESULT 88  
US-08-887-505-61  
Sequence 61, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilhuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A11 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-6000  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-61

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 83.3%; Pred. NO. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
|||:|:|  
Db 13 GGGGTCCTGAG 24

RESULT 89  
US-08-887-505-62  
Sequence 62, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilnuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A11 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESS: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-62

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 83.3%; Pred. NO. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
|||:|:|  
Db 1 GGGGTCCTGAG 12

RESULT 90  
US-08-887-505-63  
Sequence 63, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilnuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A11 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESS: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-63

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 83.3%; Pred. NO. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12

Db 13 GGGGCTCTGGAG 24

RESULT 91  
US-08-887-505-64  
Sequence 64, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: Walthers, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 64:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-64

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCTCTGGAG 12  
Db 1 GGGGCTCTGGAG 12

RESULT 92  
US-08-887-505-65  
Sequence 65, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.

APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: Walthers, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-65

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCTCTGGAG 12  
Db 13 GGGGCTCTGGAG 24

RESULT 93  
US-08-887-505-66  
Sequence 66, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: Walthers, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP

STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-66

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCCUGAG 12  
Db 1 GGGGTCCTCGAG 12

RESULT 94  
US-08-887-505-148  
Sequence 148, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 148:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-148

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCCUGAG 12  
Db 7 GGGGUCUCCUGAG 18

RESULT 95  
US-08-887-505-149  
Sequence 149, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
TITLE OF INVENTION: HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 149:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-149

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||||  
Db 7 GGGGUCCUGAG 18

RESULT 96  
US-08-887-505-150  
Sequence 150, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-5000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 150:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES

US-08-887-505-150

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||||  
Db 7 GGGGUCCUGAG 18

RESULT 97

US-08-887-505-151  
Sequence 151, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilkuskie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 151:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-151

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||||  
Db 13 GGGGUCCUGAG 24



RESULT 98  
US-08-887-505-152  
Sequence 152, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
TITLE OF INVENTION: HEPATITIS C VIRUS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-6000  
INFORMATION FOR SEQ ID NO: 152:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-152

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
Db 7 GGGGUCCUGAG 18

RESULT 99  
US-08-887-505-153  
Sequence 153, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.

APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HY2-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-6000  
INFORMATION FOR SEQ ID NO: 153:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-153

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
Db 13 GGGGUCCUGAG 24

RESULT 100  
US-08-887-505-154  
Sequence 154, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
HEPATITIS C VIRUS  
NUMBER OF SEQUENCES: 172  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA

ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 154:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-154

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
Db 7 GGGGUCGAG 18

RESULT 101  
US-08-887-505-155  
Sequence 155, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
TITLE OF INVENTION: HEPATITIS C VIRUS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 155:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-155

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
Db 13 GGGGUCGAG 24

RESULT 102  
US-08-887-505-156  
Sequence 156, Application US/08887505  
Publication No. US20020081577A1  
GENERAL INFORMATION:  
APPLICANT: Kilbuckie, Robert E.  
APPLICANT: Frank, Bruce L.  
APPLICANT: Goodchild, John  
APPLICANT: Wolfe, Jia L.  
APPLICANT: Roberts, Peter C.  
APPLICANT: Hamlin, Jr., Henry A.  
APPLICANT: Roberts, No. US20020081577A1 A.  
APPLICANT: Walther, Debra M.  
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
NUMBER OF SEQUENCES: 172  
TITLE OF INVENTION: HEPATITIS C VIRUS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hale and Dorr LLP  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,505  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 156:  
SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA/RNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-156

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
DB 7 GGGGUCGAG 18

## RESULT 103

US-08-887-505-157

Sequence 157, Application US/08887505  
Publication No. US20020081577A1

GENERAL INFORMATION:

APPLICANT: Kilbuckle, Robert E.

APPLICANT: Frank, Bruce L.

APPLICANT: Goodchild, John

APPLICANT: Wolfe, Jia L.

APPLICANT: Roberts, Peter C.

APPLICANT: Hamlin, Jr., Henry A.

APPLICANT: Roberts, No. US20020081577A1 A.

APPLICANT: Walther, Debra M.

TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR

NUMBER OF SEQUENCES: 172

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hale and Dorr LLP

STREET: 60 State Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,505

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/471,968

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523

REFERENCE/DOCKET NUMBER: HYZ-040CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 526-5000

TELEFAX: (617) 526-5000

INFORMATION FOR SEQ ID NO: 157:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA/RNA

HYPOTHETICAL: NO

ANTI-SENSE: YES

US-08-887-505-157

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
DB 7 GGGGUCGAG 18

## RESULT 104

US-08-887-505-158

Sequence 158, Application US/08887505  
Publication No. US20020081577A1

GENERAL INFORMATION:

APPLICANT: Kilbuckle, Robert E.

APPLICANT: Frank, Bruce L.

APPLICANT: Goodchild, John

APPLICANT: Wolfe, Jia L.

APPLICANT: Roberts, Peter C.

APPLICANT: Hamlin, Jr., Henry A.

APPLICANT: Roberts, No. US20020081577A1 A.

TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR

NUMBER OF SEQUENCES: 172

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hale and Dorr LLP

STREET: 60 State Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,505

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/471,968

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523

REFERENCE/DOCKET NUMBER: HYZ-040CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 526-5000

TELEFAX: (617) 526-5000

INFORMATION FOR SEQ ID NO: 158:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA/RNA

HYPOTHETICAL: NO

ANTI-SENSE: YES

US-08-887-505-158

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
DB 7 GGGGUCGAG 18

## RESULT 105

US-10-098-263B-87040/C

Sequence 87040, Application US/10098263B  
Publication No. US20030104410A1

Query Match 66.7%; Score 12; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

```
;; GENERAL INFORMATION:
;; APPLICANT: Miltman, Michael
;; TITLE OF INVENTION: Human Microarray
;; FILE REFERENCE: 3118.1
;; CURRENT APPLICATION NUMBER: US/10/098,263B
;; PRIOR FILING DATE: 2003-01-08
;; PRIOR APPLICATION NUMBER: 60/276,759
;; PRIOR FILING DATE: 2001-03-16
;; NUMBER OF SEQ ID NOS: 131066
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
;; SEQ ID NO 87040
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-10-098-263B-87040

Query Match      66.7%; Score 12; DB 15; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      1 GGGGUCUGGAG 12
Db      24 GGGGTCCTGGAG 13

RESULT 106
US-10-291-230-39/c
;; Sequence 39, Application US/10291230
;; Publication No. US20030108939A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruffner, Duane E.
;; APPLICANT: Pierce, Michael L.
;; APPLICANT: Chen, Zhidong
;; TITLE OF INVENTION: Directed Antisense Libraries
;; FILE REFERENCE: T6678.US.A
;; CURRENT APPLICATION NUMBER: US/10/291,230
;; CURRENT FILING DATE: 2002-11-07
;; PRIOR APPLICATION NUMBER: US 09/647,344
;; PRIOR FILING DATE: 2000-12-04
;; PRIOR APPLICATION NUMBER: PCT/US99/06742
;; PRIOR FILING DATE: 1999-03-28
;; PRIOR APPLICATION NUMBER: US 60/079,792
;; PRIOR FILING DATE: 1998-03-28
;; PRIOR APPLICATION NUMBER: US 60/107,504
;; PRIOR FILING DATE: 1998-11-06
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 39
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: 14 bp variable sequence fragment of a deletion library including
;; OTHER INFORMATION: flanking portions of multiple cloning site.
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (6)..(19)
;; OTHER INFORMATION: The "n" in the sequence means a or g or c or t/u.
US-10-291-230-39

Query Match      66.7%; Score 12; DB 15; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      7 CUGAGNNNNNN 18
Db      25 CTGAGNNNNNN 14

RESULT 107
US-10-291-230-47/c
;; Sequence 47, Application US/10291230
;; Publication No. US20030108939A1
```

```
;; GENERAL INFORMATION:
;; APPLICANT: Ruffner, Duane E.
;; APPLICANT: Pierce, Michael L.
;; APPLICANT: Chen, Zhidong
;; TITLE OF INVENTION: Directed Antisense Libraries
;; FILE REFERENCE: T6678.US.A
;; CURRENT APPLICATION NUMBER: US/10/291,230
;; CURRENT FILING DATE: 2002-11-07
;; PRIOR APPLICATION NUMBER: US 09/647,344
;; PRIOR FILING DATE: 2000-12-04
;; PRIOR APPLICATION NUMBER: PCT/US99/06742
;; PRIOR FILING DATE: 1999-03-28
;; PRIOR APPLICATION NUMBER: US 60/079,792
;; PRIOR FILING DATE: 1998-03-28
;; PRIOR APPLICATION NUMBER: US 60/107,504
;; PRIOR FILING DATE: 1998-11-06
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 47
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Sequence flanking the chloramphenicol (CAT) gene after insertion
;; OTHER INFORMATION: into the antisense library.
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (14)..(19)
;; OTHER INFORMATION: The "n" in the sequence means a or g or c or t.
US-10-291-230-47

Query Match      66.7%; Score 12; DB 15; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      7 CUGAGNNNNNN 18
Db      25 CTGAGNNNNNN 14

RESULT 108
US-10-291-249-39/c
;; Sequence 39, Application US/10291249
;; Publication No. US20030119041A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruffner, Duane E.
;; APPLICANT: Pierce, Michael L.
;; APPLICANT: Chen, Zhidong
;; TITLE OF INVENTION: Directed Antisense Libraries
;; FILE REFERENCE: T6678.US.B
;; CURRENT APPLICATION NUMBER: US/10/291,249
;; CURRENT FILING DATE: 2002-11-07
;; PRIOR APPLICATION NUMBER: US 09/647,344
;; PRIOR FILING DATE: 2000-12-04
;; PRIOR APPLICATION NUMBER: PCT/US99/06742
;; PRIOR FILING DATE: 1999-03-28
;; PRIOR APPLICATION NUMBER: US 60/079,792
;; PRIOR FILING DATE: 1998-03-28
;; PRIOR APPLICATION NUMBER: US 60/107,504
;; PRIOR FILING DATE: 1998-11-06
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 39
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: 14 bp variable sequence fragment of a deletion library including
;; OTHER INFORMATION: flanking portions of multiple cloning site.
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (6)..(19)
;; OTHER INFORMATION: The "n" in the sequence means a or g or c or t/u.
```

US-10-291-249-39

Query Match 66.7%; Score 12; DB 15; Length 25;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 CUGAGNNNNNN 18  
|:|||||  
Db 25 CTGAGNNNNNN 14

RESULT 109

US-10-291-249-47/c  
; Sequence 47, Application US/10291249  
; Publication No. US20030119041A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruffner, Duane E.  
; APPLICANT: Pierce, Michael L.  
; APPLICANT: Chen, Zhidong  
; TITLE OF INVENTION: Directed Antisense Libraries  
; FILE REFERENCE: 16678.US.8  
; CURRENT APPLICATION NUMBER: US/10/291,249  
; CURRENT FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US 09/647,344  
; PRIOR FILING DATE: 2000-12-04  
; PRIOR APPLICATION NUMBER: PCT/US99/06742  
; PRIOR FILING DATE: 1999-03-28  
; PRIOR APPLICATION NUMBER: US 60/079,792  
; PRIOR FILING DATE: 1998-03-28  
; PRIOR APPLICATION NUMBER: US 60/107,504  
; PRIOR FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 47  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Sequence flanking the chloramphenicol (CAT) gene after insertion  
; OTHER INFORMATION: Into the antisense library.  
; NAME/KEY: misc feature  
; LOCATION: (14)-(19)  
; OTHER INFORMATION: The "n" in the sequence means a or g or c or t.  
US-10-291-249-47

Query Match 66.7%; Score 12; DB 15; Length 25;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 CUGAGNNNNNN 18  
|:|||||  
Db 25 CTGAGNNNNNN 14

RESULT 110

US-10-719-900-205441/c  
; Sequence 205441, Application US/10719900  
; Publication No. US2005026164A1  
; GENERAL INFORMATION:  
; APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002-11-20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 205441  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus

US-10-719-900-205441

Query Match 66.7%; Score 12; DB 19; Length 25;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUGGAG 12  
|:|:|:|:|:|  
Db 22 GGGGTCTCGAG 11

RESULT 111

US-10-053-883-12  
; Sequence 12, Application US/10053883  
; Publication No. US20030113737A1  
; GENERAL INFORMATION:  
; APPLICANT: PEDERSEN, Morten Lorentz  
; TITLE OF INVENTION: ASSAY AND KIT FOR ANALYZING GENE EXPRESSION  
; FILE REFERENCE: PEDERSEN-1A  
; CURRENT APPLICATION NUMBER: US/10/053,883  
; CURRENT FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: PA 2001 00126  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: US 60/267,704  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 12  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
; NAME/KEY: misc feature  
; LOCATION: (11)-(27)  
; OTHER INFORMATION: n is a, c, g or t  
US-10-053-883-12

Query Match 66.7%; Score 12; DB 15; Length 27;  
Best Local Similarity 91.7%; Pred. No. 1.2e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 CUGAGNNNNNN 18  
|:|||||  
Db 5 CTGAGNNNNNN 16

RESULT 112

US-10-053-883-13/c  
; Sequence 13, Application US/10053883  
; Publication No. US20030113737A1  
; GENERAL INFORMATION:  
; APPLICANT: PEDERSEN, Morten Lorentz  
; TITLE OF INVENTION: ASSAY AND KIT FOR ANALYZING GENE EXPRESSION  
; FILE REFERENCE: PEDERSEN-1A  
; CURRENT APPLICATION NUMBER: US/10/053,883  
; CURRENT FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: PA 2001 00126  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: US 60/267,704  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 148  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 13  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
; NAME/KEY: misc feature  
; LOCATION: (1)-(17)

```
; OTHER INFORMATION: n is a, c, g or t
US-10-053-883-13

Query Match      66.7%; Score 12; DB 15; Length 27;
Best Local Similarity 91.7%; Pred. No. 1.2e+03;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      7  CUGAGANNNNNN 18
      ||:|||||
Db      23  CTGAGANNNNNN 12

RESULT 113
US-09-935-338-192/c
; Sequence 192, Application US/09935338
; Publication No. US20030073081A1
; GENERAL INFORMATION:
; APPLICANT: MUKAI, Hiroyuki
; APPLICANT: SAGAWA, Hiroaki
; APPLICANT: UEMORI, Takashi
; APPLICANT: YAMAMOTO, Junko
; APPLICANT: TOMONO, Jun
; APPLICANT: KOBAYASHI, Eiji
; APPLICANT: ENOKI, Tatsuji
; APPLICANT: TAKEDA, Osamu
; APPLICANT: MIYAKE, Kazuo
; APPLICANT: SATO, Yoshimi
; APPLICANT: MORIYAMA, Mariko
; APPLICANT: SAMURAGI, Haruhisa
; APPLICANT: HIGITA, Michio
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: A method for amplification of nucleic acids
; FILE REFERENCE: MUKAI-1
; CURRENT APPLICATION NUMBER: US/09/935,338
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: JP11-370035
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: JP11-370035
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: JP2000-251981
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: JP2000-284419
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: JP2000-288750
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: JP2001-104191
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PCT/JP00/01534
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 192
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Designed oligonucleotide probe to detect a DNA fragment amplifying
; OTHER INFORMATION: portion of HCV.
US-09-935-338-192

Query Match      66.7%; Score 12; DB 10; Length 30;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GGGGUCUGAG 12
      ||||:||||
Db      30  GGGGTCCTGAG 19

RESULT 114
US-10-169-371-71
; Sequence 71, Application US/10169371
```

```
; Publication No. US20030175729A1
; GENERAL INFORMATION:
; APPLICANT: VAN EICK, Michael Josephus Theresia
; APPLICANT: HOGERS, Rene Cornelis Josephus
; APPLICANT: HEIJNEN, Leo
; TITLE OF INVENTION: Method for generating oligonucleotides, in particular for the
; TITLE OF INVENTION: detection of amplified restriction fragments obtained using AFLP
; FILE REFERENCE: VAN EICK-2
; CURRENT APPLICATION NUMBER: US/10/169,371
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: EPC 99204614.4
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: PCT/NL00/00963
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: misc feature
; LOCATION: (1)..(16)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (23)..(36)

US-10-169-371-71

Query Match      66.7%; Score 12; DB 16; Length 36;
Best Local Similarity 91.7%; Pred. No. 1.1e+03;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      7  CUGAGANNNNNN 18
      ||:|||||
Db      17  CTGAGANNNNNN 28

RESULT 115
US-10-169-371-79
; Sequence 79, Application US/10169371
; Publication No. US20030175729A1
; GENERAL INFORMATION:
; APPLICANT: VAN EICK, Michael Josephus Theresia
; APPLICANT: HOGERS, Rene Cornelis Josephus
; APPLICANT: HEIJNEN, Leo
; TITLE OF INVENTION: Method for generating oligonucleotides, in particular for the
; TITLE OF INVENTION: detection of amplified restriction fragments obtained using AFLP
; FILE REFERENCE: VAN EICK-2
; CURRENT APPLICATION NUMBER: US/10/169,371
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: EPC 99204614.4
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: PCT/NL00/00963
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: misc feature
; LOCATION: (1)..(16)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (23)..(36)
```

OTHER INFORMATION: n is a, c, g, or t  
US-10-169-371-79

Query Match 66.7%; Score 12; DB 16; Length 36;  
Best Local Similarity 91.7%; Pred. No. 1.1e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 CUGAGNNNNNN 18  
|:|||||  
DB 17 CTGAGNNNNNN 28

## RESULT 116

US-10-291-230-48/c  
Sequence 48, Application US/10291230  
Publication No. US20030108939A1  
GENERAL INFORMATION:  
APPLICANT: Ruffner, Duane E.  
APPLICANT: Pierce, Michael L.  
APPLICANT: Chen, Zhidong  
TITLE OF INVENTION: Directed Antisense Libraries  
FILE REFERENCE: T6678.US.A  
CURRENT APPLICATION NUMBER: US/10/291,230  
CURRENT FILING DATE: 2002-11-07  
PRIOR APPLICATION NUMBER: US 09/647,344  
PRIOR FILING DATE: 2000-12-04  
PRIOR APPLICATION NUMBER: PCT/US99/06742  
PRIOR FILING DATE: 1999-03-28  
PRIOR APPLICATION NUMBER: US 60/079,792  
PRIOR FILING DATE: 1998-03-28  
PRIOR APPLICATION NUMBER: US 60/107,504  
PRIOR FILING DATE: 1998-11-06  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 48  
LENGTH: 46  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Hammerhead ribozyme library with flanking sequences.  
NAME/KEY: misc feature  
LOCATION: (6)-(12)  
OTHER INFORMATION: The "n" in the sequence means a or g or c or t.  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (35)-(40)  
OTHER INFORMATION: The "n" in the sequence means a or g or c or t.  
US-10-291-230-48

Query Match 66.7%; Score 12; DB 15; Length 46;  
Best Local Similarity 91.7%; Pred. No. 1e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 CUGAGNNNNNN 18  
|:|||||  
DB 46 CTGAGNNNNNN 35

## RESULT 117

US-10-291-249-48/c  
Sequence 48, Application US/10291249  
Publication No. US20030119041A1  
GENERAL INFORMATION:  
APPLICANT: Ruffner, Duane E.  
APPLICANT: Pierce, Michael L.  
APPLICANT: Chen, Zhidong  
TITLE OF INVENTION: Directed Antisense Libraries  
FILE REFERENCE: T6678.US.B  
CURRENT APPLICATION NUMBER: US/10/291,249  
CURRENT FILING DATE: 2002-11-07  
PRIOR APPLICATION NUMBER: US 09/647,344  
PRIOR FILING DATE: 2000-12-04

PRIOR APPLICATION NUMBER: PCT/US99/06742  
PRIOR FILING DATE: 1999-03-28  
PRIOR APPLICATION NUMBER: US 60/079,792  
PRIOR FILING DATE: 1998-03-28  
PRIOR APPLICATION NUMBER: US 60/107,504  
PRIOR FILING DATE: 1998-11-06  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 48  
LENGTH: 46  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Hammerhead ribozyme library with flanking sequences.  
NAME/KEY: misc feature  
LOCATION: (6)-(12)  
OTHER INFORMATION: The "n" in the sequence means a or g or c or t.  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (35)-(40)  
OTHER INFORMATION: The "n" in the sequence means a or g or c or t.  
US-10-291-249-48

Query Match 66.7%; Score 12; DB 15; Length 46;  
Best Local Similarity 91.7%; Pred. No. 1e+03;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 CUGAGNNNNNN 18  
|:|||||  
DB 46 CTGAGNNNNNN 35

## RESULT 118

US-10-349-143-2597  
Sequence 2597, Application US/10349143  
Publication No. US20040005584A1  
GENERAL INFORMATION:  
APPLICANT: Cohen, Daniel  
APPLICANT: Blumenfeld, Marla  
APPLICANT: Chumakov, Ilya  
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
FILE REFERENCE: GENSRT.020C01  
CURRENT APPLICATION NUMBER: US/10/349,143  
CURRENT FILING DATE: 2003-01-21  
PRIOR APPLICATION NUMBER: US/09/422,978  
PRIOR FILING DATE: 1999-10-20  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21  
NUMBER OF SEQ ID NOS: 11796  
SEQ ID NO 2597  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: allele  
LOCATION: 24  
OTHER INFORMATION: 99-1211-59 : polymorphic base C or T  
US-10-349-143-2597

Query Match 66.7%; Score 12; DB 17; Length 47;  
Best Local Similarity 83.3%; Pred. No. 1e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCUGAG 12  
|:|||||  
DB 25 GGGGTCTGAG 36

RESULT 119  
US-10-156-306-7157  
; Sequence 7157, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; FILE REFERENCE: Levels of IKK-Gamma and PKR  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn Version 3.0  
; SEQ ID NO 7157  
; LENGTH: 48  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid  
US-10-156-306-7157

Query Match 66.7%; Score 12; DB 15; Length 48;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCGAG 12  
|||||  
Db 1 GGGGUCUCGAG 12

RESULT 120  
US-10-322-138-6/c  
; Sequence 6, Application US/10322138  
; Publication No. US20030175765A1  
; GENERAL INFORMATION:  
; APPLICANT: Kessler, Christoph  
; APPLICANT: Haberkusen, Gerd  
; APPLICANT: Bartl, Knut  
; APPLICANT: Otum, Henrik  
; TITLE OF INVENTION: SPECIFIC AND SENSITIVE METHOD FOR DETECTING NUCLEIC ACIDS  
; FILE REFERENCE: 4817/OO  
; CURRENT APPLICATION NUMBER: US/10/322,138  
; CURRENT FILING DATE: 2002-12-17  
; PRIOR APPLICATION NUMBER: US/09/530,746B  
; PRIOR FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn Version 3.1  
; SEQ ID NO 6  
; LENGTH: 48  
; TYPE: DNA  
; ORGANISM: HCV  
US-10-322-138-6

Query Match 66.7%; Score 12; DB 16; Length 48;  
Best Local Similarity 83.3%; Pred. No. 1e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCGAG 12  
|||||  
Db 31 GGGGUCUCGAG 20

RESULT 121  
US-10-322-138-7/c  
; Sequence 7, Application US/10322138  
; Publication No. US20030175765A1  
; GENERAL INFORMATION:  
; APPLICANT: Kessler, Christoph  
; APPLICANT: Haberkusen, Gerd  
; APPLICANT: Bartl, Knut  
; APPLICANT: Otum, Henrik  
; TITLE OF INVENTION: SPECIFIC AND SENSITIVE METHOD FOR DETECTING NUCLEIC ACIDS

; FILE REFERENCE: 4817/OO  
; CURRENT APPLICATION NUMBER: US/10/322,138  
; CURRENT FILING DATE: 2002-12-17  
; PRIOR APPLICATION NUMBER: US/09/530,746B  
; PRIOR FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn Version 3.1  
; SEQ ID NO 7  
; LENGTH: 48  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-322-138-7

Query Match 66.7%; Score 12; DB 16; Length 48;  
Best Local Similarity 83.3%; Pred. No. 1e+03;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCGAG 12  
|||||  
Db 31 GGGGUCUCGAG 20

RESULT 122  
US-10-461-790-141/c  
; Sequence 141, Application US/10461790  
; Publication No. US20040029111A1  
; GENERAL INFORMATION:  
; APPLICANT: Linmen, Jeffery M.  
; APPLICANT: Kolk, Daniel P.  
; APPLICANT: Dockter, Janel M.  
; APPLICANT: German, Damon K.  
; APPLICANT: Yoshimura, Tadashi  
; APPLICANT: Ho-Sing-Loy, Marcy  
; APPLICANT: Stringfellow, Leslie A.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GP134-02 UT  
; CURRENT APPLICATION NUMBER: US/10/461,790  
; CURRENT FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: 60/389,393  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 141  
; LENGTH: 86  
; TYPE: DNA  
; ORGANISM: Hepatitis C Virus  
US-10-461-790-141

Query Match 66.7%; Score 12; DB 17; Length 86;  
Best Local Similarity 83.3%; Pred. No. 8.7e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUCGAG 12  
|||||  
Db 32 GGGGUCUCGAG 21

RESULT 123  
US-10-029-386-15052  
; Sequence 15052, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: ABEMTCA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1



SEQ ID NO 15052  
LENGTH: 97  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC024195.2  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.99  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1  
OTHER INFORMATION: EST\_HUMAN HIT: AL538246.1, EVALUATE 1.80e+00  
US-10-029-386-15052

Query Match 66.7%; Score 12; DB 16; Length 97;  
Best Local Similarity 83.3%; Pred. No. 8.4e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
DB 78 GGGGCTCTGGAG 89

RESULT 124  
US-10-029-386-14059/c  
Sequence 14059, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
FILE REFERENCE: AECOMICA-X-2  
CURRENT FILING DATE: 2001-12-20  
CURRENT APPLICATION NUMBER: US/10/029,386  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 14059  
LENGTH: 124  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AL136366.3  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6  
OTHER INFORMATION: NT HIT: g115303560, EVALUATE 1.60e+00  
OTHER INFORMATION: EST\_HUMAN HIT: W90458.1, EVALUATE 1.50e-01  
OTHER INFORMATION: SWISSPROT HIT: O15529, EVALUATE 2.30e-01  
US-10-029-386-14059

Query Match 66.7%; Score 12; DB 16; Length 124;  
Best Local Similarity 83.3%; Pred. No. 7.9e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
DB 34 GGGGCTCTGGAG 23

RESULT 125  
US-10-029-386-15594  
Sequence 15594, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
FILE REFERENCE: AECOMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 15594  
LENGTH: 138  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO CHR19.1  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.83  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.6  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.98  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.6  
OTHER INFORMATION: SWISSPROT HIT: Q92SR8, EVALUATE 5.20e-01  
OTHER INFORMATION: NT HIT: g14786907, EVALUATE 3.00e-67  
OTHER INFORMATION: EST\_HUMAN HIT: BG479422.1, EVALUATE 4.00e-67  
US-10-029-386-15594

Query Match 66.7%; Score 12; DB 16; Length 138;  
Best Local Similarity 83.3%; Pred. No. 7.7e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
DB 113 GGGGCTCTGGAG 124

RESULT 126  
US-10-425-115-1205  
Sequence 1205, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovacic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 369326  
SEQ ID NO 1205  
LENGTH: 168  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: M74577\_101098C.1  
OTHER INFORMATION: NT HIT: g115303560, EVALUATE 1.60e+00  
OTHER INFORMATION: EST\_HUMAN HIT: W90458.1, EVALUATE 1.50e-01  
OTHER INFORMATION: SWISSPROT HIT: O15529, EVALUATE 2.30e-01  
US-10-425-115-1205

Query Match 66.7%; Score 12; DB 18; Length 168;  
Best Local Similarity 83.3%; Pred. No. 7.3e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
DB 133 GGGGCTCTGGAG 144

RESULT 127  
US-10-424-599-11511  
Sequence 11511, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovacic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 115511  
LENGTH: 175  
TYPE: DNA  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_75317C.1  
US-10-424-599-115511

Query Match 66.7%; Score 12; DB 17; Length 175;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
|||:|:|:|:|  
Db 140 GGGGTCCTGGAG 151

RESULT 128  
US-09-294-121A-61/c  
Sequence 61, Application US/09294121A  
Patent No. US20020069422A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCY  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,121A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:  
CLONE: be82 (also referred to as be99)  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-294-121A-61

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
|||:|:|:|:|  
Db 26 GGGGTCCTGGAG 15

RESULT 129  
US-09-294-121A-67/c  
Sequence 67, Application US/09294121A  
Patent No. US20020069422A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCY  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,121A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb48  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-294-121A-67

Query Match 66.7%; Score 12; DB 9; Length 177;

Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCTCTGGAG 15

## RESULT 130

US-09-294-121A-68/c  
; Sequence 68, Application US/09294121A  
; Patent No. US20020069422A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/294,121A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 68:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: gp16  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; US-09-294-121A-68

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCTCTGGAG 15

RESULT 131  
US-09-294-121A-69/c

; Sequence 69, Application US/09294121A  
; Patent No. US20020069422A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/294,121A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 69:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: gp569  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; US-09-294-121A-69

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCTCTGGAG 15

RESULT 132  
US-09-294-121A-70/c  
; Sequence 70, Application US/09294121A  
; Patent No. US20020069422A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;

APPLICANT: ROSSAU, RUDI; VAN HEUVERSWM, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,121A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: gp358  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-294-121A-70  
Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
DB 26 GGGGTCCTGGAG 15  
RESULT 133  
US-09-294-121A-72/c  
Sequence 72, Application US/09294121A  
Patent No. US20020069422A1  
GENERAL INFORMATION:  
APPLICANT: MARTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWM, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE

CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,121A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: cam600  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-294-121A-72  
Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCUGAG 12  
DB 26 GGGGTCCTGGAG 15  
RESULT 134  
US-09-294-121A-73/c  
Sequence 73, Application US/09294121A  
Patent No. US20020069422A1  
GENERAL INFORMATION:  
APPLICANT: MARTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWM, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/294,121A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: cam736
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-09-294-121A-73

Query Match          66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGCUCCUGAG 12
        ||||:|||||
Db      26 GGGGTCTCTGGAG 15

RESULT 135
US-09-294-121A-74/c
Sequence 74, Application US/09294121A
Patent No. US20020069422A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/294,121A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
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APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: gb809
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-09-294-121A-74

Query Match          66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGCUCCUGAG 12
        ||||:|||||
Db      26 GGGGTCTCTGGAG 15

RESULT 136
US-09-294-121A-75/c
Sequence 75, Application US/09294121A
Patent No. US20020069422A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/294,121A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
```

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: 9B487  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-294-121A-75

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
||||:|||||  
DB 26 GGGGTCTCTGAG 15

RESULT 137  
US-09-294-121A-76/c  
Sequence 76, Application US/09294121A  
Patent No. US20020069422A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,121A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: 9B724  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-294-121A-76

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCCTGGAG 12  
||||:|||||  
DB 26 GGGGTCTCTGAG 15

RESULT 138  
US-09-294-121A-77/c  
Sequence 77, Application US/09294121A  
Patent No. US20020069422A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,121A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: be97  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-294-121A-77

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGGANG 12  
DB 26 GGGGTCTCGAG 15

RESULT 139  
US-09-294-121A-78/c  
Sequence 78, Application US/09294121A  
Patent No. US20020069422A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWM, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,121A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be95  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region

US-09-294-121A-78

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGGANG 12  
DB 26 GGGGTCTCGAG 15

RESULT 140  
US-09-294-121A-79/c  
Sequence 79, Application US/09294121A  
Patent No. US20020069422A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWM, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,121A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be96  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-294-121A-79

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGGANG 12

Db 26 GGGGTCTCTGGAG 15

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|||||:|||||
RESULT 141
US-09-294-121A-80/c
; Sequence 80, Application US/09294121A
; Patent No. US20020069422A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/294,121A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: be98
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
; US-09-294-121A-80
Query Match 66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
|||||:|||||
Db 26 GGGGTCTCTGGAG 15
RESULT 142
US-09-899-082A-61/c
; Sequence 61, Application US/09899082A
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; Patent No. US20020106638A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,082A
; FILING DATE: 06-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-AUG-1993
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: be82 (also referred to as be99)
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
; SEQUENCE DESCRIPTION: SEQ ID NO: 61:
; US-09-899-082A-61
Query Match 66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGUCCTGGAG 12
|||||:|||||
Db 26 GGGGTCTCTGGAG 15
RESULT 143
US-09-899-082A-67/c
; Sequence 67, Application US/09899082A
; Patent No. US20020106638A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
```



NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb48  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-899-082A-67

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. NO. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
|||:|||||  
Db 26 GGGGTCTGGAG 15

RESULT 144  
US-09-899-082A-68/c  
Sequence 68, Application US/09899082A  
Patent No. US20020106638A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK

COUNTRY: USA  
ZIP: 10016

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb116  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 68:  
US-09-899-082A-68

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. NO. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
|||:|||||  
Db 26 GGGGTCTGGAG 15

RESULT 145  
US-09-899-082A-69/c  
Sequence 69, Application US/09899082A  
Patent No. US20020106638A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-JUL-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gB569  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-899-082A-69

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 26 GGGGCTCTGGAG 15

RESULT 146  
US-09-899-082A-70/c  
Sequence 70, Application US/09899082A  
Patent No. US20020106638A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEIVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-JUL-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gB358  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 70:  
US-09-899-082A-70

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
Db 26 GGGGCTCTGGAG 15

RESULT 147  
US-09-899-082A-72/c  
Sequence 72, Application US/09899082A  
Patent No. US20020106638A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEIVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-JUL-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993

APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: cam600  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 72:  
US-09-899-082A-72

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
|||:|:|:|  
Db 26 GGGGTCTGGAG 15

RESULT 148  
US-09-899-082A-73/c  
Sequence 73, Application US/09899082A  
Patent No. US2002010638A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: cam736  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 73:  
US-09-899-082A-73

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGAG 12  
|||:|:|:|  
Db 26 GGGGTCTGGAG 15

RESULT 149  
US-09-899-082A-74/c  
Sequence 74, Application US/09899082A  
Patent No. US2002010638A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 74:

```

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: gb809
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
; SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-09-899-082A-74

Query Match      66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCGCGAG 12
Db      26 GGGGTCCTGGAG 15

RESULT 150
US-09-899-082A-75/c
; Sequence 75, Application US/09899082A
; Patent No. US20020106638A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,082A
; FILING DATE: 06-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-Jul-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-Nov-1993
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-Aug-1993
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-Nov-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410,004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
; SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-09-899-082A-76
```

```

;
; IMMEDIATE SOURCE:
; CLONE: gb487
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
; SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-09-899-082A-75

Query Match      66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCGCGAG 12
Db      26 GGGGTCCTGGAG 15

RESULT 151
US-09-899-082A-76/c
; Sequence 76, Application US/09899082A
; Patent No. US20020106638A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,082A
; FILING DATE: 06-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/378,900
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-Jul-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-Nov-1993
; APPLICATION NUMBER: EP/93/402,129.6
; FILING DATE: 31-Aug-1993
; APPLICATION NUMBER: EP/92/403,222.0
; FILING DATE: 27-Nov-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410,004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; POSITION IN GENOME:
; MAP POSITION: 5' untranslated region
; SEQUENCE DESCRIPTION: SEQ ID NO: 76:
US-09-899-082A-76
```

Query Match 66.7% Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
||||:|||||  
Db 26 GGGGTCTGAG 15

## RESULT 152

US-09-899-082A-77/c  
; Sequence 77, Application US/09899082A  
; Patent No. US20020106638A1

## GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWM, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES

NUMBER OF SEQUENCES: 97

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA

ZIP: 10016

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/378,900

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/256,568

FILING DATE: 18-JUL-1994

APPLICATION NUMBER: PCT/EP93/03325

FILING DATE: 26-NOV-1993

APPLICATION NUMBER: EP/93/402,129.6

FILING DATE: 31-AUG-1993

APPLICATION NUMBER: EP/92/403,222.0

FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 77:

SEQUENCE CHARACTERISTICS:

LENGTH: 177 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

LIBRARY: Be97

POSITION IN GENOME:

MAP POSITION: 5' untranslated region

SEQUENCE DESCRIPTION: SEQ ID NO: 77:

US-09-899-082A-77

Query Match 66.7% Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12

Db 26 GGGGTCTGAG 15  
||||:|||||

## RESULT 153

US-09-899-082A-78/c  
; Sequence 78, Application US/09899082A  
; Patent No. US20020106638A1

## GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWM, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES

NUMBER OF SEQUENCES: 97

## CORRESPONDENCE ADDRESSES:

ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA

ZIP: 10016

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/378,900

FILING DATE: <Unknown>

APPLICATION NUMBER: 08/256,568

FILING DATE: 18-JUL-1994

APPLICATION NUMBER: PCT/EP93/03325

FILING DATE: 26-NOV-1993

APPLICATION NUMBER: EP/93/402,129.6

FILING DATE: 31-AUG-1993

APPLICATION NUMBER: EP/92/403,222.0

FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 78:

SEQUENCE CHARACTERISTICS:

LENGTH: 177 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

CLONE: be95

POSITION IN GENOME:

MAP POSITION: 5' untranslated region

SEQUENCE DESCRIPTION: SEQ ID NO: 78:

US-09-899-082A-78

Query Match 66.7% Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCGAG 12  
||||:|||||  
Db 26 GGGGTCTGAG 15

RESULT 154  
US-09-899-082A-79/c

```
Sequence 79, Application US/09899082A
Patent No. US20020106638A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,082A
FILING DATE: 06-JUL-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/378,900
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: be96
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-899-082A-79

Query Match      66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGGUCUUGAG 12
DB      26 GGGGTCCTGAG 15
```

```
RESULT 155
US-09-899-082A-80/c
Sequence 80, Application US/09899082A
Patent No. US20020106638A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
```

```
ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,082A
FILING DATE: 06-JUL-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/378,900
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: be98
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-899-082A-80

Query Match      66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGGUCUUGAG 12
DB      26 GGGGTCCTGAG 15
```

```
RESULT 156
US-09-899-302-61/c
Sequence 61, Application US/09899302
Patent No. US2002016626A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
```

```
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,302
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/378,900
FILING DATE:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8002
FAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: ba82 (also referred to as ba99)
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-09-899-302-61

Query Match      66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
Db      26 GGGGCTCCTGGAG 15

RESULT 157
US-09-899-302-67/c
Sequence 67, Application US/09899302
Patent No. US20020168626A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWM, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
```

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,302
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/378,900
FILING DATE:
APPLICATION NUMBER: 08/256,568
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8002
FAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: gb48
POSITION IN GENOME:
MAP POSITION: 5' untranslated region
US-09-899-302-67

Query Match      66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCTGGAG 12
Db      26 GGGGCTCCTGGAG 15

RESULT 158
US-09-899-302-68/c
Sequence 68, Application US/09899302
Patent No. US20020168626A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWM, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,302
```

```

      FILING DATE:
      CLASSIFICATION:
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 09/378,900
      FILING DATE:
      APPLICATION NUMBER: 08/256,568
      FILING DATE: 18-JUL-1994
      APPLICATION NUMBER: PCT/EP93/03325
      FILING DATE: 26-NOV-1993
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: EP/93/402,129.6
      FILING DATE: 31-AUG-1993
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: EP/92/403,222.0
      FILING DATE: 27-NOV-1992
      ATTORNEY/AGENT INFORMATION:
      NAME: CHARLES A. MUSERLIAN
      REGISTRATION NUMBER: 19,683
      REFERENCE/DOCKET NUMBER: 410.004
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (212) 661-8000
      TELEFAX: (212) 661-8002
      INFORMATION FOR SEQ ID NO: 68:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 177 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      IMMEDIATE SOURCE:
      CLONE: gbl16
      POSITION IN GENOME:
      MAP POSITION: 5' untranslated region
US-09-899-302-68

Query Match      66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGUCUCUGAG 12
Db      26 GGGGTCTCTGAG 15

RESULT 159
US-09-899-302-69/c
; Sequence 69, Application US/09899302
; Patent No. US20020168626A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,302
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/378,900
; FILING DATE:
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:

```

```

      APPLICATION NUMBER: 08/256,568
      FILING DATE: 18-JUL-1994
      APPLICATION NUMBER: PCT/EP93/03325
      FILING DATE: 26-NOV-1993
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: EP/93/402,129.6
      FILING DATE: 31-AUG-1993
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: EP/92/403,222.0
      FILING DATE: 27-NOV-1992
      ATTORNEY/AGENT INFORMATION:
      NAME: CHARLES A. MUSERLIAN
      REGISTRATION NUMBER: 19,683
      REFERENCE/DOCKET NUMBER: 410.004
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (212) 661-8000
      TELEFAX: (212) 661-8002
      INFORMATION FOR SEQ ID NO: 69:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 177 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      IMMEDIATE SOURCE:
      CLONE: gbs69
      POSITION IN GENOME:
      MAP POSITION: 5' untranslated region
US-09-899-302-69

```

```

Query Match      66.7%; Score 12; DB 9; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 GGGGUCUCUGAG 12
Db      26 GGGGTCTCTGAG 15

```

```

RESULT 160
US-09-899-302-70/c
; Sequence 70, Application US/09899302
; Patent No. US20020168626A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,302
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/378,900
; FILING DATE:
; APPLICATION NUMBER: 08/256,568
; FILING DATE: 18-JUL-1994
; APPLICATION NUMBER: PCT/EP93/03325
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:

```



APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:  
CLONE: gb358  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-899-302-70

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
|||:|:|:|  
Db 26 GGGGTCTCGAG 15

RESULT 161  
US-09-899-302-72/c  
Sequence 72, Application US/09899302  
Patent No. US20020168626A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,302  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:  
CLONE: cam600  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-899-302-72

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12  
|||:|:|:|  
Db 26 GGGGTCTCGAG 15

RESULT 162  
US-09-899-302-73/c  
Sequence 73, Application US/09899302  
Patent No. US20020168626A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,302  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: cam36  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-899-302-73

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
|||:|||||  
Db 26 GGGCTCCTGAG 15

RESULT 163  
US-09-899-302-74/c  
Sequence 74, Application US/09899302  
Patent No. US20020168626A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,302  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb809  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-899-302-74

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
|||:|||||  
Db 26 GGGCTCCTGAG 15

RESULT 164  
US-09-899-302-75/c  
Sequence 75, Application US/09899302  
Patent No. US20020168626A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,302  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:

CLONE: gb487  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-899-302-75

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
||||:||||  
Db 26 GGGGCTCTGGAG 15

RESULT 165  
US-09-899-302-76/c  
Sequence 76, Application US/09899302  
Patent No. US2002016826A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT, STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899.302  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378.900  
FILING DATE:  
APPLICATION NUMBER: 08/256.568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402.129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403.222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19.683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb724  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-899-302-76

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGUCGAG 12  
||||:||||  
Db 26 GGGGCTCTGGAG 15

RESULT 166  
US-09-899-302-77/c  
Sequence 77, Application US/09899302  
Patent No. US2002016826A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT, STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899.302  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378.900  
FILING DATE:  
APPLICATION NUMBER: 08/256.568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402.129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403.222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19.683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: be97  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-899-302-77

OY 1 GGGGUCGAG 12

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 26 GGGGTCTCGAG 15

RESULT 167  
US-09-899-302-78/c  
; Sequence 78, Application US/09899302  
; Patent No. US20020168626A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; TITLE OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899,302  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/378,900  
; FILING DATE:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 78:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; IMMEDIATE SOURCE:  
; CLONE: be95  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
US-09-899-302-78

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGGAG 12  
||||:|||||  
Db 26 GGGGTCTCGAG 15

RESULT 168

US-09-899-302-79/c  
; Sequence 79, Application US/09899302  
; Patent No. US20020168626A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; TITLE OF INVENTION: ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899,302  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/378,900  
; FILING DATE:  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-JUL-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 79:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; IMMEDIATE SOURCE:  
; CLONE: be96  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
US-09-899-302-79

Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUGGAG 12  
||||:|||||  
Db 26 GGGGTCTCGAG 15

RESULT 169  
US-09-899-302-80/c  
; Sequence 80, Application US/09899302  
; Patent No. US20020168626A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;

APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESS: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,302  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: be98  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-899-302-80  
Query Match 66.7%; Score 12; DB 9; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCTCTGGAG 15  
RESULT 170  
US-09-899-044-61/c  
Sequence 61, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: be82 (also referred to as be99)  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 61:  
US-09-899-044-61  
Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCTCTGGAG 15  
RESULT 171  
US-09-899-044-67/c  
Sequence 67, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/899,044
  FILING DATE: 06-Jul-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 09/378,900
  FILING DATE: <Unknown>
  APPLICATION NUMBER: PCT/EP93/03325
  FILING DATE: 26-NOV-1993
  APPLICATION NUMBER: EP/93/402,129.6
  FILING DATE: 31-AUG-1993
  APPLICATION NUMBER: EP/92/403,222.0
  FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
  NAME: CHARLES A. MUSERLIAN
  REGISTRATION NUMBER: 19,683
  REFERENCE/DOCKET NUMBER: 410,004
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 661-8000
  TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 67:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 177 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
  CLONE: 9b48
POSITION IN GENOME:
  MAP POSITION: 5' untranslated region
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-899-044-67

Query Match      66.7%; Score 12; DB 10; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCUGGAG 12
        |||:|:|:|
Db      26 GGGGTCCTGGAG 15

RESULT 172
US-09-899-044-68/c
  Sequence 68, Application US/09899044
  Publication No. US20030036053A1
  GENERAL INFORMATION:
    APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
    ROSSAU, RUDI; VAN HEUVERSWEYN, HUGO
    TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
    ISOLATES
    NUMBER OF SEQUENCES: 97
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: BIERMAN & MUSERLIAN
      STREET: 600 THIRD AVENUE
      CITY: NEW YORK
      STATE: NEW YORK
      COUNTRY: USA
      ZIP: 10016
  COMPUTER READABLE FORM:
    MEDIUM TYPE: floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: ASCII
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/899,044
    FILING DATE: 06-Jul-2001
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 09/378,900
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
  NAME: CHARLES A. MUSERLIAN
  REGISTRATION NUMBER: 19,683
  REFERENCE/DOCKET NUMBER: 410,004
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 661-8000
  TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 68:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 177 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
  CLONE: 9b16
POSITION IN GENOME:
  MAP POSITION: 5' untranslated region
SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-899-044-68

Query Match      66.7%; Score 12; DB 10; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCCUGGAG 12
        |||:|:|:|
Db      26 GGGGTCCTGGAG 15

RESULT 173
US-09-899-044-69/c
  Sequence 69, Application US/09899044
  Publication No. US20030036053A1
  GENERAL INFORMATION:
    APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
    ROSSAU, RUDI; VAN HEUVERSWEYN, HUGO
    TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
    ISOLATES
    NUMBER OF SEQUENCES: 97
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: BIERMAN & MUSERLIAN
      STREET: 600 THIRD AVENUE
      CITY: NEW YORK
      STATE: NEW YORK
      COUNTRY: USA
      ZIP: 10016
  COMPUTER READABLE FORM:
    MEDIUM TYPE: floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: ASCII
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/899,044
    FILING DATE: 06-Jul-2001
    CLASSIFICATION: <Unknown>
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 09/378,900
    FILING DATE: <Unknown>
    APPLICATION NUMBER: PCT/EP93/03325
    FILING DATE: 26-NOV-1993
    APPLICATION NUMBER: EP/93/402,129.6
    FILING DATE: 31-AUG-1993
    APPLICATION NUMBER: EP/92/403,222.0
    FILING DATE: 27-NOV-1992
```

ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: gb569  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 69:  
US-09-899-044-69

Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGCCUGGAG 12  
|||:|:|:|  
Db 26 GGGGTCTGGAG 15

RESULT 174  
US-09-899-044-70/c  
Sequence 70, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: gb358  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 70:  
US-09-899-044-70

Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGCCUGGAG 12  
|||:|:|:|  
Db 26 GGGGTCTGGAG 15

RESULT 175  
US-09-899-044-72/c  
Sequence 72, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: cam600

POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 72:  
US-09-899-044-72

Query Match 66.7% Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 26 GGGGTCTCTGAG 15

RESULT 176  
US-09-899-044-73/C  
Sequence 73, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900

FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8002  
TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:  
CLONE: cam736  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 73:  
US-09-899-044-73

Query Match 66.7% Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 26 GGGGTCTCTGAG 15

RESULT 177  
US-09-899-044-74/C  
Sequence 74, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992

ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
IMMEDIATE SOURCE:  
CLONE: gb809  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 74:  
US-09-899-044-74

Query Match 66.7% Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
|||:|||||  
Db 26 GGGGTCTCTGAG 15

RESULT 178  
US-09-899-044-75/C



Sequence 75, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWMY, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb487  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 75:  
US-09-899-044-75  
Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
|||:|||||  
Db 26 GGGGTCTCGAG 15  
RESULT 179  
US-09-899-044-76/c  
Sequence 76, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWMY, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:

CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410,004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb724  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 76:  
US-09-899-044-76  
Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
|||:|||||  
Db 26 GGGGTCTCGAG 15  
RESULT 180  
US-09-899-044-77/c  
Sequence 77, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWMY, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: be97  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 77:  
US-09-899-044-77

Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:||||  
Db 26 GGGGTCTCTGAG 15

RESULT 181  
US-09-899-044-78/c  
Sequence 78, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVESWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be95  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 78:  
US-09-899-044-78

Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCUGAG 12  
||||:||||  
Db 26 GGGGTCTCTGAG 15

RESULT 182  
US-09-899-044-79/c  
Sequence 79, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVESWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0

FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: be96  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 79:  
US-09-899-044-79

Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCCTGGAG 12  
|||:|:|:|  
Db 26 GGGGTCTGTGAG 15

RESULT 183  
US-09-899-044-80/C  
Sequence 80, Application US/09899044  
Publication No. US20030036053A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWM, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,044  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: be98  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 80:  
US-09-899-044-80

Query Match 66.7%; Score 12; DB 10; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGUCCTGGAG 12  
|||:|:|:|  
Db 26 GGGGTCTGTGAG 15

RESULT 184  
US-10-822-711-61/C  
Sequence 61, Application US/10822711  
Publication No. US20040191768A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWM, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/822,711  
FILING DATE: 13-Apr-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be82 (also referred to as be99)  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 61  
US-10-822-711-61

Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
DB 26 GGGGTCCTGGAG 15

RESULT 185  
US-10-822-711-67/c  
Sequence 67, Application US/10822711  
Publication No. US20040191768A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/822,711  
FILING DATE: 13-Apr-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-Jul-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-Nov-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-Aug-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-Nov-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8000  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:

CLONE: gb48  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 67  
US-10-822-711-67

Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTGGAG 12  
DB 26 GGGGTCCTGGAG 15

RESULT 186  
US-10-822-711-68/c  
Sequence 68, Application US/10822711  
Publication No. US20040191768A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/922,711  
FILING DATE: 13-Apr-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-Jul-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-Nov-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-Aug-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-Nov-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8000  
INFORMATION FOR SEQ ID NO: 68:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb116  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 68;

US-10-822-711-68

Query Match 66.7%; Score 12; DB 18; Length 177;

Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12

Db 26 GGGGCTCTGAG 15

## RESULT 187

US-10-822-711-69/c

; Sequence 69, Application US/10822711

; Publication No. US20040191768A1

; GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;

ROSSAU, RUDI; VAN HEUVERSWYN, HUGO

TITLE OF INVENTION: PROCESS FOR TYPING OF HCV

ISOLATES

NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN &amp; MUSERLIAN

STREET: 600 THIRD AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/822,711

FILING DATE: 13-Apr-2004

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/899,082A

FILING DATE: 06-Jul-2001

APPLICATION NUMBER: US/09/378,900

FILING DATE: &lt;Unknown&gt;

APPLICATION NUMBER: 08/256,568

FILING DATE: 18-Jul-1994

APPLICATION NUMBER: PCT/EP93/03325

FILING DATE: 26-Nov-1993

APPLICATION NUMBER: EP/93/402,129,6

FILING DATE: 31-Aug-1993

APPLICATION NUMBER: EP/92/403,222,0

FILING DATE: 27-Nov-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 177 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

CLONE: gb569

POSITION IN GENOME:

MAP POSITION: 5' untranslated region

SEQUENCE DESCRIPTION: SEQ ID NO: 69;

US-10-822-711-69

Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCGAG 12

Db 26 GGGGCTCTGAG 15

## RESULT 188

US-10-822-711-70/c

; Sequence 70, Application US/10822711

; Publication No. US20040191768A1

; GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;

ROSSAU, RUDI; VAN HEUVERSWYN, HUGO

TITLE OF INVENTION: PROCESS FOR TYPING OF HCV

ISOLATES

NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN &amp; MUSERLIAN

STREET: 600 THIRD AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/822,711

FILING DATE: 13-Apr-2004

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/899,082A

FILING DATE: 06-Jul-2001

APPLICATION NUMBER: US/09/378,900

FILING DATE: &lt;Unknown&gt;

APPLICATION NUMBER: 08/256,568

FILING DATE: 18-Jul-1994

APPLICATION NUMBER: PCT/EP93/03325

FILING DATE: 26-Nov-1993

APPLICATION NUMBER: EP/93/402,129,6

FILING DATE: 31-Aug-1993

APPLICATION NUMBER: EP/92/403,222,0

FILING DATE: 27-Nov-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 177 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

CLONE: gb358

POSITION IN GENOME:

MAP POSITION: 5' untranslated region

SEQUENCE DESCRIPTION: SEQ ID NO: 70;

US-10-822-711-70

Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 26 GGGGTCCTCGAG 15

## RESULT 189

US-10-822-711-72/c  
; Sequence 72, Application US/10822711  
; Publication No. US20040191768A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/822,711  
; FILING DATE: 13-Apr-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899,082A  
; FILING DATE: 06-Jul-2001  
; APPLICATION NUMBER: US/09/378,900  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-Jul-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-Nov-1993  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-Aug-1993  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-Nov-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 72:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: cam600  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; SEQUENCE DESCRIPTION: SEQ ID NO: 72:  
US-10-822-711-72

Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12

Db 26 GGGGTCCTCGAG 15

RESULT 190

US-10-822-711-73/c  
; Sequence 73, Application US/10822711  
; Publication No. US20040191768A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/822,711  
; FILING DATE: 13-Apr-2004  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/899,082A  
; FILING DATE: 06-Jul-2001  
; APPLICATION NUMBER: US/09/378,900  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/256,568  
; FILING DATE: 18-Jul-1994  
; APPLICATION NUMBER: PCT/EP93/03325  
; FILING DATE: 26-Nov-1993  
; APPLICATION NUMBER: EP/93/402,129.6  
; FILING DATE: 31-Aug-1993  
; APPLICATION NUMBER: EP/92/403,222.0  
; FILING DATE: 27-Nov-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CHARLES A. MUSERLIAN  
; REGISTRATION NUMBER: 19,683  
; REFERENCE/DOCKET NUMBER: 410.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 661-8000  
; TELEFAX: (212) 661-8002  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 177 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; IMMEDIATE SOURCE:  
; CLONE: cam736  
; POSITION IN GENOME:  
; MAP POSITION: 5' untranslated region  
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:  
US-10-822-711-73

Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;

Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCCTCGAG 12

Db 26 GGGGTCCTCGAG 15

RESULT 191

US-10-822-711-74/c  
; Sequence 74, Application US/10822711  
; Publication No. US20040191768A1  
; GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/822,711  
FILING DATE: 13-Apr-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 74:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb809  
POSITION IN GENOME:  
MAP POSITION: 5', untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 74:  
US-10-822-711-74  
Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCTCTGGAG 15  
RESULT 192  
US-10-822-711-75/c  
Sequence 75, Application US/10822711  
Publication No. US20040191768A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES

NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/822,711  
FILING DATE: 13-Apr-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb487  
POSITION IN GENOME:  
MAP POSITION: 5', untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 75:  
US-10-822-711-75  
Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCCTGGAG 12  
Db 26 GGGGTCTCTGGAG 15  
RESULT 193  
US-10-822-711-76/c  
Sequence 76, Application US/10822711  
Publication No. US20040191768A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE

CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/822,711  
FILING DATE: 13-Apr-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-Jul-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-Nov-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-Aug-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-Nov-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: gb124  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 76:  
US-10-822-711-76  
Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
Db 26 GGGGCTCTGGAG 15  
RESULT 194  
US-10-822-711-77/c  
; Sequence 77, Application US/10822711  
; Publication No. US20040191768A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; ROSSAU, RUDI; VAN HEUVERSWM, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/822,711  
FILING DATE: 13-Apr-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-Jul-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-Nov-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-Aug-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-Nov-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 77:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
LIBRARY: be97  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 77:  
US-10-822-711-77  
Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGUCGAG 12  
Db 26 GGGGCTCTGGAG 15  
RESULT 195  
US-10-822-711-78/c  
; Sequence 78, Application US/10822711  
; Publication No. US20040191768A1  
; GENERAL INFORMATION:  
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
; ROSSAU, RUDI; VAN HEUVERSWM, HUGO  
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
; ISOLATES  
; NUMBER OF SEQUENCES: 97  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIERMAN & MUSERLIAN  
; STREET: 600 THIRD AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS



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SOFTWARE: ASCII
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/822,711
  FILING DATE: 13-Apr-2004
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/899,082A
  FILING DATE: 06-Jul-2001
  APPLICATION NUMBER: US/09/378,900
  FILING DATE: <Unknown>
  APPLICATION NUMBER: 08/256,568
  FILING DATE: 18-Jul-1994
  APPLICATION NUMBER: PCT/EP93/03325
  FILING DATE: 26-Nov-1993
  APPLICATION NUMBER: EP/93/402,129.6
  FILING DATE: 31-Aug-1993
  APPLICATION NUMBER: EP/92/403,222.0
  FILING DATE: 27-Nov-1992
ATTORNEY/AGENT INFORMATION:
  NAME: CHARLES A. MUSERLIAN
  REGISTRATION NUMBER: 19,683
  REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 661-8000
  TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 78:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 177 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
  CLONE: be95
POSITION IN GENOME:
  MAP POSITION: 5' untranslated region
  SEQUENCE DESCRIPTION: SEQ ID NO: 78:
US-10-822-711-78

Query Match      66.7%; Score 12; DB 18; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCGCGANG 12
        |||:|:|:|
Db      26 GGGGTCTCTGAG 15

RESULT 196
US-10-822-711-79/c
; Sequence 79, Application US/10822711
; Publication No. US20040191768A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/822,711
; FILING DATE: 13-Apr-2004
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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/899,082A
  FILING DATE: 06-Jul-2001
  APPLICATION NUMBER: US/09/378,900
  FILING DATE: <Unknown>
  APPLICATION NUMBER: 08/256,568
  FILING DATE: 18-Jul-1994
  APPLICATION NUMBER: PCT/EP93/03325
  FILING DATE: 26-Nov-1993
  APPLICATION NUMBER: EP/93/402,129.6
  FILING DATE: 31-Aug-1993
  APPLICATION NUMBER: EP/92/403,222.0
  FILING DATE: 27-Nov-1992
ATTORNEY/AGENT INFORMATION:
  NAME: CHARLES A. MUSERLIAN
  REGISTRATION NUMBER: 19,683
  REFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (212) 661-8000
  TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 79:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 177 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
  CLONE: be96
POSITION IN GENOME:
  MAP POSITION: 5' untranslated region
  SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-10-822-711-79

Query Match      66.7%; Score 12; DB 18; Length 177;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGUCGCGANG 12
        |||:|:|:|
Db      26 GGGGTCTCTGAG 15

RESULT 197
US-10-822-711-80/c
; Sequence 80, Application US/10822711
; Publication No. US20040191768A1
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
; ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
; TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; ISOLATES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/822,711
; FILING DATE: 13-Apr-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,082A
; FILING DATE: 06-Jul-2001
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APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 177 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: be98  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-10-822-711-80

Query Match 66.7%; Score 12; DB 18; Length 177;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
||||:||||  
Db 26 GGGGTCTCGAG 15

RESULT 198  
US-09-294-121A-59/c  
Sequence 59, Application US/09294121A  
Patent No. US20020069422A1  
GENERAL INFORMATION:  
APPLICANT: MARTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,121A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6

FILING DATE: 31-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: bu74  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-294-121A-59

Query Match 66.7%; Score 12; DB 9; Length 178;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGUCUUGAG 12  
||||:||||  
Db 26 GGGGTCTCGAG 15

RESULT 199  
US-09-294-121A-71/c  
Sequence 71, Application US/09294121A  
Patent No. US20020069422A1  
GENERAL INFORMATION:  
APPLICANT: MARTENS, GEERT; STUYVER, LIEVEN;  
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
TITLE OF INVENTION: ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/294,121A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-JUL-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-AUG-1993  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: gbs49  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
US-09-294-121A-71

Query Match 66.7%; Score 12; DB 9; Length 178;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
|||:||||  
Db 26 GGGGTCTCTGGAG 15

RESULT 200  
US-09-899-082A-59/c  
Sequence 59, Application US/09899082A  
Patent No. US20020106638A1  
GENERAL INFORMATION:  
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;  
ROSSAU, RUDI; VAN HEUVERSWYN, HUGO  
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV  
ISOLATES  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIERMAN & MUSERLIAN  
STREET: 600 THIRD AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10016

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/899,082A  
FILING DATE: 06-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/378,900  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/256,568  
FILING DATE: 18-Jul-1994  
APPLICATION NUMBER: PCT/EP93/03325  
FILING DATE: 26-Nov-1993  
APPLICATION NUMBER: EP/93/402,129.6  
FILING DATE: 31-Aug-1993  
APPLICATION NUMBER: EP/92/403,222.0  
FILING DATE: 27-Nov-1992

ATTORNEY/AGENT INFORMATION:  
NAME: CHARLES A. MUSERLIAN  
REGISTRATION NUMBER: 19,683  
REFERENCE/DOCKET NUMBER: 410.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 661-8000  
TELEFAX: (212) 661-8002  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
IMMEDIATE SOURCE:  
CLONE: bu74  
POSITION IN GENOME:  
MAP POSITION: 5' untranslated region  
SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
US-09-899-082A-59

Query Match 66.7%; Score 12; DB 9; Length 178;  
Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCTGGAG 12  
|||:||||  
Db 26 GGGGTCTCTGGAG 15

Search completed: April 25, 2005, 16:27:33  
Job time: 264.474 secs

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